

GenCore version 5.1.6
 OM protein - protein search, using sw model
 Run on: December 22, 2005, 02:28:47 ; Search time 51.4286 Seconds
 (without alignments)
 153.783 Million cell updates/sec

Title: US-10-063-553-48_COPY_32_49
 Perfect score: 93
 Sequence: 1 VSLVEDQFSQNPISCFE 18
 Scoring table: BLOSUM62
 Gapop 10.0 , Capext 0.5
 Searched: 2443163 seqs, 439378781 residues
 Total number of hits satisfying chosen parameters: 2443163
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1500 summaries

Database : A_Geneseq_21.*
 1: Geneseqp1980s.*
 2: Geneseqp1990s.*
 3: Geneseqp2000s.*
 4: Geneseqp2001s.*
 5: Geneseqp2002s.*
 6: Geneseqp2003as.*
 7: Geneseqp2003bs.*
 8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Match Length	DB	ID	Description
RESULT 1					SUMMARIES
ID	AA66703	standard; protein; 229 AA.			
DE	Membrane-bound protein PRO994.				
PN	W09963088-A2.				
PD	09-DEC-1999.				
PA	(GETH) GENENTECH INC.				
Query Match	100.0%;	Score 93;	DB 3;	Length 229;	
Best Local Similarity	100.0%;	Pred. No. 2.1e-07;			
RESULT 2					
ID	AAU29122	standard; protein; 229 AA.			
DE	Human PRO polypeptide sequence #99.				
PN	W0200168848-A2.				
PD	20-SEP-2001.				
PA	(GETH) GENENTECH INC.				
Query Match	100.0%;	Score 93;	DB 4;	Length 229;	
Best Local Similarity	100.0%;	Pred. No. 2.1e-07;			
RESULT 3					
ID	AA87549	standard; protein; 229 AA.			
DE	Human PRO994.				
PN	W0200116318-A2.				
PD	08-MAR-2001.				
PA	(GETH) GENENTECH INC.				
Query Match	100.0%;	Score 93;	DB 4;	Length 229;	
Best Local Similarity	100.0%;	Pred. No. 2.1e-07;			
RESULT 4					
ID	AA65226	standard; protein; 229 AA.			
DE	Human PRO994 (UNQ518) protein sequence SEQ ID NO:258.				
PN	W0200073454-A1.				
PD	07-DEC-2000.				
PA	(GETH) GENENTECH INC.				
Query Match	100.0%;	Score 93;	DB 4;	Length 229;	
Best Local Similarity	100.0%;	Pred. No. 2.1e-07;			
RESULT 5					
ID	AG95874	standard; protein; 229 AA.			
DE	Human secreted/transmembrane protein PRO994.				
PN	US2002119130-A1.				
PD	29-AUG-2002.				
PA	(GETH) GENENTECH INC.				
Query Match	100.0%;	Score 93;	DB 5;	Length 229;	
Best Local Similarity	100.0%;	Pred. No. 2.1e-07;			
RESULT 6					
ID	ABU58498	standard; protein; 229 AA.			

DE Human PRO polypeptide #99.
 PN US2003027272-A1.
 PD 06-FEB-2003.
 Query Match 100.0%; Score 93; DB 6; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 RESULT 7
 ID ABU88046 standard; protein; 229 AA.
 DE Novel human secreted and transmembrane protein PRO994.
 PN US2003032127-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 93; DB 6; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 RESULT 8
 ID ABU84361 standard; protein; 229 AA.
 DE Human secreted/transmembrane protein (PRO) #99.
 PN US2003032112-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 93; DB 6; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 RESULT 9
 ID ABR66235 standard; protein; 229 AA.
 DE Human secreted polypeptide PRO994, SEQ ID NO:198.
 PN US2003027278-A1.
 PD 06-FEB-2003.
 Query Match 100.0%; Score 93; DB 6; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 RESULT 10
 ID ABR65625 standard; protein; 229 AA.
 DE Human secreted polypeptide PRO994, SEQ ID NO:198.
 PN US2003036159-A1.
 PD 20-FEB-2003.
 Query Match 100.0%; Score 93; DB 6; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 RESULT 11
 ID ABU99565 standard; protein; 229 AA.
 DE Human secreted/transmembrane protein (PRO) #99.
 PN US2003040070-A1.
 PD 27-FEB-2003.
 Query Match 100.0%; Score 93; DB 6; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 RESULT 12
 ID ABU58041 standard; protein; 229 AA.
 DE Human PRO polypeptide #73.
 PN US2003027163-A1.
 PD 06-FEB-2003.
 Query Match 100.0%; Score 93; DB 6; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 RESULT 13
 ID ABU59119 standard; protein; 229 AA.
 DE Novel human secreted or transmembrane protein PRO994.
 PN US2002132252-A1.
 PD 19-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 93; DB 6; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 RESULT 14
 ID ABU82631 standard; protein; 229 AA.
 DE Human secreted/transmembrane protein PRO994.
 PN US2003032023-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 93; DB 6; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 RESULT 15
 ID ABU82804 standard; protein; 229 AA.
 DE Human PRO polypeptide #99.
 PN US2003032113-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 93; DB 6; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 RESULT 16
 ID ABU89925 standard; protein; 229 AA.
 DE Novel human secreted and transmembrane protein PRO994.
 PN US2003036147-A1.

PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 17
ID ABR69174 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 18
ID ABU60550 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, #103.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 19
ID ABU96227 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 20
ID ASU92658 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 21
ID ABO08735 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 22
ID ABO02787 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 23
ID ABR74941 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 24
ID ABR94703 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 25
ID ABU13932 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 26
ID ABU85676 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036140-A1.
PD 20-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 27
ID ABU98836 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 28
ID ABU98051 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 29
ID ABU91757 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 30
ID ABU89450 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 31
ID ABU86291 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 32
ID ABU67504 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 33
ID ABU80532 standard; protein; 229 AA.
DE Human PRO protein #99.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 34
ID ABU72517 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 35
ID ABU90899 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 36
ID ABO33958 standard; protein; 229 AA.

DE Human secreted/transmembrane protein PRO994.
PN US200309013-A1.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Pred. No. 2.1e-07;
RESULT 37
ID ABR99450 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Pred. No. 2.1e-07;
RESULT 38
ID ABR98840 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Pred. No. 2.1e-07;
RESULT 39
ID ABO16363 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Pred. No. 2.1e-07;
RESULT 40
ID ABR92263 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Pred. No. 2.1e-07;
RESULT 41
ID ABO18904 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Pred. No. 2.1e-07;
RESULT 42
ID ABR78325 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Pred. No. 2.1e-07;
RESULT 43
ID ABR71975 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Pred. No. 2.1e-07;
RESULT 44
ID ABR85061 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Pred. No. 2.1e-07;
RESULT 45
ID ABO00200 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Pred. No. 2.1e-07;
RESULT 46
ID ABO11532 standard; protein; 229 AA.

DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Pred. No. 2.1e-07;
RESULT 47
ID ABO02177 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Pred. No. 2.1e-07;
RESULT 48
ID ABR8751 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Pred. No. 2.1e-07;
RESULT 49
ID ABR83446 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Pred. No. 2.1e-07;
RESULT 50
ID ABO06247 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Pred. No. 2.1e-07;
RESULT 51
ID ABR59283 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Pred. No. 2.1e-07;
RESULT 52
ID ABO09345 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Pred. No. 2.1e-07;
RESULT 53
ID ABO19209 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Pred. No. 2.1e-07;
RESULT 54
ID ABO11227 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Pred. No. 2.1e-07;
RESULT 55
ID ABR66845 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
Pred. No. 2.1e-07;
RESULT 56
ID ABO16058 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040060-A1.

PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 57
ID ABO13764 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 58
ID ABU71529 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 59
ID ABU65667 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, SEQ ID 198.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 60
ID ABO07515 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 61
ID ABO03702 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 62
ID ABR67150 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 63
ID ABO15753 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 64
ID ASU56034 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, PRO994.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 65
ID ASU72310 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 66
ID ABU65362 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032102-A1.

PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 67
ID ABU95307 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 68
ID ABU71210 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 69
ID ABO07820 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 70
ID ABR70061 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 71
ID ABR69394 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 72
ID ABO1535 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 73
ID ABU81337 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 74
ID ABR60134 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 75
ID ABU90983 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003018188-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 76
ID ABR67869 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027269-A1.


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Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 97
ID ABR66540 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027281-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 98
ID ABR90958 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 99
ID ABO08125 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 100
ID ABO53284 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003027986-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 101
ID ABR92499 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 102
ID ABR66000 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 103
ID ABR8169 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 104
ID ABR59829 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 105
ID ABR94017 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 106
ID ABR99870 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 107
ID ABR66540 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 108
ID ABR90958 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 109
ID ABO53284 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 110
ID ABR58972 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, #103.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 111
ID ABR94385 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 112
ID ABR79267 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 113
ID ABR6596 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 114
ID ABR6901 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 115
ID ABR94690 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 116
ID ABO04617 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
```

RESULT 117
ID ABR70366 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 118
ID ABU92350 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 119
ID ABU98531 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 120
ID ABR65930 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 121
ID ABR64647 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 122
ID ABU59415 standard; protein; 229 AA.
DE Novel human secreted or transmembrane protein PRO812.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 123
ID ABU79572 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 124
ID ABU92963 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 125
ID ABU95922 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 126
ID ABU91142 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 127
ID ABU90235 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 128
ID ABO09650 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 129
ID ABO10922 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 130
ID ABR70976 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 131
ID ABU98286 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 132
ID ASU87584 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 133
ID ABU91452 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 134
ID ABU92991 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 135
ID ABU84666 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 136
ID ABR69756 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 137
ID ABU80133 standard; protein; 229 AA.
DE Human PRO protein #99.

PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 138
ID ABU82498 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 139
ID ABU92181 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 140
ID ABU93402 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 141
ID ABO09955 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 142
ID ABO09040 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 143
ID ABU96462 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 144
ID ABU10887 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 145
ID ABU10608 standard; protein; 229 AA.
DE Human secreted/transmembrane protein #99.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 146
ID ABU81639 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002171164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 147
ID ABO09955 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 148
ID ABU95617 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 149
ID ABU96826 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 150
ID ABR70671 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 151
ID ABO05022 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US200308352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 152
ID ABO08430 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 153
ID ABU88578 standard; protein; 229 AA.
DE Human secreted and transmembrane polypeptide PRO994.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 154
ID ABO34092 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 155
ID ABO05637 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 156
ID ABR74026 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;

RESULT 157
ID ABR95618 standard; protein: 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 158
ID ABR80915 standard; protein: 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 159
ID ABR81220 standard; protein: 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 160
ID ABR80916 standard; protein: 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 161
ID ABR88518 standard; protein: 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 162
ID ABR77339 standard; protein: 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 163
ID ABO28823 standard; protein: 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 164
ID ABO31568 standard; protein: 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 165
ID ABR07985 standard; protein: 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 166
ID ABO40465 standard; protein: 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 167
ID ABO35890 standard; protein: 229 AA.
DE Human PRO polypeptide #99.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 168
ID ABO44029 standard; protein: 229 AA.
DE Human PRO polypeptide #99.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 169
ID ADA77950 standard; protein: 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 170
ID ABM24824 standard; protein: 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 171
ID ABO03092 standard; protein: 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 172
ID ABR90348 standard; protein: 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 173
ID ABM17262 standard; protein: 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 174
ID ABR95008 standard; protein: 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 175
ID ABR95313 standard; protein: 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 176
ID ADB17105 standard; protein; 229 AA.
DE Human transmembrane PRO polypeptide (SeqID 48).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 177
ID ABO21551 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 178
ID ABR97815 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 179
ID ABR87603 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 180
ID ABR77644 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 181
ID ASB27874 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 182
ID ASB06155 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 183
ID ASB03661 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 184
ID ASB35112 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 185
ID ASB26349 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 186
ID ABO48131 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 187
ID ABR92873 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 188
ID ABO24634 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 189
ID ADA37769 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US200308297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 190
ID ASB11645 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 191
ID ASB02746 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 192
ID ASB16042 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 193
ID ABO27603 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 194

ID ABM29094 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 195
ID ABM07070 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 196
ID ABM21164 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 197
ID ABM09510 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 198
ID ABO41380 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 199
ID ABO36195 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 200
ID ABO43724 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 201
ID ABM76424 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 202
ID ABM76120 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 203
ID ABM25739 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.

PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 204
ID ABM26044 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 205
ID ADA21455 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO994.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 206
ID ABO03397 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 207
ID ABO02482 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 208
ID ABO44262 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO 994.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 209
ID ABR90653 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 210
ID ABR73721 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 211
ID ABO16973 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 212
ID ABR94398 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 213
ID ABR75905 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.

PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 214
ID ABR71281 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 215
ID ABR93178 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 216
ID ABR93483 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 217
ID ADA10242 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, PRO994.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 218
ID ABR87908 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 219
ID ABO27908 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 220
ID ABO30043 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 221
ID ABO33252 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 222
ID ABO4940 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 223
ID ABO08900 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 224
ID ABO36500 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 225
ID ABO35585 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 226
ID ABO39550 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 227
ID ABO10425 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 228
ID ABO11950 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 229
ID ABO52096 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 230
ID ABO52401 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 231
ID ADA19910 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;

Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 232
ID ABO23719 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 233
ID ADB17293 standard; protein; 229 AA.
DE Human transmembrane PRO polypeptide (SeqID 48).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 234
ID ADA17786 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 235
ID ABR97205 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 236
ID ABR8993 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 237
ID ABR11035 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 238
ID ABR28179 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 239
ID ABO32178 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 240
ID ABR15305 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 241
ID ABR06460 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040055-A1.

DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 242
ID ABR04271 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 243
ID ABR22384 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 244
ID ABR07680 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 245
ID ABR040770 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 246
ID ABR35417 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 247
ID ABR33180 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 248
ID ABO52706 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 249
ID ABO50266 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 250
ID ASU99260 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040055-A1.

PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 251
ID ABO04312 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 252
ID ABO05942 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 253
ID ABO18482 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 254
ID ADA27894 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 255
ID ABR97510 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 256
ID ABR0610 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003045740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 257
ID ABM01221 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 258
ID ABR8823 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 259
ID ABM13475 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 260
ID ABM20859 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 261
ID ABO41990 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 262
ID ABO42600 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 263
ID ABM10120 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 264
ID ABO38635 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 265
ID ABM32875 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 266
ID ABM22689 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 267
ID ABM74900 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 268
ID ADA79742 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 269
ID ABR96290 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;

Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 270
ID ABO2441 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 271
ID ABR86383 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 272
ID ABR86688 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 273
ID ABR86688 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 274
ID ABR29704 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 275
ID ABO29128 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 276
ID ABR23909 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 277
ID ABR23299 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 278
ID ABR22079 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 279
ID ABO37720 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 280
ID ABR28484 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 281
ID ABR28789 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 282
ID ABR66433 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 283
ID ABR75615 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 284
ID ABR34095 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 285
ID ABR34400 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 286
ID ABO20331 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 287
ID ABO21246 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 288
ID ABO22161 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054477-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 289
ID ADA20082 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 290
ID ABO34190 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO 994.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 291
ID ABR96595 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 292
ID ADA94474 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 293
ID ABR85773 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 294
ID ABR99755 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 295
ID ABM00306 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 296
ID ABM00611 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 297
ID ABO29738 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 298

ID ABM23604 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 299
ID ABM29399 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003088679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 300
ID ABO38330 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 301
ID ABO45630 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 302
ID ABM20554 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 303
ID ADA81469 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 304
ID ABO16668 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 305
ID ABO18294 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 306
ID ABO22721 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 307
ID ABO23026 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003054461-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 308
ID ABR2568 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 309
ID ABR1525 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 310
ID ABR77949 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 311
ID ABR89738 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 312
ID ASM26654 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 313
ID ABM13780 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 314
ID ABO28518 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 315
ID ABO30348 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 316
ID ABM07375 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 317
ID ABM03966 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 318
ID ABO37110 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 319
ID ABO41685 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 320
ID ABO35280 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 321
ID ABM25129 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104540-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 322
ID ABO47521 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 323
ID ABO47826 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 324
ID ABO48436 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 325
ID ABO51486 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 6; Length 229;
RESULT 326
ID ABO51791 standard; protein; 229 AA.

DE Human PRO polypeptide #99.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 327
ID ABO50571 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 328
ID ABR79695 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 329
ID ABM16957 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 330
ID ABO17989 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 331
ID ABO20941 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 332
ID ABR96900 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 333
ID ADA38699 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 334
ID ABM12255 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 335
ID ABM16347 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 336
ID ABO24214 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 337
ID ABM14695 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 338
ID ABO4576 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 339
ID ABM06765 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 340
ID ABM03205 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 341
ID ABO39245 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 342
ID ABM75510 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 343
ID ABM25434 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 344
ID ABM19944 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 345
ID ABO46950 standard; protein; 229 AA.
DE Human PRO polypeptide #99.

PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 346
ID ABO47155 standard; protein; 229 AA.
DE Human secreted polypeptide #99.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 347
ID ADA83267 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 348
ID ABR71586 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 349
ID ABR72196 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 350
ID ABR98535 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036129-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 351
ID ABO06905 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 352
ID ABR84858 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 353
ID ABR73416 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 354
ID ABR76510 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044932-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 355
ID ABR73111 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027270-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 356
ID ABM18177 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 357
ID ABO20636 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032126-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 358
ID ABO25379 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 359
ID ABO25684 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 360
ID ABR94093 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 361
ID ADA92820 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 362
ID ABR80000 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 363
ID ABM1340 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 364
ID ABO32947 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;

Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 365
ID ABO30653 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 366
ID ABO30958 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 367
ID ABM27264 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 368
ID ABM30009 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 369
ID ABM05545 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 370
ID ABM15610 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 371
ID ABM08595 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 372
ID ABO42295 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 373
ID ABO38025 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 374
ID ABO45935 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 375
ID ABM66738 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 376
ID ADB20310 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 377
ID ABM19639 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 378
ID ABO49351 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 379
ID ABO49656 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 380
ID ADA78562 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 381
ID ABR88213 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 382
ID ADA00379 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO 994.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 383
ID ABM26959 standard; protein; 229 AA.

DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 384
ID AMO03356 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 385
ID ABO339855 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 386
ID ABO49961 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 387
ID ABO50876 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 388
ID ABO05332 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036126-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 389
ID ABR74636 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044924-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 390
ID ABR77115 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044927-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 391
ID ABR17872 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040072-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 392
ID ABR95923 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040073-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 393
ID ABR95923 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040073-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;

RESULT 393
ID ABO21856 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
FN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 394
ID ABO20026 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
FN US2003032124-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 395
ID ABO24329 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
FN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 396
ID ABR86078 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
FN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 397
ID ABM10730 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
FN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 398
ID ABW6729 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
FN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 399
ID ABR89433 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
FN US2003073170-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 400
ID ABM12560 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
FN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 401
ID ABW05850 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
FN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 402
ID ABO34975 standard; protein; 229 AA.
DE Human PRO polypeptide #99.

PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 403
ID ABO18599 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 404
ID ABR19029 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 405
ID ABR19334 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 406
ID ABO46545 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 407
ID ABO49046 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 408
ID ABR63089 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 409
ID ABR89128 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 410
ID ABR72501 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 411
ID ABR74331 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 412
ID ABO18599 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 413
ID ABR80305 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 414
ID ABO1526 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 415
ID ABO2136 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 416
ID ABR87298 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 417
ID ABR12865 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 418
ID ABR30619 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 419
ID ABR24519 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 420
ID ABO29433 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 421

ID ABO31263 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 422
ID ABO14390 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 423
ID ABO09815 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 424
ID ABO38940 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 425
ID ABO34705 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 426
ID ABO51181 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 427
ID ABO04007 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 428
ID ABO10477 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 429
ID ABO53178 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 430
ID ABR7720 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 431
ID ABR78930 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 432
ID ABO24024 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 433
ID ABR93788 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 434
ID ABO1831 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 435
ID ABR78254 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 436
ID ABR90043 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 437
ID ADA22381 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO994.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 438
ID ABR27569 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 439
ID ABR13170 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 440
ID ABO31873 standard; protein; 229 AA.

DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068731-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 441
ID ABO15448 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 442
ID ABO15448 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068754-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 443
ID ABO15448 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 444
ID ABO15448 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068681-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 445
ID ABO15448 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068681-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 446
ID ABO15448 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068681-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 447
ID ABO15448 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068681-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 448
ID ABO15448 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068681-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 449
ID ABO15448 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068681-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 450
ID ABO15448 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 451
ID ABO15448 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 452
ID ABO15448 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040077-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 453
ID ABO15448 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 454
ID ABO15448 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 455
ID ABO15448 standard; protein; 229 AA.
DE Human secreted/transmembrane PRO polypeptide #73.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 456
ID ABO15448 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 457
ID ABO15448 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 458
ID ABO15448 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 459
ID ABO15448 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 460
ID ABM22994 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 461
ID ABM30314 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 462
ID ABM21774 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 463
ID ABM21469 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 464
ID ABM15000 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 465
ID AB041075 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 466
ID ABQ36805 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 467
ID ABQ37415 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 468
ID ABM75205 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;

Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 469
ID ABM33485 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US200306357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 470
ID ABQ46240 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 471
ID ADA82633 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 472
ID ADB85621 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 473
ID ADB96266 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 474
ID ABM31839 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 475
ID ABM31229 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 476
ID ADB85941 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 477
ID ABM32144 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 478
ID ABM32449 standard; protein; 229 AA.

DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 479
ID ADB68300 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 480
ID ADB68107 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 481
ID ADB31534 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 482
ID ADB30924 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 483
ID ADB90924 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 484
ID ADC57738 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 485
ID ADC55102 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 486
ID ADC11969 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 487
ID ADC07004 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 488
ID ADC56391 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 489
ID ADC17183 standard; protein; 229 AA.
DE Mammalian PRO polypeptide (SeqID 48).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 490
ID ADC07446 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 491
ID ADC11436 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 492
ID ADC14881 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 493
ID ADC52376 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 494
ID ADC14558 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 495
ID ADD08090 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 496
ID ADC81915 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 497
ID ADD07557 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002193299-A1.
PD 19-DEC-2002.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 498
ID ADC82448 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 499
ID ADD05671 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 500
ID ADD08628 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 501
ID ADD06877 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 502
ID ADC83124 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 503
ID ADD55231 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 504
ID ADD36052 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 505
ID ADD56189 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 506
ID ADD54627 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 507
ID ADE26781 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.

PN US2003087304-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 508
ID ADE26248 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 509
ID ADF67185 standard; protein; 229 AA.
DE Human PRO994 amino acid sequence SEQ ID NO:258.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 510
ID ADG01053 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 511
ID ADG08606 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 512
ID ADG02666 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 513
ID ADG01373 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 514
ID ADF95548 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 515
ID ADF95227 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 516
ID ADG12363 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;

Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 517
ID ADH24080 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 518
ID ADH34106 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 519
ID ADH29939 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 520
ID ADH23910 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 521
ID ADH09023 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 522
ID ADG85314 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 523
ID ADH24590 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 524
ID ADH37446 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 525
ID ADH02035 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 526
ID ADH37616 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 527
ID ADG85654 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 528
ID ADH24250 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 529
ID ADH38544 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 530
ID ADG83665 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 531
ID ADH29473 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 532
ID ADH27589 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 533
ID ADH37786 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 534
ID ADH37963 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 535
ID ADH02035 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;

ID ADH57383 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
FN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 536
ID ADH53525 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
FN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 537
ID ADH53695 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
FN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 538
ID ADH52031 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
FN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 539
ID ADH49886 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
FN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 540
ID ADI25396 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
FN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 541
ID ADH90189 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
FN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 542
ID ADI25566 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
FN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 543
ID ADH97740 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
FN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 544
ID ADI35439 standard; protein; 229 AA.

DE Human PRO polypeptide #73.
FN US2003050457-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 545
ID ADI03588 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
FN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 546
ID ADI11945 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
FN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 547
ID ADH90019 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
FN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 548
ID ADH99931 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
FN US2003049682-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 549
ID ADH98420 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
FN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 550
ID ADI11095 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
FN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 551
ID ADI11605 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
FN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 552
ID ADH98250 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
FN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 7; Length 229;
RESULT 553
ID ADH98590 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
FN US2003181708-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 554
ID ADH9080 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 555
ID ADI05068 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 556
ID ADI03418 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 557
ID ADI04813 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 558
ID ADH78267 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 559
ID ADI19611 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 560
ID ADH90359 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 561
ID ADI03078 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 562
ID ADH7927 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 563
ID ADH97910 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 564
ID ADI01295 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 565
ID ADI01990 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 566
ID ADI03248 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 567
ID ADI11435 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 568
ID ADI02337 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 569
ID ADI11775 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 570
ID ADI05412 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 571
ID ADH79484 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;

Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 572
ID ADI19441 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 573
ID ADI05242 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 574
ID ADH79654 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 575
ID ADI01480 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 576
ID ADI01650 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 577
ID ADH79824 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 578
ID ADI04642 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 579
ID ADI04642 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 580
ID ADI02778 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;

RESULT 581
ID ADH78097 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
FN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 582
ID ADI25736 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
FN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 583
ID ADI25906 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
FN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 584
ID ADK65418 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
FN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 585
ID ADH98760 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
FN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 586
ID ADH80001 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
FN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 587
ID ADL32804 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
FN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 588
ID ADL32804 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
FN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 589
ID ADL93732 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
FN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 590
ID ADL93732 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
FN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;

ID ABM5217 standard; protein; 229 AA.
DE Human protein sequence hCP1734062.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 100.0%; Score 93; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 591
ID ADC52186 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 592
ID ADE74335 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 593
ID ADE74947 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 594
ID ADF35384 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 595
ID ADG11634 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 596
ID ADF96160 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 597
ID ADG04431 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 598
ID ADG00591 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 599
ID ADH06618 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 600
ID ADH06448 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 601
ID ADG6869 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 602
ID ADH27759 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 603
ID ADH25100 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 604
ID ADH33732 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 605
ID ADG82847 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 606
ID ADH02375 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 607
ID ADH07982 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 608
ID ADG69379 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;

Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 609
ID ADH39200 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 610
ID ADH26128 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 611
ID ADG83940 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 612
ID ADH19504 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 613
ID ADG85484 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003168848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 614
ID ADH06278 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 615
ID ADH30108 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 616
ID ADH24420 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 617
ID ADH33097 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 618
ID ADG69549 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 619
ID ADH07812 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 620
ID ADG85824 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 621
ID ADH39370 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 622
ID ADH33562 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 623
ID ADH33902 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 624
ID ADH01112 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 625
ID ADG69719 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 626
ID ADH20997 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 627
ID ADH02205 standard; protein; 229 AA.

DE Human PRO polypeptide #24.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 628
ID ADG69209 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 629
ID ADG85994 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 630
ID ADH24930 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 631
ID ADH39547 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 632
ID ADH20037 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 633
ID ADH02545 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 634
ID ADG69039 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 635
ID ADH07642 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
DE ADG86164 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.

PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 637
ID ADH24760 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 638
ID ADH25808 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 639
ID ADH38374 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 640
ID ADH57213 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 641
ID ADH52201 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 642
ID ADH49567 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 643
ID ADH90529 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 644
ID ADI1265 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 93; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
RESULT 645
ID ADH98930 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003190698-A1.

PD 09-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 93; DB 8; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 RESULT 646
 ID ADI02160 standard; protein; 229 AA.
 DE Novel human secreted and transmembrane protein PRO994.
 PN US2003190699-A1.
 PD 09-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 93; DB 8; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 RESULT 647
 ID ADH90699 standard; protein; 229 AA.
 DE Novel human secreted and transmembrane protein PRO994.
 PN US2003181701-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 93; DB 8; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 RESULT 648
 ID ADJ54836 standard; protein; 229 AA.
 DE Human PRO polypeptide #99.
 PN US2004023321-A1.
 PD 05-FEB-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 93; DB 8; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 RESULT 649
 ID ADJ98574 standard; protein; 229 AA.
 DE Novel human secreted and transmembrane protein PRO994.
 PN US2003181797-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 93; DB 8; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 RESULT 650
 ID ADJ98744 standard; protein; 229 AA.
 DE Novel human secreted and transmembrane protein PRO994.
 PN US2003187228-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 93; DB 8; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 RESULT 651
 ID ADH78903 standard; protein; 229 AA.
 DE Novel human secreted and transmembrane protein PRO994.
 PN US2003181703-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 93; DB 8; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 RESULT 652
 ID ADJ99137 standard; protein; 229 AA.
 DE Novel human secreted and transmembrane protein PRO994.
 PN US2003186408-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 93; DB 8; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 RESULT 653
 ID ADJ99307 standard; protein; 229 AA.
 DE Novel human secreted and transmembrane protein PRO994.
 PN US2003187196-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 93; DB 8; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 RESULT 654
 ID ADJ98925 standard; protein; 229 AA.
 DE Novel human secreted and transmembrane protein PRO994.
 PN US2003187242-A1.
 PD 02-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 93; DB 8; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 RESULT 655
 ID ADH79073 standard; protein; 229 AA.
 DE Novel human secreted and transmembrane protein PRO994.
 PN US2003181702-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 93; DB 8; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 RESULT 656
 ID ADK00933 standard; protein; 229 AA.
 DE Human PRO polypeptide #24.
 PN US2003186407-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 93; DB 8; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 RESULT 657
 ID ADK14454 standard; protein; 229 AA.
 DE Novel human secreted and transmembrane protein PRO994.
 PN US2003187229-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 93; DB 8; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 RESULT 658
 ID ADJ64607 standard; protein; 229 AA.
 DE Human PRO polypeptide #99.
 PN US2004038337-A1.
 PD 26-FEB-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 93; DB 8; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 RESULT 659
 ID ADM31503 standard; protein; 229 AA.
 DE Novel human secreted and transmembrane protein PRO994.
 PN US2004048334-A1.
 PD 11-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 93; DB 8; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 RESULT 660
 ID ADM36550 standard; protein; 229 AA.
 DE Novel human secreted and transmembrane protein PRO994.
 PN US2004053358-A1.
 PD 18-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 93; DB 8; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 RESULT 661
 ID ADM40355 standard; protein; 229 AA.
 DE Novel human secreted and transmembrane protein PRO994.
 PN US2004048335-A1.
 PD 11-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 93; DB 8; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 RESULT 662
 ID ADM80903 standard; protein; 229 AA.
 DE Human PRO polypeptide #24.
 PN US2004058411-A1.
 PD 25-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 93; DB 8; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 RESULT 663
 ID ADN37963 standard; protein; 229 AA.
 DE Novel human secreted and transmembrane protein PRO994.
 PN US2004091959-A1.
 PD 13-MAY-2004.
 PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 93; DB 8; Length 229;
RESULT 664
ID ADR14507 standard; protein; 229 AA.
DE Human NF- κ B pathway-associated protein SeqID508.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match
Best Local Similarity 100.0%; Score 93; DB 8; Length 229;
RESULT 665
ID ADY77743 standard; protein; 229 AA.
DE Neoplastic disease detection protein PRO994.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (ZATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 100.0%; Score 93; DB 9; Length 229;
RESULT 666
ID AEA38511 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, #141.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 93; DB 9; Length 229;
RESULT 667
ID ABM85216 standard; protein; 230 AA.
DE Mouse protein sequence MCP5099.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match
Best Local Similarity 75.3%; Score 70; DB 7; Length 230;
RESULT 668
ID ABB60457 standard; protein; 410 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 8163.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 48.4%; Score 45; DB 4; Length 410;
RESULT 669
ID AAW15074 standard; protein; 420 AA.
DE M. leprae gyrase intein.
PN FR2739859-A1.
PD 18-APR-1997.
PA (INSP) INST PASTEUR.
Query Match
Best Local Similarity 47.3%; Score 44; DB 2; Length 420;
RESULT 670
ID ABU35713 standard; protein; 1249 AA.
DE Protein encoded by Prokaryotic essential gene #21240.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (SLIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 47.3%; Score 44; DB 6; Length 1249;
RESULT 671
ID AAW15078 standard; protein; 1273 AA.
DE M. leprae gyra precursor.
PN FR2739859-A1.
PD 18-APR-1997.
PA (INSP) INST PASTEUR.
Query Match
47.3%; Score 44; DB 2; Length 1273;

Best Local Similarity 46.7%; Pred. No. 3.6e+02;
RESULT 672
ID ABO00725 standard; protein; 232 AA.
DE Novel human polypeptide #312.
PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 46.2%; Score 43; DB 6; Length 232;
RESULT 673
ID AAU31159 standard; protein; 1058 AA.
DE Novel human secreted protein #1650.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 46.2%; Score 43; DB 4; Length 1058;
RESULT 674
ID AAR71333 standard; protein; 1110 AA.
DE Deduced sequence encoded by Wilson's disease gene cDNA.
PN WO9506714-A1.
PD 09-MAR-1995.
PA (UYCO) UNIV COLUMBIA NEW YORK.
PA (GEHO) GEN HOSPITAL CORP.
Query Match
Best Local Similarity 46.2%; Score 43; DB 2; Length 1110;
RESULT 675
ID AAE36368 standard; protein; 149 AA.
DE Human neuron-restrictive silencer factor repressor splice variant.
PN WO200297044-A2.
PD 05-DEC-2002.
PA (UYJE-) UNIV JEFFERSON THOMAS.
Query Match
Best Local Similarity 45.2%; Score 42; DB 6; Length 149;
RESULT 676
ID AAM58345 standard; protein; 222 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 30450.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 45.2%; Score 42; DB 4; Length 222;
RESULT 677
ID ABU03573 standard; protein; 222 AA.
DE Human expressed protein tag (EPT) #239.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match
Best Local Similarity 45.2%; Score 42; DB 6; Length 222;
RESULT 678
ID AAR99364 standard; protein; 252 AA.
DE Human REST protein DNA binding domain.
PN WO9629433-A1.
PD 26-SEP-1996.
PA (UVNY) UNIV NEW YORK STATE RES FOUND.
Query Match
Best Local Similarity 45.2%; Score 42; DB 2; Length 252;
RESULT 679
ID AAR99388 standard; protein; 428 AA.
DE Human REST protein (aa9-436).
PN WO9629433-A1.
PD 26-SEP-1996.
PA (UVNY) UNIV NEW YORK STATE RES FOUND.
Query Match
Best Local Similarity 45.2%; Score 42; DB 2; Length 428;
RESULT 680
ID AAR99367 standard; protein; 468 AA.
DE Human REST protein partial sequence (aa73-540).
PN WO9629433-A1.
PD 26-SEP-1996.
PA (UVNY) UNIV NEW YORK STATE RES FOUND.
Query Match
45.2%; Score 42; DB 2; Length 468;

Best Local Similarity 53.3%; Pred. No. 2.6e+02;
RESULT 681
ID AAR99387 standard; protein; 487 AA.
DE Human REST protein (aa41-527).
PN WO9629433-A1.
PD 26-SEP-1996.
PA (UNYU) UNIV NEW YORK STATE RES FOUND.
Query Match 45.2%; Score 42; DB 2; Length 487;
Best Local Similarity 53.3%; Pred. No. 2.7e+02;
RESULT 682
ID AAR99370 standard; protein; 538 AA.
DE Human REST protein partial sequence (aa1-538).
PN WO9629433-A1.
PD 26-SEP-1996.
PA (UNYU) UNIV NEW YORK STATE RES FOUND.
Query Match 45.2%; Score 42; DB 2; Length 538;
Best Local Similarity 53.3%; Pred. No. 3e+02;
RESULT 683
ID AAW02288 standard; protein; 678 AA.
DE Human neuron restrictive silencer factor (partial sequence).
PN WO9627665-A2.
PD 12-SEP-1996.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 45.2%; Score 42; DB 2; Length 678;
Best Local Similarity 53.3%; Pred. No. 3.9e+02;
RESULT 684
ID ABG19842 standard; protein; 875 AA.
DE Novel human diagnostic protein #19833.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 45.2%; Score 42; DB 4; Length 875;
Best Local Similarity 46.7%; Pred. No. 5.2e+02;
RESULT 685
ID AAW02289 standard; protein; 976 AA.
DE Mouse neuron restrictive silencer factor.
PN WO9627665-A2.
PD 12-SEP-1996.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 45.2%; Score 42; DB 2; Length 976;
Best Local Similarity 53.3%; Pred. No. 5.9e+02;
RESULT 686
ID ADU08035 standard; protein; 1082 AA.
DE Murine NRSP protein.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GHEO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1082;
Best Local Similarity 53.3%; Pred. No. 6.7e+02;
RESULT 687
ID AAR99365 standard; protein; 1097 AA.
DE Human REST protein.
PN WO9629433-A1.
PD 26-SEP-1996.
PA (UNYU) UNIV NEW YORK STATE RES FOUND.
Query Match 45.2%; Score 42; DB 2; Length 1097;
Best Local Similarity 53.3%; Pred. No. 6.8e+02;
RESULT 688
ID ADU08060 standard; protein; 1097 AA.
DE Human NRSP protein finger 4 variant F4v6.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GHEO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 6.8e+02;
RESULT 689
ID ADU08070 standard; protein; 1097 AA.
DE Human NRSP protein finger 5 variant F5v8.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GHEO) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 6.8e+02;

RESULT 690			
ID	ADU08063 standard; protein; 1097 AA.		
DE	Human NRSP protein finger 5 variant F5v1.		
PN	WO2004099367-A2.		
PD	18-NOV-2004.		
PA	(GHO) GEN HOSPITAL CORP.		
Query Match	45.2%;	Score 42;	DB 8; Length 1097;
Best Local Similarity	53.3%;	Pred. No. 6.8e+02;	
RESULT 691			
ID	ADU08068 standard; protein; 1097 AA.		
DE	Human NRSP protein finger 5 variant F5v6.		
PN	WO2004099367-A2.		
PD	18-NOV-2004.		
PA	(GHO) GEN HOSPITAL CORP.		
Query Match	45.2%;	Score 42;	DB 8; Length 1097;
Best Local Similarity	53.3%;	Pred. No. 6.8e+02;	
RESULT 692			
ID	ADU08067 standard; protein; 1097 AA.		
DE	Human NRSP protein finger 5 variant F5v5.		
PN	WO2004099367-A2.		
PD	18-NOV-2004.		
PA	(GHO) GEN HOSPITAL CORP.		
Query Match	45.2%;	Score 42;	DB 8; Length 1097;
Best Local Similarity	53.3%;	Pred. No. 6.8e+02;	
RESULT 693			
ID	ADU08061 standard; protein; 1097 AA.		
DE	Human NRSP protein finger 4 variant F4v7.		
PN	WO2004099367-A2.		
PD	18-NOV-2004.		
PA	(GHO) GEN HOSPITAL CORP.		
Query Match	45.2%;	Score 42;	DB 8; Length 1097;
Best Local Similarity	53.3%;	Pred. No. 6.8e+02;	
RESULT 694			
ID	ADU08066 standard; protein; 1097 AA.		
DE	Human NRSP protein finger 5 variant F5v4.		
PN	WO2004099367-A2.		
PD	18-NOV-2004.		
PA	(GHO) GEN HOSPITAL CORP.		
Query Match	45.2%;	Score 42;	DB 8; Length 1097;
Best Local Similarity	53.3%;	Pred. No. 6.8e+02;	
RESULT 695			
ID	ADU08059 standard; protein; 1097 AA.		
DE	Human NRSP protein finger 4 variant F4v5.		
PN	WO2004099367-A2.		
PD	18-NOV-2004.		
PA	(GHO) GEN HOSPITAL CORP.		
Query Match	45.2%;	Score 42;	DB 8; Length 1097;
Best Local Similarity	53.3%;	Pred. No. 6.8e+02;	
RESULT 696			
ID	ADU08062 standard; protein; 1097 AA.		
DE	Human NRSP protein finger 4 variant F4v8.		
PN	WO2004099367-A2.		
PD	18-NOV-2004.		
PA	(GHO) GEN HOSPITAL CORP.		
Query Match	45.2%;	Score 42;	DB 8; Length 1097;
Best Local Similarity	53.3%;	Pred. No. 6.8e+02;	
RESULT 697			
ID	ADU08069 standard; protein; 1097 AA.		
DE	Human NRSP protein finger 5 variant F5v7.		
PN	WO2004099367-A2.		
PD	18-NOV-2004.		
PA	(GHO) GEN HOSPITAL CORP.		
Query Match	45.2%;	Score 42;	DB 8; Length 1097;
Best Local Similarity	53.3%;	Pred. No. 6.8e+02;	
RESULT 698			
ID	ADU08058 standard; protein; 1097 AA.		
DE	Human NRSP protein finger 4 variant F4v4.		
PN	WO2004099367-A2.		
PD	18-NOV-2004.		
PA	(GHO) GEN HOSPITAL CORP.		
Query Match	45.2%;	Score 42;	DB 8; Length 1097;
Best Local Similarity	53.3%;	Pred. No. 6.8e+02;	
RESULT 699			
ID	ADU08065 standard; protein; 1097 AA.		
DE	Human NRSP protein finger 5 variant F5v3.		
PN	WO2004099367-A2.		
PD	18-NOV-2004.		
PA	(GHO) GEN HOSPITAL CORP.		
Query Match	45.2%;	Score 42;	DB 8; Length 1097;
Best Local Similarity	53.3%;	Pred. No. 6.8e+02;	

ID ADU08064 standard; protein; 1097 AA.
DE Human NRSP protein finger 5 variant F5v2.
PN WO200409367-A2.
PD 18-NOV-2004.
PA (GENE) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 6.8e+02;
RESULT 700
ID ADU08033 standard; protein; 1097 AA.
DE Human NRSP protein.
PN WO200409367-A2.
PD 18-NOV-2004.
PA (GENE) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 6.8e+02;
RESULT 701
ID ADU08057 standard; protein; 1097 AA.
DE Human NRSP protein finger 4 variant F4v1.
PN WO200409367-A2.
PD 18-NOV-2004.
PA (GENE) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 6.8e+02;
RESULT 702
ID ADU08065 standard; protein; 1097 AA.
DE Human NRSP protein finger 5 variant F5v3.
PN WO200409367-A2.
PD 18-NOV-2004.
PA (GENE) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 6.8e+02;
RESULT 703
ID ADU08065 standard; protein; 1097 AA.
DE Human NRSP protein finger 5 variant F5v3.
PN WO200409367-A2.
PD 18-NOV-2004.
PA (GENE) GEN HOSPITAL CORP.
Query Match 45.2%; Score 42; DB 8; Length 1097;
Best Local Similarity 53.3%; Pred. No. 6.8e+02;
RESULT 704
ID AAO02944 standard; protein; 1350 AA.
DE Angiotensin converting enzyme (ACEV) splice variant protein #44.
PN WO200136632-A2.
PD 25-MAY-2001.
PA (COMP.) COMFUGEN LTD.
Query Match 45.2%; Score 42; DB 4; Length 1350;
Best Local Similarity 46.7%; Pred. No. 8.6e+02;
RESULT 705
ID AAR65039 standard; protein; 1464 AA.
DE Human N-methyl-D-aspartate receptor subunit 2A protein.
PN WO9424284-A1.
PD 27-OCT-1994.
PA (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
Query Match 45.2%; Score 42; DB 2; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 706
ID AAR55529 standard; protein; 1464 AA.
DE Human NMDA R2A receptor subunit.
PN WO9411501-A1.
PD 26-MAY-1994.
PA (MERI) MERCK SHARP & DOHME LTD.
Query Match 45.2%; Score 42; DB 2; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 707
ID AAR80970 standard; protein; 1464 AA.
DE Human excitatory amino acid receptor modulatory protein NR2A-1.
PN EP674003-A2.
PD 27-SEP-1995.
PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
Query Match 45.2%; Score 42; DB 2; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 708
ID AAW85576 standard; protein; 1464 AA.

DE Human N-methyl-D-aspartate receptor subunit NMDAR2A.
PN US549895-A.
PD 15-DEC-1998.
PA (SIBI-) SIBIA NEUROSCIENCES INC.
Query Match 45.2%; Score 42; DB 2; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 709
ID AAY56113 standard; protein; 1464 AA.
DE Human NMDAR2A subunit protein sequence SEQ ID NO:11.
PN US5985586-A.
PD 16-NOV-1999.
PA (SIBI-) SIBIA NEUROSCIENCES INC.
Query Match 45.2%; Score 42; DB 3; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 710
ID AAB28215 standard; protein; 1464 AA.
DE Human N-methyl-D-aspartate receptor subunit NMDAR2A.
PN US6111091-A.
PD 29-AUG-2000.
PA (MERI) MERCK & CO INC.
Query Match 45.2%; Score 42; DB 3; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 711
ID ABB56507 standard; protein; 1464 AA.
DE Human NMDAR2A SEQ ID NO 11.
PN US6316611-B1.
PD 13-NOV-2001.
PA (MERI) MERCK & CO INC.
Query Match 45.2%; Score 42; DB 5; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 712
ID AAO18063 standard; protein; 1464 AA.
DE Human NMDAR2A SEQ ID NO: 11.
PN US6376660-B1.
PD 23-APR-2002.
PA (MERI) MERCK & CO INC.
Query Match 45.2%; Score 42; DB 5; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 713
ID ABG32158 standard; protein; 1464 AA.
DE N-methyl D-aspartate (NMDA) receptor related protein #2.
PN WO200264772-A1.
PD 22-AUG-2002.
PA (SHIO) SHIONOGI & CO LTD.
Query Match 45.2%; Score 42; DB 5; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 714
ID ABU65878 standard; protein; 1464 AA.
DE Human N-methyl D-aspartate receptor subunit associated protein #1.
PN US2002161215-A1.
PD 31-OCT-2002.
PA (DAGG/) DAGGETT L P.
PA (ELLI/) ELLIS S B.
PA (LIAW/) LIAW C W.
PA (LUCC/) LU C.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 715
ID ABU61423 standard; protein; 1464 AA.
DE Human N-methyl-D-aspartate (NMDA) receptor subunit #5.
PN US2002161193-A1.
PD 31-OCT-2002.
PA (DAGG/) DAGGETT L P.
PA (LUCC/) LU C.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 716
ID ABU03575 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #241.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;

Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 717
ID ABU03578 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #244.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 718
ID ABU03574 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #240.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 719
ID ABU03577 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #243.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 720
ID ABU03572 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #238.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 721
ID ABU03579 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #245.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 722
ID ABU03571 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #237.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 723
ID ABU03576 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #242.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 724
ID ABU03580 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #246.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 725
ID ABU03570 standard; protein; 1464 AA.
DE Human expressed protein tag (EPT) #236.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 726
ID ABU03575 standard; protein; 1464 AA.
DE Human N-methyl-D-aspartate (NMDA) receptor sub-unit #3.
PN US6469142-B1.
PD 22-OCT-2002.
PA (MERI) MERCK & CO INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 727
ID ABO43070 standard; protein; 1464 AA.
DE Human NMDA receptor subunit NMDAR2A.
PN US2003013866-A1.
PD 16-JAN-2003.
PA (MERI) MERCK & CO INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 728
ID AAE39234 standard; protein; 1464 AA.
DE Human NMDA receptor subunit, NMDAR2A protein.
PN US621413-B1.
PD 18-FEB-2003.
PA (MERI) MERCK & CO INC.
Query Match 45.2%; Score 42; DB 6; Length 1464;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
RESULT 729
ID ABU16324 standard; protein; 355 AA.
DE Protein encoded by Prokaryotic essential gene #1851.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 44.6%; Score 41.5; DB 6; Length 355;
Best Local Similarity 34.6%; Pred. No. 2.3e+02;
RESULT 730
ID ADW94654 standard; protein; 355 AA.
DE Proliferation-required gene SAV0920 protein, SEQ ID 594.
PN US2005026189-A1.
PD 03-FEB-2005.
PA (WANG/) WANG L.
PA (ZAMU/) ZAMUDIO C.
Query Match 44.6%; Score 41.5; DB 9; Length 355;
Best Local Similarity 34.6%; Pred. No. 2.3e+02;
RESULT 731
ID AAW48794 standard; protein; 117 AA.
DE Homo sapiens sprouty 1 cysteine rich protein.
PN WO9820032-A1.
PD 14-MAY-1998.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 44.1%; Score 41; DB 2; Length 117;
Best Local Similarity 58.3%; Pred. No. 79;
RESULT 732
ID AAB41184 standard; protein; 139 AA.
DE Human ORFX ORF948 polypeptide sequence SEQ ID NO:1896.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 44.1%; Score 41; DB 3; Length 139;
Best Local Similarity 58.3%; Pred. No. 97;
RESULT 733
ID ADE83550 standard; protein; 139 AA.
DE Human Protein O43609, SEQ ID NO 11168.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 44.1%; Score 41; DB 7; Length 139;
Best Local Similarity 58.3%; Pred. No. 97;
RESULT 734
ID ADE58772 standard; protein; 139 AA.
DE Human Protein O43609, SEQ ID NO 4658.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.

Query Match 44.1%; Score 41; DB 7; Length 139;
Best Local Similarity 58.3%; Pred. No. 97;
RESULT 735
ID ADN95257 standard; protein; 139 AA.
DE Human BRC/LSC-related protein sequence SeqID179.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 44.1%; Score 41; DB 7; Length 139;
Best Local Similarity 58.3%; Pred. No. 97;
RESULT 736
ID ADG47835 standard; protein; 139 AA.
DE Human sprouty-1 protein.
PN US6485920-B1.
PD 26-NOV-2002.
PA (HYSE-) HYSEQ INC.
Query Match 44.1%; Score 41; DB 8; Length 139;
Best Local Similarity 58.3%; Pred. No. 97;
RESULT 737
ID ADJ95402 standard; protein; 139 AA.
DE Human sprouty-1 polypeptide.
PN US6706871-B1.
PD 16-MAR-2004.
PA (NUVE-) NUVELO INC.
Query Match 44.1%; Score 41; DB 8; Length 139;
Best Local Similarity 58.3%; Pred. No. 97;
RESULT 738
ID AAW48793 standard; protein; 140 AA.
DE Homo sapiens sprouty 1 protein.
PN WO9820032-A1.
PD 14-MAY-1998.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 44.1%; Score 41; DB 2; Length 140;
Best Local Similarity 58.3%; Pred. No. 97;
RESULT 739
ID AAY87596 standard; protein; 156 AA.
DE Human SPROUTY protein short consensus sequence.
PN WO200015781-A1.
PD 23-MAR-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 44.1%; Score 41; DB 3; Length 156;
Best Local Similarity 58.3%; Pred. No. 1.1e+02;
RESULT 740
ID AAY87595 standard; protein; 167 AA.
DE Human SPROUTY-1 protein, SEQ ID NO:9.
PN WO200015781-A1.
PD 23-MAR-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 44.1%; Score 41; DB 3; Length 167;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
RESULT 741
ID ADP29852 standard; protein; 188 AA.
DE Human secreted protein SEQ ID #619.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 44.1%; Score 41; DB 8; Length 188;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
RESULT 742
ID AAY87597 standard; protein; 288 AA.
DE Human SPROUTY protein long consensus sequence.
PN WO200015781-A1.
PD 23-MAR-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 44.1%; Score 41; DB 3; Length 288;
Best Local Similarity 58.3%; Pred. No. 2.2e+02;
RESULT 743
ID AAY87592 standard; protein; 294 AA.
DE Human SPROUTY-1 protein, SEQ ID NO:3.
PN WO200015781-A1.
PD 23-MAR-2000.
PA (ELIL) LILLY & CO ELI.

Query Match 44.1%; Score 41; DB 3; Length 294;
Best Local Similarity 58.3%; Pred. No. 2.3e+02;
RESULT 744
ID AAY87593 standard; protein; 295 AA.
DE Human SPROUTY-1 protein, SEQ ID NO:5.
PN WO200015781-A1.
PD 23-MAR-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 44.1%; Score 41; DB 3; Length 295;
Best Local Similarity 58.3%; Pred. No. 2.3e+02;
RESULT 745
ID AAU69508 standard; protein; 315 AA.
DE Human purified secretory polypeptide #77.
PN WO200162918-A2.
PD 30-AUG-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 44.1%; Score 41; DB 4; Length 315;
Best Local Similarity 40.0%; Pred. No. 2.4e+02;
RESULT 746
ID AEB51826 standard; protein; 318 AA.
DE Human Sprouty-1 protein.
PN WO2005065686-A1.
PD 21-JUL-2005.
PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
Query Match 44.1%; Score 41; DB 9; Length 318;
Best Local Similarity 58.3%; Pred. No. 2.5e+02;
RESULT 747
ID AAY87591 standard; protein; 319 AA.
DE Human SPROUTY-1 protein, SEQ ID NO:24.
PN WO200015781-A1.
PD 23-MAR-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 44.1%; Score 41; DB 3; Length 319;
Best Local Similarity 58.3%; Pred. No. 2.5e+02;
RESULT 748
ID AAB64377 standard; protein; 319 AA.
DE Amino acid sequence of human intracellular signalling molecule INTRA9.
PN WO200077040-A2.
PD 21-DEC-2000.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 44.1%; Score 41; DB 4; Length 319;
Best Local Similarity 58.3%; Pred. No. 2.5e+02;
RESULT 749
ID AAM38688 standard; protein; 319 AA.
DE Human polypeptide SEQ ID NO 1833.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 44.1%; Score 41; DB 4; Length 319;
Best Local Similarity 58.3%; Pred. No. 2.5e+02;
RESULT 750
ID ADY16807 standard; protein; 319 AA.
DE PRO polypeptide SEQ ID NO 2613.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GRTH) GENENTECH INC.
Query Match 44.1%; Score 41; DB 9; Length 319;
Best Local Similarity 58.3%; Pred. No. 2.5e+02;
RESULT 751
ID AAM40474 standard; protein; 326 AA.
DE Human polypeptide SEQ ID NO 5405.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 44.1%; Score 41; DB 4; Length 326;
Best Local Similarity 58.3%; Pred. No. 2.5e+02;
RESULT 752
ID ABB84246 standard; protein; 335 AA.
DE Human germinal protein 36.85.
PN CN139486-A.
PD 13-MAR-2002.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.

Query Match 44.1%; Score 41; DB 5; Length 335;
Best Local Similarity 58.3%; Pred. No. 2.6e+02;
RESULT 753
ID ADE08605 standard; protein; 336 AA.
DE Novel protein (useful for identifying genetic disorders) #760.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 44.1%; Score 41; DB 7; Length 336;
Best Local Similarity 40.0%; Pred. No. 2.6e+02;
RESULT 754
ID AAY87594 standard; protein; 338 AA.
DE Human SPROUTY-1 protein, SEQ ID NO:7.
PN WO200015781-A1.
PD 23-MAR-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 44.1%; Score 41; DB 3; Length 338;
Best Local Similarity 58.3%; Pred. No. 2.6e+02;
RESULT 755
ID AAG30407 standard; protein; 449 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36346.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 44.1%; Score 41; DB 3; Length 449;
Best Local Similarity 42.9%; Pred. No. 3.7e+02;
RESULT 756
ID ABB92109 standard; protein; 449 AA.
DE Herbicidally active polypeptide SEQ ID NO 1320.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 44.1%; Score 41; DB 5; Length 449;
Best Local Similarity 42.9%; Pred. No. 3.7e+02;
RESULT 757
ID AAG30406 standard; protein; 466 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36345.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 44.1%; Score 41; DB 3; Length 466;
Best Local Similarity 42.9%; Pred. No. 3.8e+02;
RESULT 758
ID AAG41728 standard; protein; 474 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51953.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 44.1%; Score 41; DB 3; Length 474;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
RESULT 759
ID ABA18817 standard; protein; 496 AA.
DE Amino acid sequence of E3 ubiquitin ligase murine Cbl-3.
PN WO2005044840-A2.
PD 19-MAY-2005.
PA (CBRB-) CBR INST BIOMEDICAL RES INC.
Query Match 44.1%; Score 41; DB 9; Length 496;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
RESULT 760
ID AAG41727 standard; protein; 497 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51952.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 44.1%; Score 41; DB 3; Length 497;
Best Local Similarity 50.0%; Pred. No. 4.1e+02;
RESULT 761
ID AAG41726 standard; protein; 512 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51951.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 44.1%; Score 41; DB 3; Length 512;
Best Local Similarity 50.0%; Pred. No. 4.2e+02;
RESULT 762
ID ADN20612 standard; protein; 597 AA.
DE Bacterial polypeptide #3265.
PN US20032333675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 44.1%; Score 41; DB 8; Length 597;
Best Local Similarity 88.9%; Pred. No. 5e+02;
RESULT 763
ID ADU08037 standard; protein; 1068 AA.
DE Rat NRSF protein.
PN WO2004099367-A2.
PD 18-NOV-2004.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 44.1%; Score 41; DB 8; Length 1068;
Best Local Similarity 58.3%; Pred. No. 9.8e+02;
RESULT 764
ID ABU26822 standard; protein; 792 AA.
DE Protein encoded by Prokaryotic essential gene #12349.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 43.5%; Score 40.5; DB 6; Length 792;
Best Local Similarity 37.5%; Pred. No. 8.5e+02;
RESULT 765
ID AAY35218 standard; protein; 797 AA.
DE C. pneumoniae protein involved in metabolism of amino acids.
PN WO9927105-A2.
PD 03-JUN-1999.
PA (GEST) GENSET.
Query Match 43.5%; Score 40.5; DB 2; Length 797;
Best Local Similarity 37.5%; Pred. No. 8.5e+02;
RESULT 766
ID ADB65067 standard; protein; 158 AA.
DE Human protein encoded by clone SMINT20049920.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
Query Match 43.0%; Score 40; DB 7; Length 158;
Best Local Similarity 46.7%; Pred. No. 1.7e+02;
RESULT 767
ID AAU23341 standard; protein; 204 AA.
DE Novel human enzyme polypeptide #427.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 43.0%; Score 40; DB 4; Length 204;
Best Local Similarity 44.4%; Pred. No. 2.2e+02;
RESULT 768
ID ADO24768 standard; protein; 281 AA.
DE Cat TRAIL protein.
PN WO2004039307-A2.
PD 13-MAY-2004.
PA (PFIZ) PFIZER PROD INC.
Query Match 43.0%; Score 40; DB 8; Length 281;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
RESULT 769
ID ADO24766 standard; protein; 281 AA.
DE Dog TRAIL protein.
PN WO2004039307-A2.
PD 13-MAY-2004.
PA (PFIZ) PFIZER PROD INC.
Query Match 43.0%; Score 40; DB 8; Length 281;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
RESULT 770
ID ADY11675 standard; protein; 358 AA.
DE Plant full length insert polypeptide seqid 67490.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.

PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 43.0%; Score 40; DB 8; Length 358;
Best Local Similarity 66.7%; Pred. No. 4.2e+02;
RESULT 771
ID ABU11564 standard; protein; 420 AA.
DE Human MDDT polypeptide SEQ ID 511.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 43.0%; Score 40; DB 6; Length 420;
Best Local Similarity 44.4%; Pred. No. 5e+02;
RESULT 772
ID ABU11734 standard; protein; 420 AA.
DE Human MDDT polypeptide SEQ ID 681.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 43.0%; Score 40; DB 6; Length 420;
Best Local Similarity 44.4%; Pred. No. 5e+02;
RESULT 773
ID ADO20208 standard; protein; 421 AA.
DE Human PRO polypeptide #557.
PN WO2004043361-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 43.0%; Score 40; DB 8; Length 421;
Best Local Similarity 44.4%; Pred. No. 5e+02;
RESULT 774
ID ABP93229 standard; protein; 430 AA.
DE Orthostomycin biosynthetic polypeptide SEQ ID NO 45.
PN WO200279505-A2.
PD 10-OCT-2002.
PA (SCOP-) ECOPIA BIOSCIENCES INC.
Query Match 43.0%; Score 40; DB 6; Length 430;
Best Local Similarity 58.3%; Pred. No. 5.2e+02;
RESULT 775
ID ABP76709 standard; protein; 430 AA.
DE Streptomyces viridochromogenes AviGrl.
PN WO200268436-A1.
PD 06-SEP-2002.
PA (COMB-) COMBINATURE BIOPHARM AG.
Query Match 43.0%; Score 40; DB 6; Length 430;
Best Local Similarity 58.3%; Pred. No. 5.2e+02;
RESULT 776
ID ABR39814 standard; protein; 600 AA.
DE Human SCAP polypeptide-Incyte Id. 3363254CD1.
PN WO2003008625-A2.
PD 30-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 43.0%; Score 40; DB 6; Length 600;
Best Local Similarity 44.4%; Pred. No. 7.5e+02;
RESULT 777
ID ADR5983 standard; protein; 600 AA.
DE Human Elk1 phosphorylation/Elk1 kinase activation protein - SEQ ID 86.
PN WO2004072277-A2.
PD 26-AUG-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 43.0%; Score 40; DB 8; Length 600;
Best Local Similarity 44.4%; Pred. No. 7.5e+02;
RESULT 778
ID ASG20261 standard; protein; 633 AA.
DE Novel human diagnostic protein #20252.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 43.0%; Score 40; DB 4; Length 633;
Best Local Similarity 58.3%; Pred. No. 8e+02;
RESULT 779
ID ABG72972 standard; protein; 735 AA.
DE Lactococcus raffinolactis alpha-galactosidase.
PN WO200281674-A1.

PD 17-OCT-2002.
PA (UYLA-) UNIV LAVAL.
Query Match 43.0%; Score 40; DB 6; Length 735;
Best Local Similarity 66.7%; Pred. No. 9.5e+02;
RESULT 780
ID ADH22524 standard; protein; 971 AA.
DE Human transporter & ion channel (TRICH) protein SeqID22.
PN WO2003093444-A2.
PD 13-NOV-2003.
PA (INCY-) INCYTE CORP.
Query Match 43.0%; Score 40; DB 8; Length 971;
Best Local Similarity 58.8%; Pred. No. 1.3e+03;
RESULT 781
ID ADZ80808 standard; protein; 1500 AA.
DE Amino acid sequence of human homologue of Drosophila gene CG1886.
PN WO2005039635-A2.
PD 06-MAY-2005.
PA (NOVS) NOVARTIS PHARMA GMBH.
Query Match 43.0%; Score 40; DB 9; Length 1500;
Best Local Similarity 58.8%; Pred. No. 2.1e+03;
RESULT 782
ID AEB28167 standard; protein; 1500 AA.
DE Human MNK protein.
PN WO2005062055-A2.
PD 07-JUL-2005.
PA (CANC-) CANCER RES TECHNOLOGY LTD.
Query Match 43.0%; Score 40; DB 9; Length 1500;
Best Local Similarity 58.8%; Pred. No. 2.1e+03;
RESULT 783
ID AEB86597 standard; protein; 1581 AA.
DE Human copper transporting ATPase ATP7A.
PN WO2005075632-A2.
PD 18-AUG-2005.
PA (CELL-) CELLZOME AG.
Query Match 43.0%; Score 40; DB 9; Length 1581;
Best Local Similarity 58.8%; Pred. No. 2.3e+03;
RESULT 784
ID AAY27134 standard; protein; 1591 AA.
DE Human munc13 (Hmunc13) polypeptide.
PN WO9931134-A1.
PD 24-JUN-1999.
PA (SILV/) SILVERMAN M.
PA (SONG/) SONG Y.
Query Match 43.0%; Score 40; DB 2; Length 1591;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
RESULT 785
ID AAE14921 standard; protein; 1591 AA.
DE Human ubiquitous Munc13-2 protein mutant (W376R).
PN WO2003039441-A2.
PD 15-MAY-2003.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 43.0%; Score 40; DB 6; Length 1591;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
RESULT 786
ID AAE14911 standard; protein; 1591 AA.
DE Mouse ubiquitous Munc13-2 protein.
PN WO2003039441-A2.
PD 15-MAY-2003.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 43.0%; Score 40; DB 6; Length 1591;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
RESULT 787
ID AAE14912 standard; protein; 1591 AA.
DE Human ubiquitous Munc13-2 protein.
PN WO2003039441-A2.
PD 15-MAY-2003.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 43.0%; Score 40; DB 6; Length 1591;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
RESULT 788
ID ADJ68886 standard; protein; 1591 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID692.

PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 43.0%; Score 40; DB 7; Length 1591;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
RESULT 798
ID AAE14913 standard; protein; 1622 AA.
DE Rat ubiquitous Munc13-2 protein.
PN WO2003039441-A2.
PD 15-MAY-2003.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 43.0%; Score 40; DB 6; Length 1622;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
RESULT 799
ID AAE14922 standard; protein; 1622 AA.
DE Rat ubiquitous Munc13-2 protein mutant (W387R).
PN WO2003039441-A2.
PD 15-MAY-2003.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 43.0%; Score 40; DB 6; Length 1622;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
RESULT 791
ID AAE14914 standard; protein; 1985 AA.
DE Rat brain-specific Munc13-2 protein.
PN WO2003039441-A2.
PD 15-MAY-2003.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 43.0%; Score 40; DB 6; Length 1985;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
RESULT 792
ID ABP76679 standard; protein; 1938 AA.
DE Streptomyces viridochromogenes Avi Gene cluster polypeptide frame 3.
PN WO200268436-A1.
PD 06-SEP-2002.
PA (COMB-) COMBINATURE BIOPHARM AG.
Query Match 43.0%; Score 40; DB 6; Length 1938;
Best Local Similarity 58.3%; Pred. No. 4e+04;
RESULT 793
ID AAU61252 standard; protein; 87 AA.
DE Propionibacterium acnes immunogenic protein #22148.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 41.9%; Score 39; DB 4; Length 87;
Best Local Similarity 43.8%; Pred. No. 1.2e+02;
RESULT 794
ID ABW57771 standard; protein; 87 AA.
DE Propionibacterium acnes Predicted ORF-encoded polypeptide #22447.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 41.9%; Score 39; DB 6; Length 87;
Best Local Similarity 43.8%; Pred. No. 1.2e+02;
RESULT 795
ID ADT58157 standard; protein; 114 AA.
DE Plant polypeptide, SEQ ID 8234.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 41.9%; Score 39; DB 8; Length 114;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
RESULT 796
ID ABW58677 standard; protein; 152 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 2823.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 41.9%; Score 39; DB 4; Length 152;
Best Local Similarity 41.2%; Pred. No. 2.4e+02;
RESULT 797
ID ABU00656 standard; protein; 165 AA.
DE S. pneumoniae type 4 strain protein from coding region #223.

PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 41.9%; Score 39; DB 6; Length 165;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
RESULT 798
ID ABU44451 standard; protein; 198 AA.
DE Protein encoded by Prokaryotic essential gene #29978.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 41.9%; Score 39; DB 6; Length 198;
Best Local Similarity 61.5%; Pred. No. 3.2e+02;
RESULT 799
ID AAU36069 standard; protein; 215 AA.
DE Klebsiella pneumoniae cellular proliferation protein #57.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 41.9%; Score 39; DB 4; Length 215;
Best Local Similarity 43.8%; Pred. No. 3.5e+02;
RESULT 800
ID AAU38623 standard; protein; 238 AA.
DE S. pneumoniae BSCELABCD NCBI gi: 895746.
PN WO9743303-A1.
PD 20-NOV-1997.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 41.9%; Score 39; DB 2; Length 238;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
RESULT 801
ID ABU31150 standard; protein; 266 AA.
DE Protein encoded by Prokaryotic essential gene #16677.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 41.9%; Score 39; DB 6; Length 266;
Best Local Similarity 43.8%; Pred. No. 4.4e+02;
RESULT 802
ID AAY93593 standard; protein; 268 AA.
DE Amino acid sequence of a human phosphodiesterase enzyme.
PN EP1018559-A1.
PD 12-JUL-2000.
PA (PFIZ) PFIZER LTD.
Query Match 41.9%; Score 39; DB 3; Length 268;
Best Local Similarity 63.6%; Pred. No. 4.5e+02;
RESULT 803
ID ABU45046 standard; protein; 271 AA.
DE Protein encoded by Prokaryotic essential gene #30573.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 41.9%; Score 39; DB 6; Length 271;
Best Local Similarity 43.8%; Pred. No. 4.5e+02;
RESULT 804
ID AEB06770 standard; protein; 277 AA.
DE E. coli xanthosine phosphorolysis enzyme SEQ ID NO:10.
PN JP2005151962-A.
PD 16-JUN-2005.
PA (KOKU-) KOKURITSU DAIGAKU HOJIN NARA SENTAN KAGA.
Query Match 41.9%; Score 39; DB 9; Length 277;
Best Local Similarity 54.5%; Pred. No. 4.6e+02;
RESULT 805
ID AAY93568 standard; protein; 288 AA.
DE Amino acid sequence of a human phosphodiesterase enzyme.
PN EP1018559-A1.
PD 12-JUL-2000.
PA (PFIZ) PFIZER LTD.
Query Match 41.9%; Score 39; DB 3; Length 288;
Best Local Similarity 63.6%; Pred. No. 4.9e+02;

RESULT 806
ID ABG25942 standard; protein; 300 AA.
DE Novel human diagnostic protein #25933.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 41.9%; Score 39; DB 4; Length 300;
Best Local Similarity 54.5%; Pred. No. 5.1e+02;
RESULT 807
ID AAB36504 standard; protein; 320 AA.
DE Human short phosphodiesterase protein SEQ ID NO:3.
PN US6146876-A.
PD 14-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 41.9%; Score 39; DB 4; Length 320;
Best Local Similarity 63.6%; Pred. No. 5.5e+02;
RESULT 808
ID ADJ58906 standard; protein; 320 AA.
DE Human cyclic nucleotide phosphodiesterase protein #2.
PN US2004006016-A1.
PD 08-JAN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 41.9%; Score 39; DB 8; Length 320;
Best Local Similarity 63.6%; Pred. No. 5.5e+02;
RESULT 809
ID ABB67466 standard; protein; 328 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 29190.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 41.9%; Score 39; DB 4; Length 328;
Best Local Similarity 57.1%; Pred. No. 5.6e+02;
RESULT 810
ID ADY50214 standard; protein; 335 AA.
DE Human PDE7B phosphodiesterase domain SEQ ID NO:23.
PN US2005048573-A1.
PD 03-MAR-2005.
PA (PLEX-) PLEXKIXON INC.
Query Match 41.9%; Score 39; DB 9; Length 335;
Best Local Similarity 63.6%; Pred. No. 5.8e+02;
RESULT 811
ID ADZ46770 standard; protein; 335 AA.
DE Human PDE7B phosphodiesterase domain, SEQ ID NO: 23.
PN US2005079548-A1.
PD 14-APR-2005.
PA (PLEX-) PLEXKIXON INC.
Query Match 41.9%; Score 39; DB 9; Length 335;
Best Local Similarity 63.6%; Pred. No. 5.8e+02;
RESULT 812
ID AAY86040 standard; protein; 341 AA.
DE S. pneumoniae derived protein #249.
PN W09806734-A1.
PD 19-FEB-1998.
PA (SMIK-) SMITHKLINE BEECHAM CORP.
Query Match 41.9%; Score 39; DB 2; Length 341;
Best Local Similarity 50.0%; Pred. No. 5.9e+02;
RESULT 813
ID AAU08676 standard; protein; 391 AA.
DE Human phosphodiesterase type 7B #2.
PN W0200162940-A2.
PD 30-AUG-2001.
PA (MERE-) MERCK PATENT GMBH.
Query Match 41.9%; Score 39; DB 4; Length 391;
Best Local Similarity 63.6%; Pred. No. 6.9e+02;
RESULT 814
ID AAY93569 standard; protein; 450 AA.
DE Amino acid sequence of a human phosphodiesterase enzyme.
PN EP1018559-A1.
PD 12-JUL-2000.
PA (PFIZ-) PFIZER LTD.
PA (PFIZ-) PFIZER INC.
Query Match 41.9%; Score 39; DB 3; Length 450;
Best Local Similarity 63.6%; Pred. No. 8.1e+02;
RESULT 815
ID AAU08675 standard; protein; 450 AA.
DE Human phosphodiesterase type 7B #1.
PN W0200162940-A2.
PD 30-AUG-2001.
PA (MERE-) MERCK PATENT GMBH.
Query Match 41.9%; Score 39; DB 4; Length 450;
Best Local Similarity 63.6%; Pred. No. 8.1e+02;
RESULT 816
ID AAG78915 standard; protein; 450 AA.
DE Human type 7B phosphodiesterase, PDE7B.
PN JP2001238680-A.
PD 04-SEP-2001.
PA (TANA-) TANABE SEIYAKU CO.
Query Match 41.9%; Score 39; DB 4; Length 450;
Best Local Similarity 63.6%; Pred. No. 8.1e+02;
RESULT 817
ID ADP79549 standard; protein; 450 AA.
DE Human phosphodiesterase 7B nucleotide sequence.
PN W02004044196-A1.
PD 27-MAY-2004.
PA (FARB-) BAYER HEALTHCARE AG.
Query Match 41.9%; Score 39; DB 8; Length 450;
Best Local Similarity 63.6%; Pred. No. 8.1e+02;
RESULT 818
ID AAB36503 standard; protein; 502 AA.
DE Human long phosphodiesterase protein SEQ ID NO:1.
PN US6146876-A.
PD 14-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 41.9%; Score 39; DB 4; Length 502;
Best Local Similarity 63.6%; Pred. No. 9.1e+02;
RESULT 819
ID ABB03005 standard; protein; 502 AA.
DE Human phosphodiesterase-1.
PN W0200198471-A2.
PD 27-DEC-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 41.9%; Score 39; DB 5; Length 502;
Best Local Similarity 63.6%; Pred. No. 9.1e+02;
RESULT 820
ID ADJ58904 standard; protein; 502 AA.
DE Human cyclic nucleotide phosphodiesterase protein #1.
PN US2004006016-A1.
PD 08-JAN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 41.9%; Score 39; DB 8; Length 502;
Best Local Similarity 63.6%; Pred. No. 9.1e+02;
RESULT 821
ID ADX65729 standard; protein; 518 AA.
DE Plant full length insert polypeptide seqid 36572.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ-) LIU J.
PA (ZHOU-) ZHOU Y.
PA (KOVA-) KOVALIC D K.
PA (SCRE-) SCREEN S E.
PA (TABA-) TABASKA J E.
PA (CAOY-) CAO Y.
Query Match 41.9%; Score 39; DB 8; Length 518;
Best Local Similarity 52.9%; Pred. No. 9.5e+02;
RESULT 822
ID ADS42354 standard; protein; 524 AA.
DE Bacterial polypeptide #20784.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY-) CAO Y.
PA (HINK-) HINKLE G J.
PA (SLAT-) SLATER S C.
PA (CHEN-) CHEN X.
PA (GOLD-) GOLDMAN B S.
Query Match 41.9%; Score 39; DB 8; Length 524;
Best Local Similarity 54.5%; Pred. No. 9.6e+02;

RESULT 823
ID ADR21971 standard; protein; 576 AA.
DE Bacterial polypeptide #11004.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 41.9%; Score 39; DB 8; Length 576;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
RESULT 824
ID ADK47528 standard; protein; 659 AA.
DE Streptococcus pneumoniae protein, Seq ID No 4043.
PN US6699703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 41.9%; Score 39; DB 8; Length 659;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 825
ID ADR95065 standard; protein; 661 AA.
DE Novel S. pneumoniae protein sequence, Seq ID 3700.
PN US6800744-B1.
PD 05-OCT-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 41.9%; Score 39; DB 8; Length 661;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 826
ID ABA58935 standard; protein; 661 AA.
DE Streptococcus pneumoniae ORF amino acid sequence Seq ID NO:3700.
PN US2005136404-A1.
PD 23-JUN-2005.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 41.9%; Score 39; DB 9; Length 661;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 827
ID ADX87416 standard; protein; 739 AA.
DE Plant full length insert polypeptide seqid 50080.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 41.9%; Score 39; DB 8; Length 739;
Best Local Similarity 37.5%; Pred. No. 1.4e+03;
RESULT 828
ID ABM84355 standard; protein; 810 AA.
DE Human diagnostic and therapeutic pprotein Seq ID NO:4604.
PN W02004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 41.9%; Score 39; DB 8; Length 810;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
RESULT 829
ID ABM84354 standard; protein; 810 AA.
DE Human diagnostic and therapeutic pprotein Seq ID NO:4603.
PN W02004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 41.9%; Score 39; DB 8; Length 810;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
RESULT 830
ID ADT56766 standard; protein; 999 AA.
DE Plant polypeptide, Seq ID 6843.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 41.9%; Score 39; DB 8; Length 999;

Best Local Similarity 52.9%; Pred. No. 2e+03;
RESULT 831
ID AAY58717 standard; protein; 1001 AA.
DE Arabidopsis ran1-1 mutant protein.
PN W0200004760-A1.
PD 03-FEB-2000.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 41.9%; Score 39; DB 3; Length 1001;
Best Local Similarity 52.9%; Pred. No. 2e+03;
RESULT 832
ID AAY58677 standard; protein; 1001 AA.
DE Arabidopsis ran1 copper transporter.
PN W0200004760-A1.
PD 03-FEB-2000.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 41.9%; Score 39; DB 3; Length 1001;
Best Local Similarity 52.9%; Pred. No. 2e+03;
RESULT 833
ID AAY58718 standard; protein; 1001 AA.
DE Arabidopsis ran1-2 mutant protein.
PN W0200004760-A1.
PD 03-FEB-2000.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 41.9%; Score 39; DB 3; Length 1001;
Best Local Similarity 52.9%; Pred. No. 2e+03;
RESULT 834
ID ABP9398 standard; protein; 1001 AA.
DE Arabidopsis thaliana polypeptide Seq ID NO 81.
PN W0200266660-A2.
PD 29-AUG-2002.
PA (META-) METANOMICS GMBH & CO KGAA.
Query Match 41.9%; Score 39; DB 5; Length 1001;
Best Local Similarity 52.9%; Pred. No. 2e+03;
RESULT 835
ID ADJ70318 standard; protein; 1328 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID2124.
PN W02003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 41.9%; Score 39; DB 7; Length 1328;
Best Local Similarity 64.3%; Pred. No. 2.8e+03;
RESULT 836
ID ABP27518 standard; protein; 1368 AA.
DE Streptococcus polypeptide Seq ID NO 4212.
PN W0200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 41.9%; Score 39; DB 5; Length 1368;
Best Local Similarity 33.3%; Pred. No. 2.8e+03;
RESULT 837
ID AAR72343 standard; protein; 1411 AA.
DE Wilson disease protein ATP7B.
PN W09508641-A1.
PD 30-MAR-1995.
PA (HSCR-) HSC RES & DEV LP.
Query Match 41.9%; Score 39; DB 2; Length 1411;
Best Local Similarity 64.3%; Pred. No. 2.9e+03;
RESULT 838
ID AAR70419 standard; protein; 1456 AA.
DE Rat homologue of human Wilson disease gene ATP7B.
PN W09508641-A1.
PD 30-MAR-1995.
PA (HSCR-) HSC RES & DEV LP.
Query Match 41.9%; Score 39; DB 2; Length 1456;
Best Local Similarity 64.3%; Pred. No. 3.1e+03;
RESULT 839
ID ABB86598 standard; protein; 1464 AA.
DE Human copper transporting ATPase ATP7B.
PN W02005075632-A2.
PD 18-AUG-2005.
PA (CELL-) CELLZOME AG.

Query Match 41.9%; Score 39; DB 9; Length 1464;
Best Local Similarity 64.3%; Pred. No. 3.1e+03;
RESULT 840
ID AAV71957 standard; protein; 1513 AA.
DE Human bone marrow tissue polypeptide #35.
PN WO200179447-A2.
PD 25-OCT-2001.
PA (HY8E-) HYSEQ INC.
Query Match 41.9%; Score 39; DB 4; Length 1513;
Best Local Similarity 64.3%; Pred. No. 3.2e+03;
RESULT 841
ID ABB65616 standard; protein; 2271 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23640.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 41.9%; Score 39; DB 4; Length 2271;
Best Local Similarity 63.6%; Pred. No. 5.1e+03;
RESULT 842
ID AAU75351 standard; protein; 2291 AA.
DE Drosophila Rotkehlchen, ROT, protein.
PN WO200200864-A2.
PD 03-JAN-2002.
PA (AVET-) AVENTIS CROPSOURCE GMBH.
Query Match 41.9%; Score 39; DB 5; Length 2291;
Best Local Similarity 63.6%; Pred. No. 5.1e+03;
RESULT 843
ID AAU33909 standard; protein; 346 AA.
DE Staphylococcus aureus cellular proliferation protein #185.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 41.4%; Score 38.5; DB 4; Length 346;
Best Local Similarity 34.6%; Pred. No. 7.3e+02;
RESULT 844
ID ADG48173 standard; protein; 355 AA.
DE Staphylococcus aureus COL fabK protein.
PN US6613553-B1.
PD 02-SEP-2003.
PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
Query Match 41.4%; Score 38.5; DB 7; Length 355;
Best Local Similarity 34.6%; Pred. No. 7.5e+02;
RESULT 845
ID ADG48213 standard; protein; 355 AA.
DE Staphylococcus aureus fabK protein.
PN US6613553-B1.
PD 02-SEP-2003.
PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
Query Match 41.4%; Score 38.5; DB 7; Length 355;
Best Local Similarity 34.6%; Pred. No. 7.5e+02;
RESULT 846
ID AAU36919 standard; protein; 388 AA.
DE Staphylococcus aureus cellular proliferation protein #1089.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 41.4%; Score 38.5; DB 4; Length 388;
Best Local Similarity 34.6%; Pred. No. 8.3e+02;
RESULT 847
ID ABM72178 standard; protein; 390 AA.
DE Staphylococcus aureus protein #1418.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 41.4%; Score 38.5; DB 6; Length 390;
Best Local Similarity 34.6%; Pred. No. 8.3e+02;
RESULT 848
ID AAH89800 standard; protein; 393 AA.
DE Staphylococcus aureus protein SEQ ID #5248.
PN EP786519-A2.
PD 30-JUL-1997.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 41.4%; Score 38.5; DB 2; Length 393;

Best Local Similarity 34.6%; Pred. No. 8.4e+02;
RESULT 849
ID ABB65474 standard; protein; 438 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23214.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 41.4%; Score 38.5; DB 4; Length 438;
Best Local Similarity 55.6%; Pred. No. 9.5e+02;
RESULT 850
ID AAU12171 standard; peptide; 15 AA.
DE Human NPAT protein 12 N-terminal sequence.
PN WO200194402-A1.
PD 13-DEC-2001.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Query Match 40.9%; Score 38; DB 5; Length 15;
Best Local Similarity 75.0%; Pred. No. 25;
RESULT 851
ID AAY59902 standard; protein; 70 AA.
DE Human normal pancreas tissue derived protein 10.
PN DE19818598-A1.
PD 21-OCT-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match 40.9%; Score 38; DB 2; Length 70;
Best Local Similarity 41.7%; Pred. No. 1.4e+02;
RESULT 852
ID AAY59907 standard; protein; 70 AA.
DE Human normal pancreas tissue derived protein 15.
PN DE19818598-A1.
PD 21-OCT-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match 40.9%; Score 38; DB 2; Length 70;
Best Local Similarity 41.7%; Pred. No. 1.4e+02;
RESULT 853
ID AAY59914 standard; protein; 70 AA.
DE Human normal pancreas tissue derived protein 22.
PN DE19818598-A1.
PD 21-OCT-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match 40.9%; Score 38; DB 2; Length 70;
Best Local Similarity 41.7%; Pred. No. 1.4e+02;
RESULT 854
ID ADP07825 standard; protein; 84 AA.
DE Human secreted protein, seq id 308.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 40.9%; Score 38; DB 8; Length 84;
Best Local Similarity 60.0%; Pred. No. 1.8e+02;
RESULT 855
ID AAY11056 standard; protein; 100 AA.
DE H. pylori ORF hp2el0911_24804577_c3_104 cellular protein.
PN WO9824475-A1.
PD 11-JUN-1998.
PA (ASTR-) ASTRA AB.
Query Match 40.9%; Score 38; DB 2; Length 100;
Best Local Similarity 31.2%; Pred. No. 2.2e+02;
RESULT 856
ID AAU74692 standard; protein; 110 AA.
DE Human NPAT protein 12.
PN WO200194402-A1.
PD 13-DEC-2001.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Query Match 40.9%; Score 38; DB 5; Length 110;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
RESULT 857
ID ADC24809 standard; protein; 140 AA.
DE Human breast specific polypeptide (BSP) DEX0238_130, SEQ ID NO:130.
PN WO2003020900-A2.
PD 13-MAR-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 40.9%; Score 38; DB 7; Length 140;
Best Local Similarity 54.5%; Pred. No. 3.2e+02;

RESULT 858
ID ADQ65969 standard; protein; 140 AA.
DE Novel human protein sequence #942.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 40.9%; Score 38; DB 8; Length 140;
Best Local Similarity 63.6%; Pred. No. 3.2e+02;
RESULT 859
ID ADR99381 standard; protein; 142 AA.
DE Chlamydia pneumoniae protein #13 for treating Chlamydia infections.
PN W02004074318-A2.
PD 02-SEP-2004.
PA (INSP) INST PASTEUR.
PA (CNRS) CENT NAT RECH SCI.
Query Match 40.9%; Score 38; DB 8; Length 142;
Best Local Similarity 47.1%; Pred. No. 3.2e+02;
RESULT 860
ID ADQ08608 standard; protein; 173 AA.
DE Clona intestinalis nervous system associated protein SeqID10.
PN JP2004057127-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 40.9%; Score 38; DB 8; Length 173;
Best Local Similarity 40.0%; Pred. No. 4e+02;
RESULT 861
ID ADJ48525 standard; protein; 178 AA.
DE Oil-associated gene related protein #25.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 40.9%; Score 38; DB 8; Length 178;
Best Local Similarity 46.7%; Pred. No. 4.2e+02;
RESULT 862
ID AAG19526 standard; protein; 215 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 21361.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 40.9%; Score 38; DB 3; Length 215;
Best Local Similarity 61.5%; Pred. No. 5.2e+02;
RESULT 863
ID AAU43540 standard; protein; 217 AA.
DE Propionibacterium acnes immunogenic protein #4436.
PN W0200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 40.9%; Score 38; DB 4; Length 217;
Best Local Similarity 33.3%; Pred. No. 5.2e+02;
RESULT 864
ID AEM40059 standard; protein; 217 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #4735.
PN W02003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 40.9%; Score 38; DB 6; Length 217;
Best Local Similarity 33.3%; Pred. No. 5.2e+02;
RESULT 865
ID ADH61297 standard; protein; 270 AA.
DE INTSIG protein 7519192CD1, SEQ ID 14.
PN W02004001005-A2.
PD 31-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match 40.9%; Score 38; DB 8; Length 270;
Best Local Similarity 54.5%; Pred. No. 6.7e+02;
RESULT 866
ID AAV35206 standard; protein; 291 AA.
DE Chlamydia pneumoniae transmembrane protein sequence.
PN W09927103-A2.
PD 03-JUN-1999.

PA (GEST) GENSET.
Query Match 40.9%; Score 38; DB 2; Length 291;
Best Local Similarity 47.1%; Pred. No. 7.3e+02;
RESULT 867
ID AAG54677 standard; protein; 296 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 69755.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 40.9%; Score 38; DB 3; Length 296;
Best Local Similarity 58.3%; Pred. No. 7.4e+02;
RESULT 868
ID ABU17283 standard; protein; 302 AA.
DE Protein encoded by Prokaryotic essential gene #2810.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 40.9%; Score 38; DB 6; Length 302;
Best Local Similarity 77.8%; Pred. No. 7.6e+02;
RESULT 869
ID ASG18959 standard; protein; 325 AA.
DE Novel human diagnostic protein #18950.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 40.9%; Score 38; DB 4; Length 325;
Best Local Similarity 41.2%; Pred. No. 8.3e+02;
RESULT 870
ID ADY50213 standard; protein; 334 AA.
DE Human PDE7A phosphodiesterase domain SEQ ID NO:22.
PN US2005048573-A1.
PD 03-MAR-2005.
PA (PLEX-) PLEXIKON INC.
Query Match 40.9%; Score 38; DB 9; Length 334;
Best Local Similarity 54.5%; Pred. No. 8.5e+02;
RESULT 871
ID ADZ46769 standard; protein; 334 AA.
DE Human PDE7A phosphodiesterase domain, SEQ ID NO: 22.
PN US2005079548-A1.
PD 14-APR-2005.
PA (PLEX-) PLEXIKON INC.
Query Match 40.9%; Score 38; DB 9; Length 334;
Best Local Similarity 54.5%; Pred. No. 8.5e+02;
RESULT 872
ID ABB07912 standard; protein; 336 AA.
DE Human PDE7a3 splice variant polypeptide.
PN W0200183772-A1.
PD 08-NOV-2001.
PA (MERE) MERCK PATENT GMBH.
Query Match 40.9%; Score 38; DB 5; Length 336;
Best Local Similarity 54.5%; Pred. No. 8.6e+02;
RESULT 873
ID AAR54070 standard; protein; 339 AA.
DE Prod. of gene participating in homologous recombination.
PN JP06141863-A.
PD 24-MAY-1994.
PA (MORI/) MORITA T.
PA (MATS/) MATSUSHIRO A.
Query Match 40.9%; Score 38; DB 2; Length 339;
Best Local Similarity 53.3%; Pred. No. 8.7e+02;
RESULT 874
ID AAR78183 standard; protein; 339 AA.
DE Human RAD51 protein, involved in DNA repair.
PN JP07143890-A.
PD 06-JUN-1995.
PA (TOYM) TOYOBO KK.
Query Match 40.9%; Score 38; DB 2; Length 339;
Best Local Similarity 53.3%; Pred. No. 8.7e+02;
RESULT 875
ID AAR78181 standard; protein; 339 AA.
DE Mouse RAD51 protein, involved in DNA repair and recombination.
PN JP07143890-A.
PD 06-JUN-1995.
PA (TOYM) TOYOBO KK.

Query Match 40.9%; Score 38; DB 2; Length 339;
Best Local Similarity 53.3%; Pred. No. 8.7e+02;
RESULT 876
ID AAW62523 standard; peptide; 339 AA.
DE Sequence of the specification.
PN WO9820030-A2.
PD 14-MAY-1998.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 40.9%; Score 38; DB 2; Length 339;
Best Local Similarity 53.3%; Pred. No. 8.7e+02;
RESULT 877
ID AAW62522 standard; peptide; 339 AA.
DE Sequence of the specification.
PN WO9820030-A2.
PD 14-MAY-1998.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 40.9%; Score 38; DB 2; Length 339;
Best Local Similarity 53.3%; Pred. No. 8.7e+02;
RESULT 878
ID AAY87918 standard; protein; 339 AA.
DE Human Rad51 protein.
PN US6057104-A.
PD 02-MAY-2000.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 40.9%; Score 38; DB 3; Length 339;
Best Local Similarity 53.3%; Pred. No. 8.7e+02;
RESULT 879
ID AAY87917 standard; protein; 339 AA.
DE Mammalian Rad51 protein.
PN US6057104-A.
PD 02-MAY-2000.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 40.9%; Score 38; DB 3; Length 339;
Best Local Similarity 53.3%; Pred. No. 8.7e+02;
RESULT 880
ID ABB07642 standard; protein; 339 AA.
DE Human RAD51 protein sequence.
PN WO200208432-A2.
PD 31-JAN-2002.
PA (RHOB-) RHOBIO.
Query Match 40.9%; Score 38; DB 5; Length 339;
Best Local Similarity 53.3%; Pred. No. 8.7e+02;
RESULT 881
ID ADK67821 standard; protein; 339 AA.
DE Human RAD51 polypeptide.
PN WO2004012755-A1.
PD 12-FEB-2004.
PA (WIST-) WISTAR INST.
Query Match 40.9%; Score 38; DB 8; Length 339;
Best Local Similarity 53.3%; Pred. No. 8.7e+02;
RESULT 882
ID ADQ07009 standard; protein; 339 AA.
DE Mouse Rad51 protein SEQ ID NO:2.
PN JP2004173512-A.
PD 24-JUN-2004.
PA (MORI/) MORITA T.
Query Match 40.9%; Score 38; DB 8; Length 339;
Best Local Similarity 53.3%; Pred. No. 8.7e+02;
RESULT 883
ID ADQ07011 standard; protein; 339 AA.
DE Human Rad51 protein SEQ ID NO:4.
PN JP2004173512-A.
PD 24-JUN-2004.
PA (MORI/) MORITA T.
Query Match 40.9%; Score 38; DB 8; Length 339;
Best Local Similarity 53.3%; Pred. No. 8.7e+02;
RESULT 884
ID ADY15466 standard; protein; 339 AA.
DE PRO polypeptide SEQ ID NO 1272.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 40.9%; Score 38; DB 9; Length 339;
Best Local Similarity 53.3%; Pred. No. 8.7e+02;
RESULT 885
ID ADZ09769 standard; protein; 339 AA.
DE Human breast cancer marker RAD51 protein.
PN EP152594-A2.
PD 13-APR-2005.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 40.9%; Score 38; DB 9; Length 339;
Best Local Similarity 53.3%; Pred. No. 8.7e+02;
RESULT 886
ID ADQ67649 standard; protein; 340 AA.
DE Novel human protein sequence #2315.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 40.9%; Score 38; DB 8; Length 340;
Best Local Similarity 53.3%; Pred. No. 8.7e+02;
RESULT 887
ID ADR46211 standard; protein; 354 AA.
DE Human phosphodiesterase 7A truncation polypeptide 2.
PN WO2004069989-A2.
PD 19-AUG-2004.
PA (AFFI-) AFFINIUM PHARM INC.
Query Match 40.9%; Score 38; DB 8; Length 354;
Best Local Similarity 54.5%; Pred. No. 9.1e+02;
RESULT 888
ID ADR46209 standard; protein; 359 AA.
DE Human phosphodiesterase 7A truncation polypeptide 1.
PN WO2004069989-A2.
PD 19-AUG-2004.
PA (AFFI-) AFFINIUM PHARM INC.
Query Match 40.9%; Score 38; DB 8; Length 359;
Best Local Similarity 54.5%; Pred. No. 9.3e+02;
RESULT 889
ID ABU01155 standard; protein; 361 AA.
DE S. pneumoniae type 4 strain protein from coding region #728.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 40.9%; Score 38; DB 6; Length 361;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
RESULT 890
ID AAG19525 standard; protein; 363 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 21360.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 40.9%; Score 38; DB 3; Length 363;
Best Local Similarity 61.5%; Pred. No. 9.4e+02;
RESULT 891
ID ADX88971 standard; protein; 365 AA.
DE Plant full length insert polypeptide seqid 51635.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J B.
PA (CAOV/) CAO Y.
Query Match 40.9%; Score 38; DB 8; Length 365;
Best Local Similarity 52.9%; Pred. No. 9.4e+02;
RESULT 892
ID ADR66273 standard; protein; 368 AA.
DE Human prostatic carcinoma derived protein SEQ ID 127 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 40.9%; Score 38; DB 8; Length 368;
Best Local Similarity 53.3%; Pred. No. 8.7e+02;
RESULT 893
ID AAW62523 standard; peptide; 339 AA.
DE Sequence of the specification.
PN WO9820030-A2.
PD 14-MAY-1998.
PA (LEXI-) LEXICON GENETICS INC.

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Best Local Similarity 70.0%; Pred. No. 9.5e+02;
ID ADR6834 standard; protein; 368 AA.
DE Human prostatic carcinoma derived DNA SEQ ID 127 #4.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ//) HINZMANN B.
PA (DAHL//) DAHL E.
PA (ROSE//) ROSENTHAL A.
PA (HERM//) HERMANN K.
PA (PILA//) PILARSKY C.
Query Match 40.9%; Score 38; DB 8; Length 368;
Best Local Similarity 70.0%; Pred. No. 9.5e+02;
ID ADK16327 standard; protein; 369 AA.
DE Nanoarchaeum equitans cancer-associated (CA) protein #139.
PN WO2003093434-A2.
PD 13-NOV-2003.
PA (DIVE-) DIVERSA CORP.
Query Match 40.9%; Score 38; DB 8; Length 369;
Best Local Similarity 63.6%; Pred. No. 9.5e+02;
ID ADN42042 standard; protein; 369 AA.
DE Amino acid sequence of human polypeptide #8.
PN WO2004033686-A1.
PD 22-APR-2004.
PA (TAKED) TAKEDA CHEM IND LTD.
Query Match 40.9%; Score 38; DB 8; Length 369;
Best Local Similarity 63.6%; Pred. No. 9.5e+02;
ID ADN42014 standard; protein; 370 AA.
DE Amino acid sequence of human polypeptide #1.
PN WO2004033686-A1.
PD 22-APR-2004.
PA (TAKED) TAKEDA CHEM IND LTD.
Query Match 40.9%; Score 38; DB 8; Length 370;
Best Local Similarity 63.6%; Pred. No. 9.6e+02;
ID AAG19524 standard; protein; 378 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 21359.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 40.9%; Score 38; DB 3; Length 378;
Best Local Similarity 61.5%; Pred. No. 9.8e+02;
ID ADN42040 standard; protein; 380 AA.
DE Amino acid sequence of human polypeptide #7.
PN WO2004033686-A1.
PD 22-APR-2004.
PA (TAKED) TAKEDA CHEM IND LTD.
Query Match 40.9%; Score 38; DB 8; Length 380;
Best Local Similarity 63.6%; Pred. No. 9.9e+02;
ID ADN42029 standard; protein; 381 AA.
DE Amino acid sequence of human polypeptide #2.
PN WO2004033686-A1.
PD 22-APR-2004.
PA (TAKED) TAKEDA CHEM IND LTD.
Query Match 40.9%; Score 38; DB 8; Length 381;
Best Local Similarity 63.6%; Pred. No. 9.9e+02;
ID ADN42038 standard; protein; 381 AA.
DE Amino acid sequence of human polypeptide #6.
PN WO2004033686-A1.
PD 22-APR-2004.
PA (TAKED) TAKEDA CHEM IND LTD.
Query Match 40.9%; Score 38; DB 8; Length 381;
Best Local Similarity 63.6%; Pred. No. 9.9e+02;
ID ADN42030 standard; protein; 382 AA.
DE Amino acid sequence of human polypeptide #3.
PN WO2004033686-A1.
PD 22-APR-2004.
PA (TAKED) TAKEDA CHEM IND LTD.
Query Match 40.9%; Score 38; DB 8; Length 382;
Best Local Similarity 63.6%; Pred. No. 9.9e+02;
ID ADN42036 standard; protein; 383 AA.
DE Amino acid sequence of human polypeptide #5.
PN WO2004033686-A1.
PD 22-APR-2004.
PA (TAKED) TAKEDA CHEM IND LTD.
Query Match 40.9%; Score 38; DB 8; Length 383;
Best Local Similarity 63.6%; Pred. No. 1e+03;
ID ADN42031 standard; protein; 384 AA.
DE Amino acid sequence of human polypeptide #4.
PN WO2004033686-A1.
PD 22-APR-2004.
PA (TAKED) TAKEDA CHEM IND LTD.
Query Match 40.9%; Score 38; DB 8; Length 384;
Best Local Similarity 63.6%; Pred. No. 1e+03;
ID AAR88225 standard; protein; 395 AA.
DE Transcription factor BTF2 complex p44 subunit.
PN WO9529245-A2.
PD 02-NOV-1995.
PA (ASRE-) ASSOC DEV RECH EN GENETIQUE MOLECULAIRE.
Query Match 40.9%; Score 38; DB 2; Length 395;
Best Local Similarity 70.0%; Pred. No. 1e+03;
ID ADN05016 standard; protein; 395 AA.
DE Antiposrotic protein sequence #688.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 40.9%; Score 38; DB 8; Length 395;
Best Local Similarity 70.0%; Pred. No. 1e+03;
ID ADQ19648 standard; protein; 395 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2467.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 40.9%; Score 38; DB 8; Length 395;
Best Local Similarity 70.0%; Pred. No. 1e+03;
ID ADP55553 standard; protein; 395 AA.
DE Human PRO protein sequence SEQ ID NO:1529.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 40.9%; Score 38; DB 8; Length 395;
Best Local Similarity 70.0%; Pred. No. 1e+03;
ID ADC94935 standard; protein; 400 AA.
DE E. faecium protein sequence SEQ ID 4562.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 40.9%; Score 38; DB 7; Length 400;
Best Local Similarity 58.3%; Pred. No. 1e+03;
ID AAU79713 standard; protein; 424 AA.
DE Human phosphodiesterase, PDE7A3 splice variant.
PN WO200222661-A2.
PD 21-MAR-2002.
PA (BEAV/) BEAVO J A.
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PA (SEEB/) SEEBECK T.
PA (SODE/) SODERLING S H.
PA (RASC/) RASCON A.
PA (ZORA/) ZORAGHI R.
PA (KUNZ/) KUNZ S.
PA (GONG/) GONG K.
PA (GLAV/) GLAVAS N.
Query Match 40.9%; Score 38; DB 5; Length 424;
Best Local Similarity 54.5%; Pred. No. 1.1e+03;
RESULT 911
ID AAU79727 standard; protein; 424 AA.
DE Human cyclic nucleotide phosphodiesterase, PDB8A variant #3.
PN WO200222661-A2.
PD 21-MAR-2002.
PA (BEAV/) BEAVO J A.
PA (SEEB/) SEEBECK T.
PA (SODE/) SODERLING S H.
PA (RASC/) RASCON A.
PA (ZORA/) ZORAGHI R.
PA (KUNZ/) KUNZ S.
PA (GONG/) GONG K.
PA (GLAV/) GLAVAS N.
Query Match 40.9%; Score 38; DB 5; Length 424;
Best Local Similarity 54.5%; Pred. No. 1.1e+03;
RESULT 912
ID ABM83119 standard; protein; 425 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3368.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 40.9%; Score 38; DB 8; Length 425;
Best Local Similarity 54.5%; Pred. No. 1.1e+03;
RESULT 913
ID AAE24528 standard; protein; 426 AA.
DE Mouse PDE7 protein.
PN WO200226954-A2.
PD 04-APR-2002.
PA (WARN) WARNER LAMBERT CO.
Query Match 40.9%; Score 38; DB 5; Length 426;
Best Local Similarity 54.5%; Pred. No. 1.1e+03;
RESULT 914
ID AAE24527 standard; protein; 426 AA.
DE Human PDE7 protein.
PN WO200226954-A2.
PD 04-APR-2002.
PA (WARN) WARNER LAMBERT CO.
Query Match 40.9%; Score 38; DB 5; Length 426;
Best Local Similarity 54.5%; Pred. No. 1.1e+03;
RESULT 915
ID AAE24529 standard; protein; 426 AA.
DE Rat PDE7 protein.
PN WO200226954-A2.
PD 04-APR-2002.
PA (WARN) WARNER LAMBERT CO.
Query Match 40.9%; Score 38; DB 5; Length 426;
Best Local Similarity 54.5%; Pred. No. 1.1e+03;
RESULT 916
ID AAE24533 standard; protein; 428 AA.
DE Rat PDE7a protein.
PN WO200226954-A2.
PD 04-APR-2002.
PA (WARN) WARNER LAMBERT CO.
Query Match 40.9%; Score 38; DB 5; Length 428;
Best Local Similarity 54.5%; Pred. No. 1.1e+03;
RESULT 917
ID AAU16967 standard; protein; 432 AA.
DE Human novel secreted protein, SEQ ID 208.
PN WO200155441-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 40.9%; Score 38; DB 4; Length 432;
Best Local Similarity 54.5%; Pred. No. 1.1e+03;
RESULT 918
PA (SEEB/) SEEBECK T.
PA (SODE/) SODERLING S H.
PA (RASC/) RASCON A.
PA (ZORA/) ZORAGHI R.
PA (KUNZ/) KUNZ S.
PA (GONG/) GONG K.
PA (GLAV/) GLAVAS N.
Query Match 40.9%; Score 38; DB 5; Length 424;
Best Local Similarity 54.5%; Pred. No. 1.1e+03;
RESULT 911
ID AAU79727 standard; protein; 424 AA.
DE Human cyclic nucleotide phosphodiesterase, PDB8A variant #3.
PN WO200222661-A2.
PD 21-MAR-2002.
PA (BEAV/) BEAVO J A.
PA (SEEB/) SEEBECK T.
PA (SODE/) SODERLING S H.
PA (RASC/) RASCON A.
PA (ZORA/) ZORAGHI R.
PA (KUNZ/) KUNZ S.
PA (GONG/) GONG K.
PA (GLAV/) GLAVAS N.
Query Match 40.9%; Score 38; DB 5; Length 424;
Best Local Similarity 54.5%; Pred. No. 1.1e+03;
RESULT 912
ID ABM83119 standard; protein; 425 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3368.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 40.9%; Score 38; DB 8; Length 425;
Best Local Similarity 54.5%; Pred. No. 1.1e+03;
RESULT 913
ID AAE24528 standard; protein; 426 AA.
DE Mouse PDE7 protein.
PN WO200226954-A2.
PD 04-APR-2002.
PA (WARN) WARNER LAMBERT CO.
Query Match 40.9%; Score 38; DB 5; Length 426;
Best Local Similarity 54.5%; Pred. No. 1.1e+03;
RESULT 914
ID AAE24527 standard; protein; 426 AA.
DE Human PDE7 protein.
PN WO200226954-A2.
PD 04-APR-2002.
PA (WARN) WARNER LAMBERT CO.
Query Match 40.9%; Score 38; DB 5; Length 426;
Best Local Similarity 54.5%; Pred. No. 1.1e+03;
RESULT 915
ID AAE24529 standard; protein; 426 AA.
DE Rat PDE7 protein.
PN WO200226954-A2.
PD 04-APR-2002.
PA (WARN) WARNER LAMBERT CO.
Query Match 40.9%; Score 38; DB 5; Length 426;
Best Local Similarity 54.5%; Pred. No. 1.1e+03;
RESULT 916
ID AAE24533 standard; protein; 428 AA.
DE Rat PDE7a protein.
PN WO200226954-A2.
PD 04-APR-2002.
PA (WARN) WARNER LAMBERT CO.
Query Match 40.9%; Score 38; DB 5; Length 428;
Best Local Similarity 54.5%; Pred. No. 1.1e+03;
RESULT 917
ID AAU16967 standard; protein; 432 AA.
DE Human novel secreted protein, SEQ ID 208.
PN WO200155441-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 40.9%; Score 38; DB 4; Length 432;
Best Local Similarity 54.5%; Pred. No. 1.1e+03;
RESULT 918
ID ABM83118 standard; protein; 437 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3367.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 40.9%; Score 38; DB 8; Length 437;
Best Local Similarity 54.5%; Pred. No. 1.2e+03;
RESULT 919
ID ABM83121 standard; protein; 441 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3370.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 40.9%; Score 38; DB 8; Length 441;
Best Local Similarity 54.5%; Pred. No. 1.2e+03;
RESULT 920
ID ABR40577 standard; protein; 445 AA.
DE Human secreted protein #SEQ ID 327.
PN WO200268628-A1.
PD 06-SEP-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 40.9%; Score 38; DB 5; Length 445;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
RESULT 921
ID AAE24532 standard; protein; 446 AA.
DE Human PDE7A2 protein.
PN WO200226954-A2.
PD 04-APR-2002.
PA (WARN) WARNER LAMBERT CO.
Query Match 40.9%; Score 38; DB 5; Length 446;
Best Local Similarity 54.5%; Pred. No. 1.2e+03;
RESULT 922
ID AAR97669 standard; protein; 448 AA.
DE Chicken Yes proto-oncogene associated protein YAP65.
PN WO9617061-A1.
PD 06-JUN-1996.
PA (UYRQ) UNIV ROCKEFELLER.
PA (DELB-) DELBRUECK CENT MOLECULAR MEDICINE MAX.
Query Match 40.9%; Score 38; DB 2; Length 448;
Best Local Similarity 58.3%; Pred. No. 1.2e+03;
RESULT 923
ID AAE24530 standard; protein; 456 AA.
DE Mouse PDE7A2 protein.
PN WO200226954-A2.
PD 04-APR-2002.
PA (WARN) WARNER LAMBERT CO.
Query Match 40.9%; Score 38; DB 5; Length 456;
Best Local Similarity 54.5%; Pred. No. 1.2e+03;
RESULT 924
ID ADO21910 standard; protein; 456 AA.
DE Human CAMP phosphodiesterase PDE7a2 protein.
PN WO2004044223-A2.
PD 27-MAY-2004.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 40.9%; Score 38; DB 8; Length 456;
Best Local Similarity 54.5%; Pred. No. 1.2e+03;
RESULT 925
ID ADY18172 standard; protein; 456 AA.
DE PRO polypeptide SEQ ID NO 3978.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 40.9%; Score 38; DB 9; Length 456;
Best Local Similarity 54.5%; Pred. No. 1.2e+03;
RESULT 926
ID ABM83120 standard; protein; 468 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3369.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 40.9%; Score 38; DB 8; Length 468;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
RESULT 927

ID ABR40523 standard; protein; 477 AA.
 DE Human secreted protein #SSQ ID 273.
 PN WO200268628-A1.
 PD 06-SEP-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 40.9%; Score 38; DB 5; Length 477;
 Best Local Similarity 60.0%; Pred. No. 1.3e+03;
 RESULT 928
 ID AAE24531 standard; protein; 482 AA.
 DE Human PDE7A1 protein.
 PN WO200226954-A2.
 PD 04-APR-2002.
 PA (WARN) WARNER LAMBERT CO.
 Query Match 40.9%; Score 38; DB 5; Length 482;
 Best Local Similarity 54.5%; Pred. No. 1.3e+03;
 RESULT 929
 ID ADO40842 standard; protein; 482 AA.
 DE Human phosphodiesterase 7a1, PDE7a1.
 PN WO2004044235-A1.
 PD 27-MAY-2004.
 PA (FARB) BAYER HEALTHCARE AG.
 Query Match 40.9%; Score 38; DB 8; Length 482;
 Best Local Similarity 54.5%; Pred. No. 1.3e+03;
 RESULT 930
 ID ADR46207 standard; protein; 482 AA.
 DE Human phosphodiesterase 7A.
 PN WO2004069989-A2.
 PD 19-AUG-2004.
 PA (AFFI-) AFFINIUM PHARM INC.
 Query Match 40.9%; Score 38; DB 8; Length 482;
 Best Local Similarity 54.5%; Pred. No. 1.3e+03;
 RESULT 931
 ID ADY18092 standard; protein; 482 AA.
 DE PRO polypeptide SEQ ID NO 3898.
 PN WO2005016962-A2.
 PD 24-FEB-2005.
 PA (GETH) GENENTECH INC.
 Query Match 40.9%; Score 38; DB 9; Length 482;
 Best Local Similarity 54.5%; Pred. No. 1.3e+03;
 RESULT 932
 ID AAW00094 standard; protein; 498 AA.
 DE cAMP phosphodiesterase encoded by plasmid pTM22 (ATCC 68601).
 PN US5527896-A.
 PD 18-JUN-1996.
 PA (COLD-) COLD SPRING HARBOR LAB.
 Query Match 40.9%; Score 38; DB 2; Length 498;
 Best Local Similarity 54.5%; Pred. No. 1.3e+03;
 RESULT 933
 ID AAY49808 standard; protein; 498 AA.
 DE Human glioblastoma cell cAMP phosphodiesterase pTM22 protein.
 PN US5977305-A.
 PD 02-NOV-1999.
 PA (COLD-) COLD SPRING HARBOR LAB.
 Query Match 40.9%; Score 38; DB 2; Length 498;
 Best Local Similarity 54.5%; Pred. No. 1.3e+03;
 RESULT 934
 ID AAB20619 standard; protein; 498 AA.
 DE pTM22 human glioblastoma cell insert protein sequence SEQ ID NO:20.
 PN US6100025-A.
 PD 08-AUG-2000.
 PA (COLD-) COLD SPRING HARBOR LAB.
 Query Match 40.9%; Score 38; DB 2; Length 498;
 Best Local Similarity 54.5%; Pred. No. 1.3e+03;
 RESULT 935
 ID ADR66097 standard; protein; 498 AA.
 DE Human prostatic carcinoma derived protein SEQ ID 293 #1.
 PN WO2004076614-A2.
 PD 10-SEP-2004.
 PA (HINZ/) HINZMANN B.
 PA (DAHL/) DAHL E.
 PA (ROSE/) ROSENTHAL A.
 PA (HERM/) HERMANN K.
 PA (PILA/) PILARSKY C.

Query Match 40.9%; Score 38; DB 8; Length 498;
 Best Local Similarity 54.5%; Pred. No. 1.3e+03;
 RESULT 936
 ID ADR66439 standard; protein; 498 AA.
 DE Human prostatic carcinoma derived protein SEQ ID 293 #2.
 PN WO2004076614-A2.
 PD 10-SEP-2004.
 PA (HINZ/) HINZMANN B.
 PA (DAHL/) DAHL E.
 PA (ROSE/) ROSENTHAL A.
 PA (HERM/) HERMANN K.
 PA (PILA/) PILARSKY C.

Query Match 40.9%; Score 38; DB 8; Length 498;
 Best Local Similarity 54.5%; Pred. No. 1.3e+03;
 RESULT 937
 ID ADY25040 standard; protein; 507 AA.
 DE Plant full length insert polypeptide seqid 72824.
 PN US2004034888-A1.
 PD 19-FEB-2004.
 PA (LIUJ/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCRENN S E.
 PA (TABR/) TABASKA J E.
 PA (CAOY/) CAO Y.

Query Match 40.9%; Score 38; DB 8; Length 507;
 Best Local Similarity 47.1%; Pred. No. 1.4e+03;
 RESULT 938
 ID ABM88992 standard; protein; 525 AA.
 DE Rice abiotic stress responsive polypeptide SEQ ID NO:7238.
 PN WO2003008540-A2.
 PD 30-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 40.9%; Score 38; DB 7; Length 525;
 Best Local Similarity 63.6%; Pred. No. 1.4e+03;
 RESULT 939
 ID ABA42693 standard; protein; 529 AA.
 DE Human ORFX ORF2457 polypeptide sequence SEQ ID NO:4914.
 PN WO200058473-A2.
 PD 05-OCT-2000.
 PA (CURA-) CURAGEN CORP.
 Query Match 40.9%; Score 38; DB 3; Length 529;
 Best Local Similarity 60.0%; Pred. No. 1.4e+03;
 RESULT 940
 ID ADU08039 standard; protein; 529 AA.
 DE Xenopus NR5F protein.
 PN WO2004099367-A2.
 PD 18-NOV-2004.
 PA (GEHO) GEN HOSPITAL CORP.
 Query Match 40.9%; Score 38; DB 8; Length 529;
 Best Local Similarity 46.7%; Pred. No. 1.4e+03;
 RESULT 941
 ID ADY70504 standard; protein; 529 AA.
 DE Human beta-amyloid precursor protein, MGC4022.
 PN WO2005023858-A1.
 PD 17-MAR-2005.
 PA (CELL-) CELLZOME AG.
 Query Match 40.9%; Score 38; DB 9; Length 529;
 Best Local Similarity 60.0%; Pred. No. 1.4e+03;
 RESULT 942
 ID ABU29965 standard; protein; 548 AA.
 DE Protein encoded by Prokaryotic essential gene #15492.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 40.9%; Score 38; DB 6; Length 548;
 Best Local Similarity 58.3%; Pred. No. 1.5e+03;
 RESULT 943
 ID ADJ50318 standard; protein; 558 AA.
 DE Oil-associated gene related protein #1818.
 PN US2004025202-A1.
 PD 05-FEB-2004.
 PA (LAUR/) LAURIE C C.

PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDRAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 40.9%; Score 38; DB 8; Length 558;
Best Local Similarity 58.3%; Pred. No. 1.5e+03;
RESULT 944
ID ADN72631 standard; protein; 558 AA.
DE Thale cress protein upregulated in E2Pa/Dpa expressing plants SeqID 526.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDESIGN NV.
Query Match 40.9%; Score 38; DB 8; Length 558;
Best Local Similarity 58.3%; Pred. No. 1.5e+03;
RESULT 945
ID ABR40445 standard; protein; 591 AA.
DE Human secreted protein #SEQ ID 195.
PN WO200268628-A1.
PD 06-SEP-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 40.9%; Score 38; DB 5; Length 591;
Best Local Similarity 60.0%; Pred. No. 1.6e+03;
RESULT 946
ID ADY80077 standard; protein; 607 AA.
DE Amino acid sequence of murine pannexin 2.
PN WO2005026170-A2.
PD 24-MAR-2005.
PA (INSP) INST PASTEUR.
Query Match 40.9%; Score 38; DB 9; Length 607;
Best Local Similarity 41.2%; Pred. No. 1.7e+03;
RESULT 947
ID ADY80065 standard; protein; 633 AA.
DE Amino acid sequence of human pannexin 2.
PN WO2005026170-A2.
PD 24-MAR-2005.
PA (INSP) INST PASTEUR.
Query Match 40.9%; Score 38; DB 9; Length 633;
Best Local Similarity 41.2%; Pred. No. 1.8e+03;
RESULT 948
ID ABR44418 standard; protein; 653 AA.
DE Human potassium channel Kv1.4.
PN WO2003035690-A2.
PD 01-MAY-2003.
PA (TMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
Query Match 40.9%; Score 38; DB 6; Length 653;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
RESULT 949
ID ADA83742 standard; protein; 653 AA.
DE Human KCNA4 protein.
PN WO2002103028-A2.
PD 27-DEC-2002.
PA (BIOM-) BIOMEDICAL CENT.
Query Match 40.9%; Score 38; DB 6; Length 653;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
RESULT 950
ID ADE57786 standard; protein; 653 AA.
DE Human Protein P22459, SEQ ID NO 3651.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 40.9%; Score 38; DB 7; Length 653;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
RESULT 951
ID ADE63497 standard; protein; 653 AA.
DE Human Protein P22459, SEQ ID NO 9441.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 40.9%; Score 38; DB 7; Length 653;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
RESULT 952
ID ADS43873 standard; protein; 757 AA.
ID ABO59441 standard; protein; 653 AA.
DE Human genome derived single exon protein #5675.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 40.9%; Score 38; DB 8; Length 653;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
RESULT 953
ID ADE63495 standard; protein; 655 AA.
DE Rat Protein CAA34133, SEQ ID NO 9439.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 40.9%; Score 38; DB 7; Length 655;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
RESULT 954
ID ADE57784 standard; protein; 655 AA.
DE Rat Protein P15385, SEQ ID NO 3649.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 40.9%; Score 38; DB 7; Length 655;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
RESULT 955
ID ADY80071 standard; protein; 664 AA.
DE Amino acid sequence of rat pannexin 2.
PN WO2005026170-A2.
PD 24-MAR-2005.
PA (INSP) INST PASTEUR.
Query Match 40.9%; Score 38; DB 9; Length 664;
Best Local Similarity 41.2%; Pred. No. 1.9e+03;
RESULT 956
ID ADM04783 standard; protein; 667 AA.
DE Human protein of the invention SEQ ID NO:3468.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 40.9%; Score 38; DB 7; Length 667;
Best Local Similarity 41.2%; Pred. No. 1.9e+03;
RESULT 957
ID ADJ38278 standard; protein; 670 AA.
DE Plastid division-related Arc5 orthologue protein 60.
PN WO2004001003-A2.
PD 31-DEC-2003.
PA (UNMS) UNIV MICHIGAN STATE.
Query Match 40.9%; Score 38; DB 8; Length 670;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
RESULT 958
ID ABO75000 standard; protein; 700 AA.
DE Pseudomonas aeruginosa polypeptide #7175.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 40.9%; Score 38; DB 7; Length 700;
Best Local Similarity 43.8%; Pred. No. 2e+03;
RESULT 959
ID ADS23975 standard; protein; 712 AA.
DE Bacterial polypeptide #13008.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 40.9%; Score 38; DB 8; Length 712;
Best Local Similarity 38.5%; Pred. No. 2e+03;
RESULT 960
ID ADS43873 standard; protein; 757 AA.

DE Bacterial polypeptide #22303.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY//) CAO Y.
 PA (HINK//) HINKLE G J.
 PA (SLAT//) SLATER S C.
 PA (CHEN//) CHEN X.
 PA (GOLD//) GOLDMAN B S.
 Query Match 40.9%; Score 38; DB 8; Length 757;
 Best Local Similarity 50.0%; Pred. No. 2.2e+03;
 RESULT 961
 ID AAE03804 standard; protein; 772 AA.
 DE Schizosaccharomyces pombe RAD 15 protein.
 PN W0200142434-A1.
 PD 14-JUN-2001.
 PA (MERI//) MERCK & CO INC.
 Query Match 40.9%; Score 38; DB 4; Length 772;
 Best Local Similarity 60.0%; Pred. No. 2.2e+03;
 RESULT 962
 ID ADN19422 standard; protein; 772 AA.
 DE Bacterial polypeptide #2075.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY//) CAO Y.
 PA (HINK//) HINKLE G J.
 PA (SLAT//) SLATER S C.
 PA (CHEN//) CHEN X.
 PA (GOLD//) GOLDMAN B S.
 Query Match 40.9%; Score 38; DB 8; Length 772;
 Best Local Similarity 60.0%; Pred. No. 2.2e+03;
 RESULT 963
 ID AEM84550 standard; protein; 793 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:4799.
 PN W02004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 40.9%; Score 38; DB 8; Length 793;
 Best Local Similarity 40.0%; Pred. No. 2.3e+03;
 RESULT 964
 ID ADT55566 standard; protein; 811 AA.
 DE Plant polypeptide, SEQ ID 5643.
 PN US2004216190-A1.
 PD 28-OCT-2004.
 PA (KOVA//) KOVALIC D K.
 Query Match 40.9%; Score 38; DB 8; Length 811;
 Best Local Similarity 46.2%; Pred. No. 2.3e+03;
 RESULT 965
 ID ADS24019 standard; protein; 822 AA.
 DE Bacterial polypeptide #13052.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY//) CAO Y.
 PA (HINK//) HINKLE G J.
 PA (SLAT//) SLATER S C.
 PA (CHEN//) CHEN X.
 PA (GOLD//) GOLDMAN B S.
 Query Match 40.9%; Score 38; DB 8; Length 822;
 Best Local Similarity 60.0%; Pred. No. 2.4e+03;
 RESULT 966
 ID ABE58526 standard; protein; 882 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 2370.
 PN W0200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE//) PE CORP NY.
 Query Match 40.9%; Score 38; DB 4; Length 882;
 Best Local Similarity 38.9%; Pred. No. 2.6e+03;
 RESULT 967
 ID ADN19659 standard; protein; 886 AA.
 DE Bacterial polypeptide #2312.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY//) CAO Y.
 PA (HINK//) HINKLE G J.

PA (SLAT//) SLATER S C.
 PA (CHEN//) CHEN X.
 PA (GOLD//) GOLDMAN B S.
 Query Match 40.9%; Score 38; DB 8; Length 886;
 Best Local Similarity 40.0%; Pred. No. 2.6e+03;
 RESULT 968
 ID ABO75893 standard; protein; 940 AA.
 DE Pseudomonas aeruginosa polypeptide #8068.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 40.9%; Score 38; DB 7; Length 940;
 Best Local Similarity 63.6%; Pred. No. 2.8e+03;
 RESULT 969
 ID AEM90649 standard; protein; 981 AA.
 DE M. xanthus protein sequence, seq id 9848.
 PN US6833447-B1.
 PD 21-DEC-2004.
 PA (MONS) MONSANTO TECHNOLOGY LLC.
 Query Match 40.9%; Score 38; DB 9; Length 981;
 Best Local Similarity 42.9%; Pred. No. 2.9e+03;
 RESULT 970
 ID ADX05670 standard; protein; 998 AA.
 DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 235.
 PN W02005012875-A2.
 PD 10-FEB-2005.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Query Match 40.9%; Score 38; DB 9; Length 998;
 Best Local Similarity 60.0%; Pred. No. 3e+03;
 RESULT 971
 ID AAR43341 standard; protein; 1068 AA.
 DE p110.
 PN W09321328-A1.
 PD 28-OCT-1993.
 PA (LUDW-) LUDWIG INST CANCER RES.
 Query Match 40.9%; Score 38; DB 2; Length 1068;
 Best Local Similarity 40.0%; Pred. No. 3.2e+03;
 RESULT 972
 ID AAR43342 standard; protein; 1068 AA.
 DE Human p110.
 PN W09321328-A1.
 PD 28-OCT-1993.
 PA (LUDW-) LUDWIG INST CANCER RES.
 Query Match 40.9%; Score 38; DB 2; Length 1068;
 Best Local Similarity 40.0%; Pred. No. 3.2e+03;
 RESULT 973
 ID AAR46294 standard; protein; 1068 AA.
 DE PtdIns 3-kinase 110 kD catalytic subunit.
 PN W09403609-A1.
 PD 17-FEB-1994.
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
 Query Match 40.9%; Score 38; DB 2; Length 1068;
 Best Local Similarity 40.0%; Pred. No. 3.2e+03;
 RESULT 974
 ID AAU09687 standard; protein; 1068 AA.
 DE Human p110alpha isoform of PI3-kinase.
 PN W0200185986-A2.
 PD 15-NOV-2001.
 PA (ICOS-) ICOS CORP.
 Query Match 40.9%; Score 38; DB 5; Length 1068;
 Best Local Similarity 40.0%; Pred. No. 3.2e+03;
 RESULT 975
 ID ADH68169 standard; protein; 1068 AA.
 DE PI3K-alpha protein.
 PN US2003182669-A1.
 PD 25-SEP-2003.
 PA (ROCK//) ROCKMAN H A.
 PA (PRAS//) NAGA PRASAD S V.
 PA (LAPO//) LAPORTE S A.
 PA (BARA//) BARAK L S.
 PA (CARO//) CARON M G.
 Query Match 40.9%; Score 38; DB 8; Length 1068;
 Best Local Similarity 40.0%; Pred. No. 3.2e+03;

RESULT 976
ID ADU06422 standard; protein; 1068 AA.
DE Novel bronchial cancer-associated human protein SeqID646.
PN D810316701-A1.
PD 04-NOV-2004.
PA (HINZ//) HINZMANN B.
PA (HERM//) HERMANN K.
PA (CAST//) HEIDEN CASTANOS-VLEZ E.
Query Match 40.9%; Score 38; DB 8; Length 1068;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
RESULT 977
ID ADZ00491 standard; protein; 1068 AA.
DE p110-beta.
PN WO2005031341-A2.
PD 07-APR-2005.
PA (PFIZ) PFIZER HEALTH AB.
Query Match 40.9%; Score 38; DB 9; Length 1068;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
RESULT 978
ID AAG70814 standard; protein; 1276 AA.
DE S cerevisiae apoptosis associated protein YPL090C.
PN WO200102550-A2.
PD 11-JAN-2001.
PA (JANC) JANSSEN PHARM NV.
Query Match 40.9%; Score 38; DB 4; Length 1276;
Best Local Similarity 70.0%; Pred. No. 3.9e+03;
RESULT 979
ID AAK1465 standard; peptide; 15 AA.
DE Lepidoptera allostatin polypeptide analogue.
PN EP421935-A.
PD 10-APR-1991.
PA (SANO) SANDOZ LTD.
PA (KRAM//) KRAMER S J.
PA (NOVS) NOVARTIS AG.
Query Match 40.3%; Score 37.5; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 31;
RESULT 980
ID ABP72616 standard; peptide; 15 AA.
DE Manduca sexta allatostatin.
PN WO2003014150-A2.
PD 20-FEB-2003.
PA (UYDU-) UNIV DURHAM.
PA (ENVI-) DEPT ENVIRONMENT FOOD & RURAL AFFAIRS.
Query Match 40.3%; Score 37.5; DB 6; Length 15;
Best Local Similarity 60.0%; Pred. No. 31;
RESULT 981
ID ADE14702 standard; peptide; 15 AA.
DE DmGPCR binding ligand #150.
PN US2003180297-A1.
PD 25-SEP-2003.
PA (LOWE//) LOWERY D E.
PA (SMIT//) SMITH V G.
PA (KUBI//) KUBIAK T M.
PA (LARS//) LARSEN M J.
Query Match 40.3%; Score 37.5; DB 7; Length 15;
Best Local Similarity 60.0%; Pred. No. 31;
RESULT 982
ID ADL83598 standard; peptide; 15 AA.
DE Manduca sexta allatostatin-C peptide.
PN US2003162223-A1.
PD 28-AUG-2003.
PA (LOWE//) LOWERY D E.
PA (SMIT//) SMITH V G.
PA (KUBI//) KUBIAK T M.
PA (LARS//) LARSEN M J.
Query Match 40.3%; Score 37.5; DB 7; Length 15;
Best Local Similarity 60.0%; Pred. No. 31;
RESULT 983
ID ADY80079 standard; protein; 392 AA.
DE Amino acid sequence of murine pannexin 3.
PN WO2005026170-A2.
PD 24-MAR-2005.
PA (INSP) INST PASTEUR.

Query Match 40.3%; Score 37.5; DB 9; Length 392;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 984
ID ADY80073 standard; protein; 392 AA.
DE Amino acid sequence of rat pannexin 3.
PN WO2005026170-A2.
PD 24-MAR-2005.
PA (INSP) INST PASTEUR.
Query Match 40.3%; Score 37.5; DB 9; Length 392;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 985
ID ADY80067 standard; protein; 392 AA.
DE Amino acid sequence of human pannexin 3.
PN WO2005026170-A2.
PD 24-MAR-2005.
PA (INSP) INST PASTEUR.
Query Match 40.3%; Score 37.5; DB 9; Length 392;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 986
ID ABM70582 standard; protein; 806 AA.
DE Photobabidus luminescens protein sequence #3679.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 40.3%; Score 37.5; DB 6; Length 806;
Best Local Similarity 36.4%; Pred. No. 2.8e+03;
RESULT 987
ID ABB91321 standard; protein; 838 AA.
DE Herbicidally active polypeptide SEQ ID NO 532.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 40.3%; Score 37.5; DB 5; Length 838;
Best Local Similarity 56.2%; Pred. No. 2.9e+03;
RESULT 988
ID ABG22709 standard; protein; 29 AA.
DE Novel human diagnostic protein #22700.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 4; Length 29;
Best Local Similarity 42.9%; Pred. No. 79;
RESULT 989
ID AAM16024 standard; protein; 42 AA.
DE Peptide #2458 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 42;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
RESULT 990
ID ABB35016 standard; peptide; 42 AA.
DE Peptide #2522 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 42;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
RESULT 991
ID AAM28525 standard; protein; 42 AA.
DE Peptide #2562 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 42;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
RESULT 992
ID AAM68206 standard; protein; 42 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 28512.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 39.8%; Score 37; DB 4; Length 42;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
RESULT 993
ID AAM55833 standard; protein; 42 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 27938.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 42;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
RESULT 994
ID ABG49853 standard; peptide; 42 AA.
DE Human liver peptide, SEQ ID NO 28501.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 42;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
RESULT 995
ID NAM03755 standard; protein; 42 AA.
DE Peptide #2437 encoded by probe for measuring breast gene expression.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 39.8%; Score 37; DB 4; Length 42;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
RESULT 996
ID AD240090 standard; peptide; 48 AA.
DE HIV-1 gp41 ectodomain peptide variant, Seq 2.
PN WO2005034842-A2.
PD 21-APR-2005.
PA (PROG-) PROGENICS PHARM INC.
Query Match 39.8%; Score 37; DB 9; Length 48;
Best Local Similarity 70.0%; Pred. No. 1.4e+02;
RESULT 997
ID ADU80332 standard; peptide; 50 AA.
DE HIV transmembrane envelope glycoprotein GP41-based peptide, SEQ ID 2.
PN WO2004103312-A2.
PD 02-DEC-2004.
PA (PROG-) PROGENICS PHARM INC.
Query Match 39.8%; Score 37; DB 8; Length 50;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
RESULT 998
ID AAY12353 standard; protein; 55 AA.
DE Human 5' EST secreted protein SEQ ID NO:384.
PN WO9906548-A2.
PD 11-FEB-1999.
PA (GSET) GENSET.
Query Match 39.8%; Score 37; DB 2; Length 55;
Best Local Similarity 46.2%; Pred. No. 1.6e+02;
RESULT 999
ID ABP43919 standard; protein; 64 AA.
DE FLJ20040 fis clone COL00417.
PN WO200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 5; Length 64;
Best Local Similarity 46.7%; Pred. No. 1.9e+02;
RESULT 1000
ID ADH32550 standard; protein; 70 AA.
DE Yeast smORF338-encoded polypeptide, SEQ ID NO:1008.
PN WO200268693-A2.
PD 06-SEP-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 39.8%; Score 37; DB 5; Length 70;
Best Local Similarity 41.7%; Pred. No. 2.1e+02;
RESULT 1001
ID AAM85399 standard; protein; 74 AA.
DE Human immune/haematopoietic antigen SEQ ID NO:12992.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 4; Length 74;

Best Local Similarity 53.8%; Pred. No. 2.3e+02;
RESULT 1002
ID AAB45011 standard; protein; 83 AA.
DE Human secreted protein encoded by gene 37 homologue.
PN WO200055200-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 3; Length 83;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
RESULT 1003
ID AAB45012 standard; protein; 83 AA.
DE Human secreted protein encoded by gene 37 homologue.
PN WO200055200-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 3; Length 83;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
RESULT 1004
ID ASP07339 standard; protein; 85 AA.
DE Human ORFX protein sequence SEQ ID NO:14660.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 39.8%; Score 37; DB 5; Length 85;
Best Local Similarity 27.8%; Pred. No. 2.7e+02;
RESULT 1005
ID ADI67220 standard; protein; 104 AA.
DE Lactobacillus rhamnosus polypeptide sequence #94.
PN US2004009490-A1.
PD 15-JAN-2004.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 39.8%; Score 37; DB 8; Length 104;
Best Local Similarity 41.2%; Pred. No. 3.4e+02;
RESULT 1006
ID ABB97814 standard; protein; 107 AA.
DE Human secretory polypeptide (SPTM) 66.
PN WO200220756-A2.
PD 14-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 39.8%; Score 37; DB 5; Length 107;
Best Local Similarity 46.2%; Pred. No. 3.5e+02;
RESULT 1007
ID ADY22702 standard; protein; 120 AA.
DE Plant full length insert polypeptide seqid 70486.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREBEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 39.8%; Score 37; DB 8; Length 120;
Best Local Similarity 53.8%; Pred. No. 4e+02;
RESULT 1008
ID AG05261 standard; protein; 149 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1600.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 149;
Best Local Similarity 47.1%; Pred. No. 5.1e+02;
RESULT 1009
ID ABG06103 standard; protein; 163 AA.
DE Novel human diagnostic protein #6094.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 4; Length 163;
Best Local Similarity 41.2%; Pred. No. 5.6e+02;
RESULT 1010
ID AGS9595 standard; protein; 166 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77099.
PN EPI033405-A2.

PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 166;
Best Local Similarity 47.1%; Pred. No. 5.7e+02;
RESULT 1011
ID AAG07269 standard; protein; 166 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4358.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 166;
Best Local Similarity 47.1%; Pred. No. 5.7e+02;
RESULT 1012
ID AAR57031 standard; protein; 178 AA.
DE Serotonin receptor encoded by human PCR S10 clone.
PN W09414957-A2.
PD 07-JUL-1994.
PA (SYNA-) SYNAPTIC PHARM CORP.
Query Match 39.8%; Score 37; DB 2; Length 178;
Best Local Similarity 26.7%; Pred. No. 6.2e+02;
RESULT 1013
ID AAG10820 standard; protein; 181 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 9294.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 181;
Best Local Similarity 53.8%; Pred. No. 6.3e+02;
RESULT 1014
ID AAG06866 standard; protein; 181 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 3798.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 181;
Best Local Similarity 53.8%; Pred. No. 6.3e+02;
RESULT 1015
ID AAG54822 standard; protein; 185 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 70045.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 185;
Best Local Similarity 53.8%; Pred. No. 6.5e+02;
RESULT 1016
ID AAG06865 standard; protein; 193 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 3797.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 193;
Best Local Similarity 53.8%; Pred. No. 6.8e+02;
RESULT 1017
ID AAG10819 standard; protein; 193 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 9293.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 193;
Best Local Similarity 53.8%; Pred. No. 6.8e+02;
RESULT 1018
ID AAG05260 standard; protein; 194 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1599.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 194;
Best Local Similarity 47.1%; Pred. No. 6.8e+02;
RESULT 1019
ID AAG05259 standard; protein; 204 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1598.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 204;
Best Local Similarity 47.1%; Pred. No. 7.2e+02;
RESULT 1020
ID AAG10818 standard; protein; 205 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 9292.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 205;
Best Local Similarity 47.1%; Pred. No. 7.3e+02;
RESULT 1021
ID AAG06864 standard; protein; 205 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 3796.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 205;
Best Local Similarity 53.8%; Pred. No. 7.3e+02;
RESULT 1022
ID AAG59594 standard; protein; 206 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77098.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 206;
Best Local Similarity 47.1%; Pred. No. 7.3e+02;
RESULT 1023
ID AAG07268 standard; protein; 206 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4357.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 206;
Best Local Similarity 47.1%; Pred. No. 7.3e+02;
RESULT 1024
ID AAG03816 standard; protein; 209 AA.
DE Novel human diagnostic protein #3807.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 4; Length 209;
Best Local Similarity 41.2%; Pred. No. 7.4e+02;
RESULT 1025
ID AAG59593 standard; protein; 215 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77097.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 215;
Best Local Similarity 47.1%; Pred. No. 7.7e+02;
RESULT 1026
ID AAG07267 standard; protein; 215 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4356.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 39.8%; Score 37; DB 3; Length 215;
Best Local Similarity 47.1%; Pred. No. 7.7e+02;
RESULT 1027
ID AAG12667 standard; protein; 225 AA.
DE Novel human diagnostic protein #12658.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 4; Length 225;
Best Local Similarity 40.0%; Pred. No. 8.1e+02;
RESULT 1028
ID AAY74526 standard; protein; 243 AA.
DE Neisseria meningitidis ORF 136 protein sequence SEQ ID NO: 526.
PN W0957280-A2.
PD 11-NOV-1999.
PA (CHIR-) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Query Match 39.8%; Score 37; DB 3; Length 243;
Best Local Similarity 60.0%; Pred. No. 8.8e+02;
RESULT 1029
ID ABU24490 standard; protein; 265 AA.
DE Protein encoded by Prokaryotic essential gene #10017.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 39.8%; Score 37; DB 6; Length 265;
Best Local Similarity 58.3%; Pred. No. 9.7e+02;
RESULT 1030
ID AAB96515 standard; protein; 271 AA.
DE Putative P. abyssi Fe-S oxidoreductase #7.
PN FR2792651-A1.

PD 27-OCT-2000.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (IPRE-) IPREMER INST FR RECH EXPL MER.
Query Match
Best Local Similarity 39.8%; Score 37; DB 4; Length 271;
Pred. No. 1e+03;
RESULT 1031
ID AM17915 standard; protein; 276 AA.
DE Peptide #4349 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 39.8%; Score 37; DB 4; Length 276;
Pred. No. 1e+03;
RESULT 1032
ID AB36945 standard; peptide; 276 AA.
DE Peptide #4451 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 39.8%; Score 37; DB 4; Length 276;
Pred. No. 1e+03;
RESULT 1033
ID AM30426 standard; protein; 276 AA.
DE Peptide #4463 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 39.8%; Score 37; DB 4; Length 276;
Pred. No. 1e+03;
RESULT 1034
ID AB31724 standard; peptide; 276 AA.
DE Peptide #4375 encoded by breast cell single exon nucleic acid probe.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 39.8%; Score 37; DB 4; Length 276;
Pred. No. 1e+03;
RESULT 1035
ID AM70098 standard; protein; 276 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 30394.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 39.8%; Score 37; DB 4; Length 276;
Pred. No. 1e+03;
RESULT 1036
ID ABG51785 standard; peptide; 276 AA.
DE Human liver peptide, SEQ ID NO 30433.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 39.8%; Score 37; DB 4; Length 276;
Pred. No. 1e+03;
RESULT 1037
ID AM05567 standard; protein; 276 AA.
DE Peptide #4249 encoded by probe for measuring breast gene expression.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 39.8%; Score 37; DB 4; Length 276;
Pred. No. 1e+03;
RESULT 1038
ID ABG39722 standard; peptide; 276 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 29387.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 39.8%; Score 37; DB 5; Length 276;
Pred. No. 1e+03;
RESULT 1039
ID ADA36649 standard; protein; 277 AA.
DE Acinetobacter baumannii protein #3810.
PN US6562958-B1.

PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 39.8%; Score 37; DB 6; Length 277;
Pred. No. 1e+03;
RESULT 1040
ID AA74527 standard; protein; 278 AA.
DE Neisseria meningitidis ORF 136 protein sequence SEQ ID NO:528.
PN WO9957280-A2.
PD 11-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Query Match
Best Local Similarity 39.8%; Score 37; DB 3; Length 278;
Pred. No. 1e+03;
RESULT 1041
ID AD30040 standard; protein; 292 AA.
DE Plant yield-related protein from clone G1453.
PN WO2003013227-A2.
PD 20-FEB-2003.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match
Best Local Similarity 39.8%; Score 37; DB 7; Length 292;
Pred. No. 1.1e+03;
RESULT 1042
ID AD14161 standard; protein; 292 AA.
DE Plant transcription factor related polypeptide #1669.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER) SHERMAN B K.
PA (RIEC) RIECHMANN J L.
PA (JIAN) JIANG C.
PA (HEAR) HEARD J E.
PA (HNAK) HAAKE V.
PA (CREE) CREELMAN R A.
PA (RATC) RATCLIFFE O.
PA (ADAM) ADAM L J.
PA (REUB) REUBER T L.
PA (KEDD) KEDDIE J.
PA (BROU) BROUN P E.
PA (FILG) FILGRIM M L.
PA (DUBE) DUBELL A N.
PA (FINE) PINEDA O.
PA (YUGG) YU G.
Query Match
Best Local Similarity 39.8%; Score 37; DB 8; Length 292;
Pred. No. 1.1e+03;
RESULT 1043
ID AAU20366 standard; protein; 301 AA.
DE Human secreted protein, Seq ID No 358.
PN WO200155326-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 39.8%; Score 37; DB 4; Length 301;
Pred. No. 1.1e+03;
RESULT 1044
ID ADX92357 standard; protein; 306 AA.
DE Plant full length insert polypeptide seqid 55021.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ) LIU J.
PA (ZHOU) ZHOU Y.
PA (KOVA) KOVALIC D K.
PA (SCRE) SCREEN S E.
PA (TABR) TABASKA J E.
PA (CAOY) CAO Y.
Query Match
Best Local Similarity 39.8%; Score 37; DB 8; Length 306;
Pred. No. 1.1e+03;
RESULT 1045
ID ABB51278 standard; protein; 307 AA.
DE Human secreted protein encoded by gene 30 SEQ ID NO:1235.
PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 39.8%; Score 37; DB 4; Length 307;
Pred. No. 1.1e+03;
RESULT 1046

ID ABB51275 standard; protein; 307 AA.
DE Human secreted protein encoded by gene 30 SEQ ID NO:1232.
PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 4; Length 307;
Best Local Similarity 46.2%; Pred. No. 1.1e+03;
RESULT 1047
ID ADX94522 standard; protein; 314 AA.
DE Plant full length insert polypeptide seqid 57186.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOV/) CAO Y.
Query Match 39.8%; Score 37; DB 8; Length 314;
Best Local Similarity 58.8%; Pred. No. 1.2e+03;
RESULT 1048
ID AAW48792 standard; protein; 315 AA.
DE Homo sapiens sprouty 2 protein.
PN WO9820032-A1.
PD 14-MAY-1998.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 39.8%; Score 37; DB 2; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1049
ID ABO07185 standard; protein; 315 AA.
DE Human p53 modifying protein, SEQ ID 145.
PN WO200299122-A1.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 39.8%; Score 37; DB 6; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1050
ID ABE61338 standard; protein; 315 AA.
DE Human Protein O43597, SEQ ID NO 7256.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 39.8%; Score 37; DB 7; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1051
ID ADQ14302 standard; protein; 315 AA.
DE Human Sprouty 2 (SPRY2), SEQ ID 4.
PN WO2003074007-A2.
PD 12-SEP-2003.
PA (RIGE-) RIGEL PHARM INC.
Query Match 39.8%; Score 37; DB 7; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1052
ID ADG47834 standard; protein; 315 AA.
DE Human sprouty-2 protein.
PN US6485920-B1.
PD 26-NOV-2002.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 8; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1053
ID ADG47837 standard; protein; 315 AA.
DE Mouse sprouty-2 protein.
PN US6485920-B1.
PD 26-NOV-2002.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 8; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1054
ID ADJ95401 standard; protein; 315 AA.
DE Human sprouty-2 polypeptide.
PN US6706871-B1.

PD 16-MAR-2004.
PA (NUVE-) NUVELO INC.
Query Match 39.8%; Score 37; DB 8; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1055
ID ADJ95404 standard; protein; 315 AA.
DE Mouse sprouty-2 polypeptide.
PN US6706871-B1.
PD 16-MAR-2004.
PA (NUVE-) NUVELO INC.
Query Match 39.8%; Score 37; DB 8; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1056
ID ADN11324 standard; protein; 315 AA.
DE Human Sprouty2, marker for breast cancer.
PN WO2004029295-A1.
PD 08-APR-2004.
PA (SCTE-) AGENCY SCI TECHNOLOGY & RES.
Query Match 39.8%; Score 37; DB 8; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1057
ID ADQ21111 standard; protein; 315 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3931.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 39.8%; Score 37; DB 8; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1058
ID ADP23634 standard; protein; 315 AA.
DE PRO polypeptide SEQ ID NO:812.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 39.8%; Score 37; DB 8; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1059
ID ADS15841 standard; protein; 315 AA.
DE Human sprouty-2 SEQ ID 4.
PN WO2004082704-A1.
PD 30-SEP-2004.
PA (DNAV-) DNAVEC RES INC.
Query Match 39.8%; Score 37; DB 8; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1060
ID ADY19896 standard; protein; 315 AA.
DE PRO polypeptide SEQ ID NO 5702.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 39.8%; Score 37; DB 9; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1061
ID ADY15230 standard; protein; 315 AA.
DE PRO polypeptide SEQ ID NO 1036.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 39.8%; Score 37; DB 9; Length 315;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1062
ID ADM25514 standard; protein; 316 AA.
DE Hyperthermophile Methanopyrus kandleri protein #120.
PN WO2003076575-A2.
PD 18-SEP-2003.
PA (FIDE-) FIDELITY SYSTEMS INC.
PA (MALY/) MALYKH A.
Query Match 39.8%; Score 37; DB 7; Length 316;
Best Local Similarity 42.9%; Pred. No. 1.2e+03;
RESULT 1063
ID ABB51277 standard; protein; 321 AA.
DE Human secreted protein encoded by gene 30 SEQ ID NO:1234.
PN WO200162891-A2.

PA 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 4; Length 321;
Best Local Similarity 46.2%; Pred. No. 1.2e+03;
RESULT 1064
ID ABU29258 standard; protein; 324 AA.
DE Protein encoded by Prokaryotic essential gene #14785.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 39.8%; Score 37; DB 6; Length 324;
Best Local Similarity 33.3%; Pred. No. 1.2e+03;
RESULT 1065
ID AAB19393 standard; protein; 325 AA.
DE Amino acid sequence of a human secreted protein.
PN W0200061755-A2.
PD 19-OCT-2000.
PA (CHIR) CHIRON CORP.
Query Match 39.8%; Score 37; DB 3; Length 325;
Best Local Similarity 46.2%; Pred. No. 1.2e+03;
RESULT 1066
ID AAB23045 standard; protein; 326 AA.
DE Human peroxisome associated protein splice variant, SECX 3884846-1.
PN W0200053742-A2.
PD 14-SEP-2000.
PA (CURA-) CURAGEN CORP.
Query Match 39.8%; Score 37; DB 3; Length 326;
Best Local Similarity 46.2%; Pred. No. 1.2e+03;
RESULT 1067
ID ADA23352 standard; protein; 326 AA.
DE Human SECX polypeptide, SEC7 #2.
PN U02003054514-A1.
PD 20-MAR-2003.
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.
Query Match 39.8%; Score 37; DB 6; Length 326;
Best Local Similarity 46.2%; Pred. No. 1.2e+03;
RESULT 1068
ID ADH87324 standard; protein; 339 AA.
DE Enterococcus faecalis polypeptide #1804.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 39.8%; Score 37; DB 7; Length 339;
Best Local Similarity 33.3%; Pred. No. 1.3e+03;
RESULT 1069
ID AAR22463 standard; protein; 343 AA.
DE Acetylpolymine amidohydrolase.
PN JF04071489-A.
PD 06-MAR-1992.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 39.8%; Score 37; DB 2; Length 343;
Best Local Similarity 58.3%; Pred. No. 1.3e+03;
RESULT 1070
ID ADO57333 standard; protein; 351 AA.
DE Kidney development associated protein seqid 100.
PN US2004068763-A1.
PD 08-APR-2004.
PA (HOPK/) HOPKINS N.
PA (GOLL/) GOLLING G.
PA (AMST/) AMSTERDAM A.
PA (SUNZ/) SUN Z.
Query Match 39.8%; Score 37; DB 8; Length 351;
Best Local Similarity 40.0%; Pred. No. 1.3e+03;
RESULT 1071
ID ADF29942 standard; protein; 351 AA.
DE Human secreted protein SEQ ID #709.
PN W02004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 39.8%; Score 37; DB 8; Length 351;
Best Local Similarity 38.5%; Pred. No. 1.3e+03;
RESULT 1072
ID ADA57263 standard; protein; 362 AA.
DE Human secreted protein #546.
PN W02002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 6; Length 362;
Best Local Similarity 46.2%; Pred. No. 1.4e+03;
RESULT 1073
ID ADA57577 standard; protein; 362 AA.
DE Human secreted protein #546.
PN W02002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 6; Length 362;
Best Local Similarity 46.2%; Pred. No. 1.4e+03;
RESULT 1074
ID ADA41146 standard; protein; 362 AA.
DE Human secreted protein.
PN W02002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 6; Length 362;
Best Local Similarity 46.2%; Pred. No. 1.4e+03;
RESULT 1075
ID ADA41471 standard; protein; 362 AA.
DE Human secreted protein.
PN W02002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 6; Length 362;
Best Local Similarity 46.2%; Pred. No. 1.4e+03;
RESULT 1076
ID ADC74585 standard; protein; 362 AA.
DE Human secreted protein - SEQ ID 1218.
PN W02003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 7; Length 362;
Best Local Similarity 46.2%; Pred. No. 1.4e+03;
RESULT 1077
ID ADC74351 standard; protein; 362 AA.
DE Human secreted protein - SEQ ID 984.
PN W02003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 7; Length 362;
Best Local Similarity 46.2%; Pred. No. 1.4e+03;
RESULT 1078
ID ADD38093 standard; protein; 362 AA.
DE Human secreted protein #276.
PN W0200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 7; Length 362;
Best Local Similarity 46.2%; Pred. No. 1.4e+03;
RESULT 1079
ID ADD37992 standard; protein; 362 AA.
DE Human secreted protein #175.
PN W0200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 7; Length 362;
Best Local Similarity 46.2%; Pred. No. 1.4e+03;
RESULT 1080
ID AAW88563 standard; protein; 363 AA.
DE Secreted protein encoded by gene 30 clone HTPBW79.
PN W09854963-A2.
PD 10-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 2; Length 363;
Best Local Similarity 46.2%; Pred. No. 1.4e+03;
RESULT 1081

ID AAY36333 standard; protein; 363 AA.
DE Human secreted protein encoded by gene 110.
PN WO931117-A1.
PD 24-JUN-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 2; Length 363;
Best Local Similarity 46.2%; Pred. No. 1.4e+03;
RESULT 1082
ID ABB50330 standard; protein; 363 AA.
DE Human secreted protein encoded by gene 30 SEQ ID NO:278.
PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 4; Length 363;
Best Local Similarity 46.2%; Pred. No. 1.4e+03;
RESULT 1083
ID ABB51276 standard; protein; 363 AA.
DE Human secreted protein encoded by gene 30 SEQ ID NO:1233.
PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 4; Length 363;
Best Local Similarity 46.2%; Pred. No. 1.4e+03;
RESULT 1084
ID ABO44587 standard; protein; 363 AA.
DE Novel human secreted protein #30.
PN US2003065160-A1.
PD 03-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 6; Length 363;
Best Local Similarity 46.2%; Pred. No. 1.4e+03;
RESULT 1085
ID ABO26067 standard; protein; 363 AA.
DE Human protein from novel secreted protein gene 30.
PN US6525174-B1.
PD 25-FEB-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 7; Length 363;
Best Local Similarity 46.2%; Pred. No. 1.4e+03;
RESULT 1086
ID ABB53913 standard; protein; 365 AA.
DE Lactococcus lactis protein serC.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 39.8%; Score 37; DB 5; Length 365;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
RESULT 1087
ID ADS29312 standard; protein; 365 AA.
DE Bacterial polypeptide #18345.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 39.8%; Score 37; DB 8; Length 365;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
RESULT 1088
ID AAW88777 standard; protein; 370 AA.
DE Polypeptide fragment encoded by gene 30.
PN WO9854963-A2.
PD 10-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 2; Length 370;
Best Local Similarity 46.2%; Pred. No. 1.4e+03;
RESULT 1089
ID ABB50610 standard; protein; 370 AA.
DE Human secreted protein encoded by gene 30 SEQ ID NO:558.
PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 39.8%; Score 37; DB 4; Length 370;
Best Local Similarity 46.2%; Pred. No. 1.4e+03;
RESULT 1090
ID ABO44867 standard; protein; 370 AA.
DE Novel human secreted protein #30 fragment #1.
PN US2003065160-A1.
PD 03-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 6; Length 370;
Best Local Similarity 46.2%; Pred. No. 1.4e+03;
RESULT 1091
ID ABO26347 standard; protein; 370 AA.
DE Protein associated with novel secreted protein gene 30 #1.
PN US6525174-B1.
PD 25-FEB-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 7; Length 370;
Best Local Similarity 46.2%; Pred. No. 1.4e+03;
RESULT 1092
ID AAY36194 standard; protein; 393 AA.
DE Human secreted protein #66.
PN WO9925825-A2.
PD 27-MAY-1999.
PA (GEST) GENSET.
Query Match 39.8%; Score 37; DB 2; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1093
ID AAY94883 standard; protein; 393 AA.
DE Human protein clone HPI0530.
PN WO200005367-A2.
PD 03-FEB-2000.
PA (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
Query Match 39.8%; Score 37; DB 3; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1094
ID AAB61136 standard; protein; 393 AA.
DE Human NOV6 protein.
PN WO200075321-A2.
PD 14-DEC-2000.
PA (CURA-) CURAGEN CORP.
Query Match 39.8%; Score 37; DB 4; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1095
ID AAM79115 standard; protein; 393 AA.
DE Human protein SEQ ID NO 1777.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 4; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1096
ID AAB93277 standard; protein; 393 AA.
DE Human protein sequence SEQ ID NO:12320.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 39.8%; Score 37; DB 4; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1097
ID ABO23238 standard; protein; 393 AA.
DE Human breast tumour associated protein 47-like polypeptide NOV6.
PN US2003027158-A1.
PD 06-FEB-2003.
PA (CURA-) CURAGEN CORP.
Query Match 39.8%; Score 37; DB 6; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1098
ID ADJ46046 standard; protein; 393 AA.
DE Novel human secreted protein-related protein sequence SeqID199.
PN US2003144490-A1.
PD 31-JUL-2003.
PA (EDWA/) EDWARDS J D M.

PA (DUC/L/) DUCLERT A.
PA (BOUG/) BOUGUELERET L.
Query Match 39.8%; Score 37; DB 7; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1099
ID ADM56375 standard; protein; 393 AA.
DE Human cell adhesion molecule NOV6.
PN US2003082554-A1.
PD 01-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match 39.8%; Score 37; DB 7; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1100
ID ADF66739 standard; protein; 393 AA.
DE Novel human protein NOV6.
PN US2003199103-A1.
PD 23-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 39.8%; Score 37; DB 8; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1101
ID ADI19776 standard; protein; 393 AA.
DE Human NOV6 protein.
PN US2004002134-A1.
PD 01-JAN-2004.
PA (CURA-) CURAGEN CORP.
Query Match 39.8%; Score 37; DB 8; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1102
ID ADO58690 standard; protein; 393 AA.
DE Human regulatory molecule HRM-11.
PN US2002058264-A1.
PD 16-MAY-2002.
PA (INCY-) INCYTE PHARM INC.
Query Match 39.8%; Score 37; DB 8; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1103
ID ADO60249 standard; protein; 393 AA.
DE Human NOV6 protein.
PN US2003134430-A1.
PD 17-JUL-2003.
PA (CURA-) CURAGEN CORP.
Query Match 39.8%; Score 37; DB 8; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1104
ID ADP19455 standard; protein; 393 AA.
DE Human secreted polypeptide #306.
PN US2004110939-A1.
PD 10-JUN-2004.
PA (GEST) GENSET SA.
Query Match 39.8%; Score 37; DB 8; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1105
ID ADO65337 standard; protein; 393 AA.
DE Novel human protein sequence #310.
PN EPI40981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 39.8%; Score 37; DB 8; Length 393;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
RESULT 1106
ID ADA57578 standard; protein; 415 AA.
DE Human secreted protein #546.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 6; Length 415;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1107
ID ADA41472 standard; protein; 415 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 6; Length 415;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1108
ID ADC74586 standard; protein; 415 AA.
DE Human secreted protein - SEQ ID 1219.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 7; Length 415;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1109
ID ADD38094 standard; protein; 415 AA.
DE Human secreted protein #277.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 7; Length 415;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1110
ID AAW88745 standard; protein; 416 AA.
DE Secreted protein encoded by gene 30 clone HTSEV09.
PN WO9854963-A2.
PD 10-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 2; Length 416;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1111
ID ABB50513 standard; protein; 416 AA.
DE Human secreted protein encoded by gene 30 SEQ ID NO:461.
PN WO200162891-A2.
PD 30-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 4; Length 416;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1112
ID AAM25861 standard; protein; 416 AA.
DE Human protein sequence SEQ ID NO:1376.
PN WO200153455-A2.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 4; Length 416;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1113
ID ABO44770 standard; protein; 416 AA.
DE Novel human secreted protein #213.
PN US2003065160-A1.
PD 03-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 6; Length 416;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1114
ID ABO26250 standard; protein; 416 AA.
DE Human protein from novel secreted protein gene 30 #2.
PN US6525174-B1.
PD 25-FEB-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 37; DB 7; Length 416;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
RESULT 1115
ID ABB1390 standard; peptide; 435 AA.
DE Human secreted protein homologue, SEQ ID NO:1760.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 4; Length 435;
Best Local Similarity 46.2%; Pred. No. 1.7e+03;
RESULT 1116
ID AAM80099 standard; protein; 435 AA.
DE Human protein SEQ ID NO 3745.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.

Query Match 39.8%; Score 37; DB 4; Length 435;
Best Local Similarity 46.2%; Pred. No. 1.7e+03;
RESULT 1117
ID AD828270 standard; protein; 445 AA.
DE Bacterial polypeptide #17303.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY//) CAO Y.
PA (HINK//) HINKLE G J.
PA (SLAT//) SLATER S C.
PA (CHEN//) CHEN X.
PA (GOLD//) GOLDMAN B S.
Query Match 39.8%; Score 37; DB 8; Length 445;
Best Local Similarity 75.0%; Pred. No. 1.8e+03;
RESULT 1118
ID ADF60384 standard; protein; 469 AA.
DE Human contig polypeptide sequence SEQ ID NO:2751.
PN W02003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 7; Length 469;
Best Local Similarity 38.5%; Pred. No. 1.9e+03;
RESULT 1119
ID AAB69271 standard; protein; 494 AA.
DE HIV-1 non-subtype B clone 92RW009-6 gag protein.
PN W0200026416-A1.
PD 11-MAY-2000.
PA (UABR-) UAB RES FOUND.
Query Match 39.8%; Score 37; DB 3; Length 494;
Best Local Similarity 47.1%; Pred. No. 2e+03;
RESULT 1120
ID ADX39491 standard; protein; 494 AA.
DE HIV gag protein #67.
PN W02005012502-A2.
PD 10-FEB-2005.
PA (SPIM-) EPIMMUNE INC.
Query Match 39.8%; Score 37; DB 9; Length 494;
Best Local Similarity 47.1%; Pred. No. 2e+03;
RESULT 1121
ID ADT57574 standard; protein; 496 AA.
DE Plant polypeptide, SEQ ID 7651.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA//) KOVALIC D K.
Query Match 39.8%; Score 37; DB 8; Length 496;
Best Local Similarity 58.3%; Pred. No. 2e+03;
RESULT 1122
ID ADN17531 standard; protein; 497 AA.
DE Bacterial polypeptide #184.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY//) CAO Y.
PA (HINK//) HINKLE G J.
PA (SLAT//) SLATER S C.
PA (CHEN//) CHEN X.
PA (GOLD//) GOLDMAN B S.
Query Match 39.8%; Score 37; DB 8; Length 497;
Best Local Similarity 60.0%; Pred. No. 2e+03;
RESULT 1123
ID ADV09236 standard; protein; 508 AA.
DE Plant full length insert polypeptide seqid 65051.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ//) LIU J.
PA (ZHOU//) ZHOU Y.
PA (KOVA//) KOVALIC D K.
PA (SCRE//) SCREEN S E.
PA (TABA//) TABASKA J E.
PA (CAOY//) CAO Y.
Query Match 39.8%; Score 37; DB 8; Length 508;
Best Local Similarity 58.3%; Pred. No. 2e+03;
RESULT 1124
ID ADX80031 standard; protein; 533 AA.
DE Plant full length insert polypeptide seqid 49397.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ//) LIU J.
PA (ZHOU//) ZHOU Y.
PA (KOVA//) KOVALIC D K.
PA (SCRE//) SCREEN S E.
PA (TABA//) TABASKA J E.
PA (CAOY//) CAO Y.
Query Match 39.8%; Score 37; DB 8; Length 533;
Best Local Similarity 52.9%; Pred. No. 2.1e+03;
RESULT 1125
ID ABU29646 standard; protein; 547 AA.
DE Protein encoded by Prokaryotic essential gene #15173.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 39.8%; Score 37; DB 6; Length 547;
Best Local Similarity 36.4%; Pred. No. 2.2e+03;
RESULT 1126
ID ADC97213 standard; protein; 549 AA.
DE E. faecium protein sequence SEQ ID 6840.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 39.8%; Score 37; DB 7; Length 549;
Best Local Similarity 36.4%; Pred. No. 2.2e+03;
RESULT 1127
ID ADP29943 standard; protein; 561 AA.
DE Human secreted protein SEQ ID #710.
PN W02004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 39.8%; Score 37; DB 8; Length 561;
Best Local Similarity 38.5%; Pred. No. 2.3e+03;
RESULT 1128
ID ABP73959 standard; protein; 569 AA.
DE Candida albicans essential protein SEQ ID NO 7796.
PN W0200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 39.8%; Score 37; DB 5; Length 569;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
RESULT 1129
ID ABG12666 standard; protein; 570 AA.
DE Novel human diagnostic protein #12657.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 4; Length 570;
Best Local Similarity 40.0%; Pred. No. 2.3e+03;
RESULT 1130
ID AAW83428 standard; protein; 611 AA.
DE Munc13-1-interacting domain of Doc2-alpha.
PN JP10313866-A.
PD 02-DEC-1998.
PA (SHIO) SHIONOGI & CO LTD.
Query Match 39.8%; Score 37; DB 2; Length 611;
Best Local Similarity 53.8%; Pred. No. 2.5e+03;
RESULT 1131
ID ADY23680 standard; protein; 616 AA.
DE Plant full length insert polypeptide seqid 71464.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ//) LIU J.
PA (ZHOU//) ZHOU Y.
PA (KOVA//) KOVALIC D K.
PA (SCRE//) SCREEN S E.
PA (TABA//) TABASKA J E.
PA (CAOY//) CAO Y.
Query Match 39.8%; Score 37; DB 8; Length 616;
Best Local Similarity 66.7%; Pred. No. 2.5e+03;
RESULT 1132

ID ADK64436 standard; protein; 647 AA.
DE Disease treating protein complex-derived protein #1157.
PN EPI338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 39.8%; Score 37; DB 7; Length 647;
Best Local Similarity 46.2%; Pred. No. 2.7e+03;
RESULT 1133
ID ADA55125 standard; protein; 707 AA.
DE Human protein, SEQ ID 2693.
PN EPI293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 39.8%; Score 37; DB 6; Length 707;
Best Local Similarity 38.5%; Pred. No. 3e+03;
RESULT 1134
ID ABP54927 standard; protein; 731 AA.
DE Mouse gelsolin.
PN W0200274982-A1.
PD 26-SEP-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 39.8%; Score 37; DB 5; Length 731;
Best Local Similarity 47.6%; Pred. No. 3.1e+03;
RESULT 1135
ID AEH04819 standard; protein; 731 AA.
DE Murine gelsolin.
PN EPI284298-A2.
PD 19-FEB-2003.
PA (WARN) WARNER LAMBERT CO.
Query Match 39.8%; Score 37; DB 6; Length 731;
Best Local Similarity 47.6%; Pred. No. 3.1e+03;
RESULT 1136
ID ADF72344 standard; protein; 731 AA.
DE Mouse gelsolin protein SEQ ID NO:40.
PN W02003103595-A2.
PD 18-DEC-2003.
PA (UTRP) UNIV ROCHESTER.
Query Match 39.8%; Score 37; DB 8; Length 731;
Best Local Similarity 47.6%; Pred. No. 3.1e+03;
RESULT 1137
ID AAM93424 standard; protein; 733 AA.
DE Human polypeptide, SEQ ID NO: 3048.
PN EPI130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 39.8%; Score 37; DB 4; Length 733;
Best Local Similarity 40.0%; Pred. No. 3.1e+03;
RESULT 1138
ID AAM93852 standard; protein; 733 AA.
DE Human polypeptide, SEQ ID NO: 3939.
PN EPI130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 39.8%; Score 37; DB 4; Length 733;
Best Local Similarity 40.0%; Pred. No. 3.1e+03;
RESULT 1139
ID AAE29757 standard; protein; 733 AA.
DE Human nucleic acid-associated protein (NAAP-4).
PN W0200277231-A2.
PD 03-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 39.8%; Score 37; DB 6; Length 733;
Best Local Similarity 40.0%; Pred. No. 3.1e+03;
RESULT 1140
ID ADL31015 standard; protein; 733 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3048.
PN EPI396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 39.8%; Score 37; DB 8; Length 733;
Best Local Similarity 40.0%; Pred. No. 3.1e+03;
RESULT 1141

ID ADL31906 standard; protein; 733 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3939.
PN EPI396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 39.8%; Score 37; DB 8; Length 733;
Best Local Similarity 40.0%; Pred. No. 3.1e+03;
RESULT 1142
ID ABU25779 standard; protein; 794 AA.
DE Aspergillus fumigatus essential gene protein #437.
PN W0200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 39.8%; Score 37; DB 6; Length 794;
Best Local Similarity 60.0%; Pred. No. 3.4e+03;
RESULT 1143
ID ABJ26379 standard; protein; 794 AA.
DE Aspergillus fumigatus essential gene protein #1037.
PN W0200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 39.8%; Score 37; DB 6; Length 794;
Best Local Similarity 60.0%; Pred. No. 3.4e+03;
RESULT 1144
ID ABB65490 standard; protein; 799 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23262.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 39.8%; Score 37; DB 4; Length 799;
Best Local Similarity 46.2%; Pred. No. 3.4e+03;
RESULT 1145
ID ABB07508 standard; protein; 802 AA.
DE Human aminoacyl tRNA synthetase (ATRS) polypeptide (ID: 7474756CD1).
PN W0200204611-A2.
PD 17-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 39.8%; Score 37; DB 5; Length 802;
Best Local Similarity 38.5%; Pred. No. 3.4e+03;
RESULT 1146
ID ADR08945 standard; protein; 922 AA.
DE Human protein useful for treating neurological disease Seq 2451.
PN EPI447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 39.8%; Score 37; DB 8; Length 922;
Best Local Similarity 53.8%; Pred. No. 4e+03;
RESULT 1147
ID ABB90849 standard; protein; 1055 AA.
DE Herbicidally active polypeptide SEQ ID NO 60.
PN W0200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 39.8%; Score 37; DB 5; Length 1055;
Best Local Similarity 63.6%; Pred. No. 4.7e+03;
RESULT 1148
ID ABP57716 standard; protein; 1073 AA.
DE Novel human protein #3.
PN W0200277257-A1.
PD 03-OCT-2002.
PA (HYSE-) HYSEQ INC.
Query Match 39.8%; Score 37; DB 6; Length 1073;
Best Local Similarity 53.8%; Pred. No. 4.8e+03;
RESULT 1149
ID ABU43426 standard; protein; 1096 AA.
DE Protein encoded by Prokaryotic essential gene #28953.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 39.8%; Score 37; DB 6; Length 1096;
Best Local Similarity 41.2%; Pred. No. 4.9e+03;
RESULT 1150
ID ADB70293 standard; protein; 1116 AA.

DE C. neoformans amino acid sequence SEQ ID NO:3337.
PN W02003052076-A2.
PD 26-JUN-2003.
PA (BLIT-) ELITRA PHARM INC.
Query Match 39.8%; Score 37; DB 7; Length 1116;
Best Local Similarity 50.0%; Pred. No. 5e+03;
RESULT 1151
ID AAR13309 standard; protein; 1180 AA.
DE Modified thermostable protoxin.
PN EF440581-A.
PD 07-AUG-1991.
PA (CIBA) CIBA GEIGY AG.
Query Match 39.8%; Score 37; DB 2; Length 1180;
Best Local Similarity 46.2%; Pred. No. 5.3e+03;
RESULT 1152
ID ABUS4638 standard; protein; 1713 AA.
DE Human NOVX polypeptide #97.
PN W0200281498-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 39.8%; Score 37; DB 6; Length 1713;
Best Local Similarity 53.8%; Pred. No. 8.1e+03;
RESULT 1153
ID AAE14920 standard; protein; 1735 AA.
DE Rat Munc13-1 protein mutant (W464R).
PN W02003039441-A2.
PD 15-MAY-2003.
PA (PLAC) MAX PLANCK GES FORDERUNG WISSENSCHAFTEN.
Query Match 39.8%; Score 37; DB 6; Length 1735;
Best Local Similarity 53.8%; Pred. No. 8.2e+03;
RESULT 1154
ID AAE14910 standard; protein; 1735 AA.
DE Rat Munc13-1 protein.
PN W02003039441-A2.
PD 15-MAY-2003.
PA (PLAC) MAX PLANCK GES FORDERUNG WISSENSCHAFTEN.
Query Match 39.8%; Score 37; DB 6; Length 1735;
Best Local Similarity 53.8%; Pred. No. 8.2e+03;
RESULT 1155
ID AAH83431 standard; protein; 1763 AA.
DE Rat Munc13-1.
PN JP10313866-A.
PD 02-DEC-1998.
PA (SHIO) SHIONOGI & CO LTD.
Query Match 39.8%; Score 37; DB 2; Length 1763;
Best Local Similarity 53.8%; Pred. No. 8.4e+03;
RESULT 1156
ID ADN24058 standard; protein; 238 AA.
DE Bacterial polypeptide #6711.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK) HINKLE G J.
PA (SLAT) SLATER S C.
PA (CHEN) CHEN X.
PA (GOLD) GOLDMAN B S.
Query Match 39.2%; Score 36.5; DB 8; Length 238;
Best Local Similarity 53.3%; Pred. No. 1e+03;
RESULT 1157
ID ABP41601 standard; protein; 261 AA.
DE Human ovarian antigen HOCPO73, SEQ ID NO:2733.
PN W0200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.2%; Score 36.5; DB 5; Length 261;
Best Local Similarity 46.2%; Pred. No. 1.2e+03;
RESULT 1158
ID AB061655 standard; protein; 291 AA.
DE Klebsiella pneumoniae polypeptide seqid 8172.
PN US610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 39.2%; Score 36.5; DB 7; Length 291;

Best Local Similarity 35.3%; Pred. No. 1.3e+03;
RESULT 1159
ID ABB70793 standard; protein; 308 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 39171.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 39.2%; Score 36.5; DB 4; Length 308;
Best Local Similarity 52.9%; Pred. No. 1.4e+03;
RESULT 1160
ID AAY72889 standard; protein; 644 AA.
DE Human pCMVN5 mutant with deleted alpha helix 4 region.
PN W0200116168-A2.
PD 08-MAR-2001.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 39.2%; Score 36.5; DB 4; Length 644;
Best Local Similarity 46.2%; Pred. No. 3.2e+03;
RESULT 1161
ID AAY72887 standard; protein; 657 AA.
DE Human pCMVN5-PP mutant (L617P/W620P).
PN W0200116168-A2.
PD 08-MAR-2001.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 39.2%; Score 36.5; DB 4; Length 657;
Best Local Similarity 46.2%; Pred. No. 3.3e+03;
RESULT 1162
ID AAY72888 standard; protein; 657 AA.
DE Human pCMVN5-R mutant (W620R).
PN W0200116168-A2.
PD 08-MAR-2001.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 39.2%; Score 36.5; DB 4; Length 657;
Best Local Similarity 46.2%; Pred. No. 3.3e+03;
RESULT 1163
ID AAY72883 standard; protein; 657 AA.
DE Human p8AN5 protein involved in cancer therapy.
PN W0200116168-A2.
PD 08-MAR-2001.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 39.2%; Score 36.5; DB 4; Length 657;
Best Local Similarity 46.2%; Pred. No. 3.3e+03;
RESULT 1164
ID ABP70646 standard; protein; 657 AA.
DE Amino acid sequence of p8AN5, an expression product of the N5 gene.
PN W02003002067-A2.
PD 03-JAN-2003.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 39.2%; Score 36.5; DB 6; Length 657;
Best Local Similarity 46.2%; Pred. No. 3.3e+03;
RESULT 1165
ID ABO52983 standard; protein; 657 AA.
DE Human putative spliceosome associated protein (SAP) #12.
PN US2003068803-A1.
PD 10-APR-2003.
PA (REED) REED R.
PA (ZHOU) ZHOU Z.
Query Match 39.2%; Score 36.5; DB 6; Length 657;
Best Local Similarity 46.2%; Pred. No. 3.3e+03;
RESULT 1166
ID ABO53063 standard; protein; 657 AA.
DE Human putative spliceosome associated protein (SAP) #40.
PN US2003068803-A1.
PD 10-APR-2003.
PA (REED) REED R.
PA (ZHOU) ZHOU Z.
Query Match 39.2%; Score 36.5; DB 6; Length 657;
Best Local Similarity 46.2%; Pred. No. 3.3e+03;
RESULT 1167
ID ABG06945 standard; protein; 673 AA.
DE Novel human diagnostic protein #6936.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.

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Query Match          39.2%; Score 36.5; DB 4; Length 673;
Best Local Similarity 46.2%; Pred. No. 3.4e+03;
RESULT 1168
ID AAU38327 standard; protein; 804 AA.
DE DE Salmonella typhi cellular proliferation protein #218.
PN W0200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match          39.2%; Score 36.5; DB 4; Length 804;
Best Local Similarity 38.1%; Pred. No. 4.2e+03;
RESULT 1169
ID ABU48260 standard; protein; 804 AA.
DE DE Protein encoded by Prokaryotic essential gene #33787.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match          39.2%; Score 36.5; DB 6; Length 804;
Best Local Similarity 38.1%; Pred. No. 4.2e+03;
RESULT 1170
ID AAW40059 standard; protein; 813 AA.
DE DE Mouse P300/CBP-associated transcriptional cofactor P/CAF.
PN W09803652-A2.
PD 29-JAN-1998.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
Query Match          39.2%; Score 36.5; DB 2; Length 813;
Best Local Similarity 53.3%; Pred. No. 4.2e+03;
RESULT 1171
ID AAW40052 standard; protein; 832 AA.
DE DE Human P300/CBP-associated transcriptional cofactor P/CAF.
PN W09803652-A2.
PD 29-JAN-1998.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
Query Match          39.2%; Score 36.5; DB 2; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.3e+03;
RESULT 1172
ID ADN06247 standard; protein; 832 AA.
DE DE Human P300/CBP-associated factor (P/CAF) protein.
PN US2004043378-A1.
PD 04-MAR-2004.
PA (AGGA/) AGGARWAL A K.
PA (ZHOU/) ZHOU M.
PA (VERD/) VERDIN E.
PA (OTTM/) OTT M.
Query Match          39.2%; Score 36.5; DB 8; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.3e+03;
RESULT 1173
ID ADN06310 standard; protein; 832 AA.
DE DE Human P300/CBP-associated factor (P/CAF) mutant protein, Y802A.
PN US2004043378-A1.
PD 04-MAR-2004.
PA (AGGA/) AGGARWAL A K.
PA (ZHOU/) ZHOU M.
PA (VERD/) VERDIN E.
PA (OTTM/) OTT M.
Query Match          39.2%; Score 36.5; DB 8; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.3e+03;
RESULT 1174
ID ADN06311 standard; protein; 832 AA.
DE DE Human P300/CBP-associated factor (P/CAF) mutant protein, Y760A.
PN US2004043378-A1.
PD 04-MAR-2004.
PA (AGGA/) AGGARWAL A K.
PA (ZHOU/) ZHOU M.
PA (VERD/) VERDIN E.
PA (OTTM/) OTT M.
Query Match          39.2%; Score 36.5; DB 8; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.3e+03;
RESULT 1175
ID ADN06309 standard; protein; 832 AA.
DE DE Human P300/CBP-associated factor (P/CAF) mutant protein, Y809A.
PN US2004043378-A1.
PD 04-MAR-2004.
PA (ZHOU/) ZHOU M.
PA (AGGA/) AGGARWAL A K.
PA (ZHOU/) ZHOU M.
PA (AGGA/) AGGARWAL A K.
PA (VERD/) VERDIN E.
PA (OTTM/) OTT M.
Query Match          39.2%; Score 36.5; DB 8; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.3e+03;
RESULT 1176
ID ADN06312 standard; protein; 832 AA.
DE DE Human P300/CBP-associated factor (P/CAF) mutant protein, V752A.
PN US2004043378-A1.
PD 04-MAR-2004.
PA (ZHOU/) ZHOU M.
PA (AGGA/) AGGARWAL A K.
PA (VERD/) VERDIN E.
PA (OTTM/) OTT M.
Query Match          39.2%; Score 36.5; DB 8; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.3e+03;
RESULT 1177
ID ADO40043 standard; protein; 832 AA.
DE DE Human P300/CBP-associated factor (P/CAF) mutant protein, Y809A.
PN US2004009613-A1.
PD 15-JAN-2004.
PA (ZHOU/) ZHOU M.
PA (AGGA/) AGGARWAL A K.
PA (VERD/) VERDIN E.
PA (OTTM/) OTT M.
Query Match          39.2%; Score 36.5; DB 8; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.3e+03;
RESULT 1178
ID ADO40046 standard; protein; 832 AA.
DE DE Human P300/CBP-associated factor (P/CAF) mutant protein, V752A.
PN US2004009613-A1.
PD 15-JAN-2004.
PA (ZHOU/) ZHOU M.
PA (AGGA/) AGGARWAL A K.
PA (VERD/) VERDIN E.
PA (OTTM/) OTT M.
Query Match          39.2%; Score 36.5; DB 8; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.3e+03;
RESULT 1179
ID ADO40045 standard; protein; 832 AA.
DE DE Human P300/CBP-associated factor (P/CAF) mutant protein, Y760A.
PN US2004009613-A1.
PD 15-JAN-2004.
PA (ZHOU/) ZHOU M.
PA (AGGA/) AGGARWAL A K.
PA (VERD/) VERDIN E.
PA (OTTM/) OTT M.
Query Match          39.2%; Score 36.5; DB 8; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.3e+03;
RESULT 1180
ID ADO40044 standard; protein; 832 AA.
DE DE Human P300/CBP-associated factor (P/CAF) mutant protein, Y802A.
PN US2004009613-A1.
PD 15-JAN-2004.
PA (ZHOU/) ZHOU M.
PA (AGGA/) AGGARWAL A K.
PA (VERD/) VERDIN E.
PA (OTTM/) OTT M.
Query Match          39.2%; Score 36.5; DB 8; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.3e+03;
RESULT 1181
ID ADO39984 standard; protein; 832 AA.
DE DE Human P300/CBP-associated factor (P/CAF) protein.
PN US2004009613-A1.
PD 15-JAN-2004.
PA (ZHOU/) ZHOU M.
PA (AGGA/) AGGARWAL A K.
PA (VERD/) VERDIN E.
PA (OTTM/) OTT M.
Query Match          39.2%; Score 36.5; DB 8; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.3e+03;
RESULT 1182
ID ADZ70677 standard; protein; 832 AA.
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DE Human protein from lung cancer marker gene PCAF.
PN WO2005032495-A2.
PD 14-APR-2005.
PA (PARB) BAYER PHARM CORP.
Query Match 39.2%; Score 36.5; DB 9; Length 832;
Best Local Similarity 53.3%; Pred. No. 4.3e+03;
RESULT 1183
ID ADE14747 standard; peptide; 14 AA.
DE Fruit fly allostatin #4.
PN US2003180297-A1.
PD 25-SEP-2003.
PA (LOWE/) LOWERY D E.
PA (SMIT/) SMITH V G.
PA (KUBI/) KUBIAK T M.
PA (LARS/) LARSEN M J.
Query Match 38.7%; Score 36; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 51;
RESULT 1184
ID ADE14700 standard; peptide; 14 AA.
DE DmgPCR binding ligand #148.
PN US2003180297-A1.
PD 25-SEP-2003.
PA (LOWE/) LOWERY D E.
PA (SMIT/) SMITH V G.
PA (KUBI/) KUBIAK T M.
PA (LARS/) LARSEN M J.
Query Match 38.7%; Score 36; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 51;
RESULT 1185
ID ADE14701 standard; peptide; 14 AA.
DE DmgPCR binding ligand #149.
PN US2003180297-A1.
PD 25-SEP-2003.
PA (LOWE/) LOWERY D E.
PA (SMIT/) SMITH V G.
PA (KUBI/) KUBIAK T M.
PA (LARS/) LARSEN M J.
Query Match 38.7%; Score 36; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 51;
RESULT 1186
ID ADL83600 standard; peptide; 14 AA.
DE Drosophila allatostatin-C peptide.
PN US2003162223-A1.
PD 28-AUG-2003.
PA (LOWE/) LOWERY D E.
PA (SMIT/) SMITH V G.
PA (KUBI/) KUBIAK T M.
PA (LARS/) LARSEN M J.
Query Match 38.7%; Score 36; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 51;
RESULT 1187
ID ADE14703 standard; peptide; 15 AA.
DE DmgPCR binding ligand #151.
PN US2003180297-A1.
PD 25-SEP-2003.
PA (LOWE/) LOWERY D E.
PA (SMIT/) SMITH V G.
PA (KUBI/) KUBIAK T M.
PA (LARS/) LARSEN M J.
Query Match 38.7%; Score 36; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 55;
RESULT 1188
ID ADL8599 standard; peptide; 15 AA.
DE Manducta sexta drostatin-C peptide.
PN US2003162223-A1.
PD 28-AUG-2003.
PA (LOWE/) LOWERY D E.
PA (SMIT/) SMITH V G.
PA (KUBI/) KUBIAK T M.
PA (LARS/) LARSEN M J.
Query Match 38.7%; Score 36; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 55;
RESULT 1189
ID AAB55895 standard; protein; 90 AA.
DE Skin cell protein, SEQ ID NO: 134.
PN WO200069884-A2.

ID ADH52754 standard; peptide; 29 AA.
DE Porphyromonas gulae B43 OprF peptide 2.
PN WO2003054755-A2.
PD 03-JUL-2003.
PA (PFIZ) PFIZER PROD INC.
Query Match 38.7%; Score 36; DB 7; Length 29;
Best Local Similarity 42.9%; Pred. No. 1.2e+02;
RESULT 1190
ID ADX88003 standard; protein; 61 AA.
DE Plant full length insert polypeptide seqid 50667.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUG/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOX/) CAO Y.
Query Match 38.7%; Score 36; DB 8; Length 61;
Best Local Similarity 54.5%; Pred. No. 2.7e+02;
RESULT 1191
ID AAG02548 standard; protein; 70 AA.
DE Human secreted protein, SEQ ID NO: 6629.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 38.7%; Score 36; DB 3; Length 70;
Best Local Similarity 42.9%; Pred. No. 3.2e+02;
RESULT 1192
ID ABP06392 standard; protein; 79 AA.
DE Human ORFX protein sequence SEQ ID NO:12766.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 5; Length 79;
Best Local Similarity 54.5%; Pred. No. 3.7e+02;
RESULT 1193
ID ABU70954 standard; protein; 85 AA.
DE Human adipocyte Selected Interacting domain, SID, #585.
PN WO200286122-A2.
PD 31-OCT-2002.
PA (HYBR-) HYBRIGENICS.
Query Match 38.7%; Score 36; DB 6; Length 85;
Best Local Similarity 50.0%; Pred. No. 4e+02;
RESULT 1194
ID AAU79594 standard; protein; 88 AA.
DE Human TRAIL splice variant 1, TRA-3-T7, protein.
PN US2002061525-A1.
PD 23-MAY-2002.
PA (YELI/) YELIN R.
PA (KHOS/) KHOSRAVI R.
PA (SAVI/) SAVITZKY K.
Query Match 38.7%; Score 36; DB 5; Length 88;
Best Local Similarity 41.7%; Pred. No. 4.1e+02;
RESULT 1195
ID AAG12285 standard; protein; 89 AA.
DE Zea mays protein fragment SEQ ID NO: 11339.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 89;
Best Local Similarity 54.5%; Pred. No. 4.2e+02;
RESULT 1196
ID AAY75956 standard; protein; 90 AA.
DE Rat skin cell protein, SEQ ID 134.
PN WO9955865-A1.
PD 04-NOV-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 38.7%; Score 36; DB 3; Length 90;
Best Local Similarity 46.2%; Pred. No. 4.2e+02;
RESULT 1197
ID AAB55895 standard; protein; 90 AA.
DE Skin cell protein, SEQ ID NO: 134.
PN WO200069884-A2.

PD 23-NOV-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 38.7%; Score 36; DB 4; Length 90;
Best Local Similarity 46.2%; Pred. No. 4.2e+02;
RESULT 1198
ID AB872095 standard; protein; 90 AA.
DE Rat protein isolated from skin cells SEQ ID NO: 134.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 38.7%; Score 36; DB 5; Length 90;
Best Local Similarity 46.2%; Pred. No. 4.2e+02;
RESULT 1199
ID AAU79595 standard; protein; 98 AA.
DE Human TRAIL splice variant 2, TRA-31-T7, protein.
PN US2002061525-A1.
PD 23-MAY-2002.
PA (VELI/) YELIN R.
PA (KHOS/) KHOSRAVI R.
PA (SAVI/) SAVITZKY K.
Query Match 38.7%; Score 36; DB 5; Length 98;
Best Local Similarity 41.7%; Pred. No. 4.7e+02;
RESULT 1200
ID AB084414 standard; protein; 98 AA.
DE Human cancer-associated protein HP7-053.2.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 38.7%; Score 36; DB 8; Length 98;
Best Local Similarity 41.7%; Pred. No. 4.7e+02;
RESULT 1201
ID AAU43074 standard; protein; 100 AA.
DE Propionibacterium acnes immunogenic protein #3970.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 38.7%; Score 36; DB 4; Length 100;
Best Local Similarity 50.0%; Pred. No. 4.8e+02;
RESULT 1202
ID AAB93388 standard; protein; 100 AA.
DE Human protein sequence SEQ ID NO:12562.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 38.7%; Score 36; DB 4; Length 100;
Best Local Similarity 55.6%; Pred. No. 4.8e+02;
RESULT 1203
ID AAM39593 standard; protein; 100 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #4269.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 38.7%; Score 36; DB 6; Length 100;
Best Local Similarity 50.0%; Pred. No. 4.8e+02;
RESULT 1204
ID AAW19790 standard; protein; 101 AA.
DE Human apoptosis inducer cytokine TRAIL deletion variant.
PN WO9701633-A1.
PD 16-JAN-1997.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 2; Length 101;
Best Local Similarity 41.7%; Pred. No. 4.8e+02;
RESULT 1205
ID AAW56761 standard; protein; 101 AA.
DE Human TRAIL deletion variant (huTRAILdv) clone protein sequence.
PN US5763223-A.
PD 09-JUN-1998.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 2; Length 101;
Best Local Similarity 41.7%; Pred. No. 4.8e+02;
RESULT 1206
ID AAY79163 standard; protein; 101 AA.
DE Human endothelial PAS domain protein-1 C-terminal polypeptide.

PN WO200009657-A2.
PD 24-FEB-2000.
PA (HARD) HARVARD COLLEGE.
Query Match 38.7%; Score 36; DB 3; Length 101;
Best Local Similarity 54.5%; Pred. No. 4.8e+02;
RESULT 1207
ID AAE11032 standard; protein; 101 AA.
DE Human TRAIL deletion variant (huTRAILdv).
PN US6284236-B1.
PD 04-SEP-2001.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 4; Length 101;
Best Local Similarity 41.7%; Pred. No. 4.8e+02;
RESULT 1208
ID ABU08559 standard; protein; 101 AA.
DE Human TNF Related Apoptosis Inducing Ligand, TRAIL, deletion variant.
PN US6521228-B1.
PD 18-FEB-2003.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 6; Length 101;
Best Local Similarity 41.7%; Pred. No. 4.8e+02;
RESULT 1209
ID ADK15500 standard; protein; 101 AA.
DE Human TRAIL protein (deletion variant).
PN US2004052788-A1.
PD 18-MAR-2004.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 8; Length 101;
Best Local Similarity 41.7%; Pred. No. 4.8e+02;
RESULT 1210
ID ABE92346 standard; protein; 101 AA.
DE Human TRAIL deletion variant (huTRAILdv), SEQ ID 4.
PN US2005158823-A1.
PD 21-JUL-2005.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 9; Length 101;
Best Local Similarity 41.7%; Pred. No. 4.8e+02;
RESULT 1211
ID AAB43222 standard; protein; 104 AA.
DE Human ORFX ORF2986 polypeptide sequence SEQ ID NO:5972.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 3; Length 104;
Best Local Similarity 54.5%; Pred. No. 5e+02;
RESULT 1212
ID AAG22301 standard; protein; 104 AA.
DE Zea mays protein fragment SEQ ID NO: 25176.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 104;
Best Local Similarity 54.5%; Pred. No. 5e+02;
RESULT 1213
ID AAG21375 standard; protein; 105 AA.
DE Zea mays protein fragment SEQ ID NO: 23910.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 105;
Best Local Similarity 54.5%; Pred. No. 5e+02;
RESULT 1214
ID AAG33020 standard; protein; 105 AA.
DE Zea mays protein fragment SEQ ID NO: 39947.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 105;
Best Local Similarity 54.5%; Pred. No. 5e+02;
RESULT 1215
ID ADT87801 standard; protein; 105 AA.
DE Plant homologue of yeast SRP YLR275W #2.
PN WO2004092398-A2.
PD 28-OCT-2004.
PA (BADI) BASF PLANT SCI GMBH.
Query Match 38.7%; Score 36; DB 8; Length 105;

Best Local Similarity 54.5%; Pred. No. 5e+02;
RESULT 1216
ID AAU79600 standard; protein; 113 AA.
DE Human TRAIL splice variant 7, TRA-54-f1, protein.
PN US2002061525-A1.
PD 23-MAY-2002.
PA (YELI/) YELIN R.
PA (KHOS/) KHOSRAVI R.
PA (SAVI/) SAVITZKY K.
Query Match 38.7%; Score 36; DB 5; Length 113;
Best Local Similarity 41.7%; Pred. No. 5.5e+02;
RESULT 1217
ID ADL98267 standard; protein; 120 AA.
DE Human TNF-related apoptosis inducing ligand splice variant protein #4.
PN US6720182-B1.
PD 13-APR-2004.
PA (COMP-) COMPUGEN LTD CORP.
Query Match 38.7%; Score 36; DB 8; Length 120;
Best Local Similarity 41.7%; Pred. No. 5.9e+02;
RESULT 1218
ID ADM0623 standard; protein; 120 AA.
DE Human protein encoded by gene splice variant #6.
PN US2004258681-A1.
PD 23-DEC-2004.
PA (COMP-) COMPUGEN LTD CORP.
Query Match 38.7%; Score 36; DB 9; Length 120;
Best Local Similarity 41.7%; Pred. No. 5.9e+02;
RESULT 1219
ID AAG03752 standard; protein; 121 AA.
DE Human secreted protein, SEQ ID NO: 7833.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST-) GENSET.
Query Match 38.7%; Score 36; DB 3; Length 121;
Best Local Similarity 41.7%; Pred. No. 5.9e+02;
RESULT 1220
ID ABH69940 standard; protein; 122 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 36612.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 38.7%; Score 36; DB 4; Length 122;
Best Local Similarity 100.0%; Pred. No. 6e+02;
RESULT 1221
ID ADL98266 standard; protein; 122 AA.
DE Human TNF-related apoptosis inducing ligand splice variant protein #3.
PN US6720182-B1.
PD 13-APR-2004.
PA (COMP-) COMPUGEN LTD CORP.
Query Match 38.7%; Score 36; DB 8; Length 122;
Best Local Similarity 41.7%; Pred. No. 6e+02;
RESULT 1222
ID ADM0622 standard; protein; 122 AA.
DE Human protein encoded by gene splice variant #5.
PN US2004258681-A1.
PD 23-DEC-2004.
PA (COMP-) COMPUGEN LTD CORP.
Query Match 38.7%; Score 36; DB 9; Length 122;
Best Local Similarity 41.7%; Pred. No. 6e+02;
RESULT 1223
ID AAY35754 standard; protein; 125 AA.
DE Chlamydia pneumoniae protein not found in C. trachomatis.
PN W09927105-A2.
PD 03-JUN-1999.
PA (GEST-) GENSET.
Query Match 38.7%; Score 36; DB 2; Length 125;
Best Local Similarity 66.7%; Pred. No. 6.2e+02;
RESULT 1224
ID ADY30583 standard; protein; 127 AA.
DE Human splice variant protein expressed in ovary cells DEX0487_010.aa.1.
PN WO2005017102-A2.
PD 24-FEB-2005.
PA (DIAD-) DIADEXUS INC.

Query Match 38.7%; Score 36; DB 9; Length 127;
Best Local Similarity 41.7%; Pred. No. 6.3e+02;
RESULT 1225
ID AAU54614 standard; protein; 130 AA.
DE Proptonibacterium acnes immunogenic protein #15510.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 38.7%; Score 36; DB 4; Length 130;
Best Local Similarity 38.9%; Pred. No. 6.4e+02;
RESULT 1226
ID ABMS1133 standard; protein; 130 AA.
DE Proptonibacterium acnes predicted ORF-encoded polypeptide #15809.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 38.7%; Score 36; DB 6; Length 130;
Best Local Similarity 38.9%; Pred. No. 6.4e+02;
RESULT 1227
ID ABP72618 standard; protein; 131 AA.
DE Snowdrop agglutinin-Manduca sexta allatostatin protein fusion.
PN WO2003014150-A2.
PD 20-FEB-2003.
PA (UYDU-) UNIV DURHAM.
PA (SNVI-) DEPT ENVIRONMENT FOOD & RURAL AFFAIRS.
Query Match 38.7%; Score 36; DB 6; Length 131;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
RESULT 1228
ID AAB67715 standard; protein; 133 AA.
DE DE Protein encoded by cDNA clone with similarity to murine GL50 cDNA.
PN WO200121796-A2.
PD 29-MAR-2001.
PA (GBMY) GENETICS INST INC.
Query Match 38.7%; Score 36; DB 4; Length 133;
Best Local Similarity 42.9%; Pred. No. 6.6e+02;
RESULT 1229
ID ABB70442 standard; protein; 137 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 38118.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 38.7%; Score 36; DB 4; Length 137;
Best Local Similarity 40.0%; Pred. No. 6.8e+02;
RESULT 1230
ID AAU67799 standard; protein; 137 AA.
DE Proptonibacterium acnes immunogenic protein #28695.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 38.7%; Score 36; DB 4; Length 137;
Best Local Similarity 38.9%; Pred. No. 6.8e+02;
RESULT 1231
ID ABM64318 standard; protein; 137 AA.
DE Proptonibacterium acnes predicted ORF-encoded polypeptide #28994.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 38.7%; Score 36; DB 6; Length 137;
Best Local Similarity 38.9%; Pred. No. 6.8e+02;
RESULT 1232
ID AAG20539 standard; protein; 144 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 22770.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 144;
Best Local Similarity 41.2%; Pred. No. 7.2e+02;
RESULT 1233
ID AAG47787 standard; protein; 144 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 60268.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 144;
Best Local Similarity 41.2%; Pred. No. 7.2e+02;

RESULT 1234
ID ADR09299 standard; protein; 151 AA.
DE Human protein useful for treating neurological disease Seq 2805.
PN EPI447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 38.7%; Score 36; DB 8; Length 151;
Best Local Similarity 46.2%; Pred. No. 7.6e+02;
RESULT 1235
ID ADV12886 standard; protein; 151 AA.
DE Plant full length insert polypeptide seqid 68701.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 38.7%; Score 36; DB 8; Length 151;
Best Local Similarity 75.0%; Pred. No. 7.6e+02;
RESULT 1236
ID AAB58333 standard; protein; 157 AA.
DE Lung cancer associated polypeptide sequence SEQ ID 671.
PN WO20055180-A2.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 38.7%; Score 36; DB 3; Length 157;
Best Local Similarity 54.5%; Pred. No. 8e+02;
RESULT 1237
ID AAG33019 standard; protein; 163 AA.
DE Zea mays protein fragment SEQ ID NO: 39946.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 163;
Best Local Similarity 54.5%; Pred. No. 8.3e+02;
RESULT 1238
ID ADL98264 standard; protein; 169 AA.
DE Human TNF-related apoptosis inducing ligand splice variant protein #1.
PN US6720182-B1.
PD 13-APR-2004.
PA (COMP-) COMPUGEN LTD CORP.
Query Match 38.7%; Score 36; DB 8; Length 169;
Best Local Similarity 41.7%; Pred. No. 8.7e+02;
RESULT 1239
ID ADM00620 standard; protein; 169 AA.
DE Human protein encoded by gene splice variant #3.
PN US2004258681-A1.
PD 23-DEC-2004.
PA (COMP-) COMPUGEN LTD CORP.
Query Match 38.7%; Score 36; DB 9; Length 169;
Best Local Similarity 41.7%; Pred. No. 8.7e+02;
RESULT 1240
ID AAG21373 standard; protein; 172 AA.
DE Zea mays protein fragment SEQ ID NO: 23908.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 172;
Best Local Similarity 54.5%; Pred. No. 8.8e+02;
RESULT 1241
ID AAG60079 standard; protein; 174 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77779.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 174;
Best Local Similarity 38.5%; Pred. No. 9e+02;
RESULT 1242
ID AAG60078 standard; protein; 176 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77778.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 176;

Best Local Similarity 38.5%; Pred. No. 9.1e+02;
RESULT 1243
ID AAG60077 standard; protein; 179 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77777.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 38.7%; Score 36; DB 3; Length 179;
Best Local Similarity 38.5%; Pred. No. 9.2e+02;
RESULT 1244
ID ADF5456 standard; protein; 179 AA.
DE Human novel polypeptide #20.
PN JP2003245081-A.
PD 02-SEP-2003.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
Query Match 38.7%; Score 36; DB 7; Length 179;
Best Local Similarity 50.0%; Pred. No. 9.2e+02;
RESULT 1245
ID ADB63818 standard; protein; 185 AA.
DE Human protein encoded by clone ADRGL20021910.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 38.7%; Score 36; DB 7; Length 185;
Best Local Similarity 42.9%; Pred. No. 9.6e+02;
RESULT 1246
ID AAU79599 standard; protein; 188 AA.
DE Human TRAIL splice variant 6, TRA-33-T7, protein.
PN US2002061525-A1.
PD 23-MAY-2002.
PA (YELI/) YELIN R.
PA (KHOS/) KHOSRAVI R.
PA (SAVI/) SAVITZKY K.
Query Match 38.7%; Score 36; DB 5; Length 188;
Best Local Similarity 41.7%; Pred. No. 9.8e+02;
RESULT 1247
ID ADY11445 standard; protein; 188 AA.
DE Plant full length insert polypeptide seqid 67260.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 38.7%; Score 36; DB 8; Length 188;
Best Local Similarity 54.5%; Pred. No. 9.8e+02;
RESULT 1248
ID ABG21529 standard; protein; 190 AA.
DE Novel human diagnostic protein #21520.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 38.7%; Score 36; DB 4; Length 190;
Best Local Similarity 50.0%; Pred. No. 9.9e+02;
RESULT 1249
ID ABG00247 standard; protein; 192 AA.
DE Novel human diagnostic protein #238.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 38.7%; Score 36; DB 4; Length 192;
Best Local Similarity 50.0%; Pred. No. 1e+03;
RESULT 1250
ID ABB72279 standard; protein; 193 AA.
DE Human protein isolated from skin cells SEQ ID NO: 491.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 38.7%; Score 36; DB 5; Length 193;
Best Local Similarity 66.7%; Pred. No. 1e+03;
RESULT 1251

ID ADU00112 standard; protein; 203 AA.
DE Amino acid sequence of G-protein coupled receptor GCRC-4.
PN W02004092350-A2.
PD 28-OCT-2004.
PA (INCY-) INCYTE CORP.
Query Match 38.7%; Score 36; DB 8; Length 203;
Best Local Similarity 46.2%; Pred. No. 1.1e+03;
RESULT 1252
ID AAY09197 standard; protein; 208 AA.
DE Human DNAX interleukin-40 (DIL-40) alternative sequence.
PN W09919491-A2.
PD 22-APR-1999.
PA (SCHE) SCHERING CORP.
Query Match 38.7%; Score 36; DB 2; Length 208;
Best Local Similarity 53.8%; Pred. No. 1.1e+03;
RESULT 1253
ID AAY09196 standard; protein; 208 AA.
DE Human DNAX interleukin-40 (DIL-40) polypeptide.
PN W09919491-A2.
PD 22-APR-1999.
PA (SCHE) SCHERING CORP.
Query Match 38.7%; Score 36; DB 2; Length 208;
Best Local Similarity 53.8%; Pred. No. 1.1e+03;
RESULT 1254
ID ADT90843 standard; protein; 208 AA.
DE Human DNAX IL-40.
PN US2004192891-A1.
PD 30-SEP-2004.
PA (SCHE) SCHERING CORP.
Query Match 38.7%; Score 36; DB 8; Length 208;
Best Local Similarity 53.8%; Pred. No. 1.1e+03;
RESULT 1255
ID ADT61031 standard; protein; 208 AA.
DE Human cytokine DNAX IL-40 (DIL-40).
PN US6800460-B1.
PD 05-OCT-2004.
PA (SCHE) SCHERING CORP.
Query Match 38.7%; Score 36; DB 8; Length 208;
Best Local Similarity 53.8%; Pred. No. 1.1e+03;
RESULT 1256
ID ADY57156 standard; protein; 208 AA.
DE Human DNAX IL-40 protein.
PN US2005048625-A1.
PD 03-MAR-2005.
PA (SCHE) SCHERING CORP.
Query Match 38.7%; Score 36; DB 9; Length 208;
Best Local Similarity 53.8%; Pred. No. 1.1e+03;
RESULT 1257
ID AAU99301 standard; protein; 212 AA.
DE Human TRAIL splice variant 8, rpl-6-6, protein.
PN US2002061525-A1.
PD 23-MAY-2002.
PA (YELI/) YELIN R.
PA (KHOS/) KHOSRAVI R.
PA (SAVI/) SAVITZKY K.
Query Match 38.7%; Score 36; DB 5; Length 212;
Best Local Similarity 41.7%; Pred. No. 1.1e+03;
RESULT 1258
ID ABB40635 standard; protein; 212 AA.
DE L. pneumophila protein SEQ ID NO 4967.
PN W02005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 38.7%; Score 36; DB 9; Length 212;
Best Local Similarity 53.8%; Pred. No. 1.1e+03;
RESULT 1259
ID ABB37312 standard; protein; 216 AA.
DE L. pneumophila protein SEQ ID NO 1644.
PN W02005049642-A2.
PD 02-JUN-2005.

PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 38.7%; Score 36; DB 9; Length 216;
Best Local Similarity 53.8%; Pred. No. 1.1e+03;
RESULT 1260
ID AAB94978 standard; protein; 226 AA.
DE Human protein sequence SEQ ID NO:16560.
PN EP1074517-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 38.7%; Score 36; DB 4; Length 226;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1261
ID AAG20538 standard; protein; 227 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 22769.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (HELI-) HELIX RES INST.
Query Match 38.7%; Score 36; DB 3; Length 227;
Best Local Similarity 41.2%; Pred. No. 1.2e+03;
RESULT 1262
ID AAG47786 standard; protein; 227 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 60267.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (FARB) BAYER AG.
Query Match 38.7%; Score 36; DB 5; Length 227;
Best Local Similarity 41.2%; Pred. No. 1.2e+03;
RESULT 1263
ID ABB92117 standard; protein; 227 AA.
DE Herbicidally active polypeptide SEQ ID NO 1328.
PN W0200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 38.7%; Score 36; DB 3; Length 227;
Best Local Similarity 41.2%; Pred. No. 1.2e+03;
RESULT 1264
ID ABP79680 standard; protein; 233 AA.
DE N. gonorrhoeae amino acid sequence SEQ ID 5890.
PN W0200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Query Match 38.7%; Score 36; DB 6; Length 233;
Best Local Similarity 41.2%; Pred. No. 1.2e+03;
RESULT 1265
ID ADD12586 standard; protein; 233 AA.
DE Human ENZW-46 protein SEQ ID NO:46.
PN W02003072729-A2.
PD 04-SEP-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 38.7%; Score 36; DB 7; Length 233;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
RESULT 1266
ID ADH71888 standard; protein; 235 AA.
DE Human protein of the invention NOV31h SEQ ID NO:784.
PN W02003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 8; Length 235;
Best Local Similarity 42.9%; Pred. No. 1.3e+03;
RESULT 1267
ID ADM05434 standard; protein; 242 AA.
DE Human protein of the invention SEQ ID NO:4119.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 38.7%; Score 36; DB 7; Length 242;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
RESULT 1268
ID ADF59116 standard; protein; 244 AA.
DE Human polypeptide sequence SEQ ID NO:1524.
PN W02003080795-A2.
PD 02-OCT-2003.

PA (HYSE-) HYSEQ INC.
 Query Match 38.7%; Score 36; DB 7; Length 244;
 Best Local Similarity 50.0%; Pred. No. 1.3e+03;
 RESULT 1269
 ID ABB65303 standard; protein; 245 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 22701.
 PN W0200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 38.7%; Score 36; DB 4; Length 245;
 Best Local Similarity 50.0%; Pred. No. 1.3e+03;
 RESULT 1270
 ID ABB50023 standard; protein; 246 AA.
 DE Listeria monocytogenes protein #2727.
 PN W0200177335-A2.
 PD 18-OCT-2001.
 PA (INSP) INST PASTEUR.
 Query Match 38.7%; Score 36; DB 5; Length 246;
 Best Local Similarity 30.8%; Pred. No. 1.3e+03;
 RESULT 1271
 ID AAU79598 standard; protein; 246 AA.
 DE Human TRAIL splice variant 5, TRA-20-SP6, protein.
 PN US2002061525-A1.
 PD 23-MAY-2002.
 PA (YELI/) YELIN R.
 PA (KHOS/) KHOSRAVI R.
 PA (SAVI/) SAVITZKY K.
 Query Match 38.7%; Score 36; DB 5; Length 246;
 Best Local Similarity 41.7%; Pred. No. 1.3e+03;
 RESULT 1272
 ID ADI17038 standard; protein; 247 AA.
 DE Human NOVX protein homologue Seqid 574.
 PN W0200268649-A2.
 PD 06-SEP-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 38.7%; Score 36; DB 5; Length 247;
 Best Local Similarity 50.0%; Pred. No. 1.3e+03;
 RESULT 1273
 ID ADX72396 standard; protein; 250 AA.
 DE Plant full length insert polypeptide seqid 41762.
 PN US2004034888-A1.
 PD 19-FEB-2004.
 PA (LIUJ/) LIU Y.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABA/) TABASKA J E.
 PA (CAOY/) CAO Y.
 Query Match 38.7%; Score 36; DB 8; Length 250;
 Best Local Similarity 35.7%; Pred. No. 1.4e+03;
 RESULT 1274
 ID ABM94614 standard; protein; 250 AA.
 DE M. xanthus protein sequence, seq id 13813.
 PN US6833447-B1.
 PD 21-DEC-2004.
 PA (MONS) MONSANTO TECHNOLOGY LLC.
 Query Match 38.7%; Score 36; DB 9; Length 250;
 Best Local Similarity 42.9%; Pred. No. 1.4e+03;
 RESULT 1275
 ID AAH84141 standard; peptide; 252 AA.
 DE Desaturase enzyme peptide sequence.
 PN W09846763-A1.
 PD 22-OCT-1998.
 PA (CALJ) CALGENE LLC.
 PA (ABBO) ABBOTT LAB.
 Query Match 38.7%; Score 36; DB 2; Length 252;
 Best Local Similarity 40.0%; Pred. No. 1.4e+03;
 RESULT 1276
 ID ADY26629 standard; protein; 262 AA.
 DE Streptomyces vinaceus VioH protein.
 PN US2005042726-A1.
 PD 24-FEB-2005.
 PA (THOM/) THOMAS M G.

PA (CHAN/) CHAN Y A.
 Query Match 38.7%; Score 36; DB 9; Length 262;
 Best Local Similarity 50.0%; Pred. No. 1.4e+03;
 RESULT 1277
 ID AAV72935 standard; protein; 266 AA.
 DE OmpA signal peptide-human TRAIL fusion protein.
 PN W0200125397-A2.
 PD 12-APR-2001.
 PA (VION-) VION PHARM INC.
 Query Match 38.7%; Score 36; DB 4; Length 266;
 Best Local Similarity 41.7%; Pred. No. 1.4e+03;
 RESULT 1278
 ID ASU09032 standard; protein; 267 AA.
 DE Human tumour wilting extract protein, Apo-2L I_100.
 PN CN1367248-A.
 PD 04-SEP-2002.
 PA (TWOM-) NO 2 MILITARY MEDICAL COLLEGE PLA.
 Query Match 38.7%; Score 36; DB 6; Length 267;
 Best Local Similarity 41.7%; Pred. No. 1.5e+03;
 RESULT 1279
 ID ABR82204 standard; protein; 270 AA.
 DE Chimeric hTNFalpha/hTRAIL protein.
 PN W02003050254-A2.
 PD 19-JUN-2003.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 38.7%; Score 36; DB 6; Length 270;
 Best Local Similarity 41.7%; Pred. No. 1.5e+03;
 RESULT 1280
 ID ADL98265 standard; protein; 271 AA.
 DE Human TNF-related apoptosis inducing ligand splice variant protein #2.
 PN US6720182-B1.
 PD 13-APR-2004.
 PA (COMP-) COMPUGEN LTD CORP.
 Query Match 38.7%; Score 36; DB 8; Length 271;
 Best Local Similarity 41.7%; Pred. No. 1.5e+03;
 RESULT 1281
 ID ADM00621 standard; protein; 271 AA.
 DE Human protein encoded by gene splice variant #4.
 PN US2004258681-A1.
 PD 23-DEC-2004.
 PA (COMP-) COMPUGEN LTD CORP.
 Query Match 38.7%; Score 36; DB 9; Length 271;
 Best Local Similarity 41.7%; Pred. No. 1.5e+03;
 RESULT 1282
 ID ADF58901 standard; protein; 274 AA.
 DE Human polypeptide sequence SEQ ID NO:1309.
 PN W02003080795-A2.
 PD 02-OCT-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match 38.7%; Score 36; DB 7; Length 274;
 Best Local Similarity 50.0%; Pred. No. 1.5e+03;
 RESULT 1283
 ID ADT59020 standard; protein; 278 AA.
 DE Plant polypeptide, SEQ ID 9097.
 PN US2004216190-A1.
 PD 28-OCT-2004.
 PA (KOVA/) KOVALIC D K.
 Query Match 38.7%; Score 36; DB 8; Length 278;
 Best Local Similarity 45.5%; Pred. No. 1.5e+03;
 RESULT 1284
 ID AAW76332 standard; protein; 279 AA.
 DE Human TL2 (TRAIL), ligand for TR5.
 PN EP867509-A2.
 PD 30-SEP-1998.
 PA (SWIK) SMITHKLINE BEECHAM CORP.
 Query Match 38.7%; Score 36; DB 2; Length 279;
 Best Local Similarity 41.7%; Pred. No. 1.5e+03;
 RESULT 1285
 ID AAW95032 standard; protein; 279 AA.
 DE Tumour necrosis factor receptor (TNF-R) related polypeptide TL2.
 PN EP897114-A2.
 PD 17-FEB-1999.

PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 38.7%; Score 36; DB 2; Length 279;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1286
ID ADX71478 standard; protein; 279 AA.
DE Plant full length insert polypeptide seqid 40844.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOV/) CAO Y.
Query Match 38.7%; Score 36; DB 8; Length 279;
Best Local Similarity 25.0%; Pred. No. 1.5e+03;
RESULT 1287
ID ADN95444 standard; protein; 280 AA.
DE Human BEC/LBC-related protein sequence SeqID367.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN-) LICENTIA LTD.
Query Match 38.7%; Score 36; DB 7; Length 280;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1288
ID AAW19777 standard; protein; 281 AA.
DE Novel cytokine Apo-2 ligand.
PN WO9725428-A1.
PD 17-JUL-1997.
PA (GETH-) GENENTECH INC.
Query Match 38.7%; Score 36; DB 2; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1289
ID AAW27134 standard; protein; 281 AA.
DE Human Apoptosis inducing molecule-I (AIM-I).
PN WO9733899-A1.
PD 18-SEP-1997.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 2; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1290
ID AAW19787 standard; protein; 281 AA.
DE Human apoptosis inducer cytokine TRAIL.
PN WO9701633-A1.
PD 16-JAN-1997.
PA (IMMV-) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 2; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1291
ID AAW76829 standard; protein; 281 AA.
DE Human TL2 protein.
PN EP870827-A2.
PD 14-OCT-1998.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 38.7%; Score 36; DB 2; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1292
ID AAW56760 standard; protein; 281 AA.
DE Human TRAIL polypeptide.
PN US5763223-A.
PD 09-JUN-1998.
PA (IMMV-) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 2; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1293
ID AAW44354 standard; protein; 281 AA.
DE Human AGP-1.
PN WO9746686-A2.
PD 11-DEC-1997.
PA (AMGE-) AMGEN INC.
Query Match 38.7%; Score 36; DB 2; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;

RESULT 1294
ID AAY01517 standard; peptide; 281 AA.
DE Protein associated with neurodegenerative and autoimmune diseases.
PN FR2766713-A1.
PD 05-FEB-1999.
PA (INMR) BIO MERIEUX.
Query Match 38.7%; Score 36; DB 2; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1295
ID AAY01516 standard; peptide; 281 AA.
DE Protein associated with neurodegenerative and autoimmune diseases.
PN FR2766713-A1.
PD 05-FEB-1999.
PA (INMR) BIO MERIEUX.
Query Match 38.7%; Score 36; DB 2; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1296
ID AAY27018 standard; protein; 281 AA.
DE Human Apo-2 ligand (Apo-2L) variant D269A.
PN WO9936535-A1.
PD 22-JUL-1999.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 2; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1297
ID AAY27019 standard; protein; 281 AA.
DE Human Apo-2 ligand (Apo-2L) variant D203A, D218A, D269A.
PN WO9936535-A1.
PD 22-JUL-1999.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 2; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1298
ID AAY27016 standard; protein; 281 AA.
DE Human Apo-2 ligand (Apo-2L) variant D203A.
PN WO9936535-A1.
PD 22-JUL-1999.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 2; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1299
ID AAY27017 standard; protein; 281 AA.
DE Human Apo-2 ligand (Apo-2L) variant D218A.
PN WO9936535-A1.
PD 22-JUL-1999.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 2; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1300
ID AAY27012 standard; protein; 281 AA.
DE Human Apo-2 ligand (Apo-2L) polypeptide.
PN WO9936535-A1.
PD 22-JUL-1999.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 2; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1301
ID AAY81956 standard; protein; 281 AA.
DE Human Apo-2 ligand protein sequence.
PN US6046048-A.
PD 04-APR-2000.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 3; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1302
ID AAB24038 standard; protein; 281 AA.
DE Human PRO1096 protein sequence SEQ ID NO:51.
PN WO200053750-A1.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 3; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1303

ID AAB08545 standard; protein; 281 AA.
DE Amino acid sequence of a human TRAIL polypeptide.
PN WO200048619-A1.
PD 24-AUG-2000.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 38.7%; Score 36; DB 3; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1304
ID AAB28691 standard; protein; 281 AA.
DE Human AGP-1.
PN WO200063253-A1.
PD 26-OCT-2000.
PA (AMGE-) AMGEN INC.
Query Match 38.7%; Score 36; DB 3; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1305
ID AAB50977 standard; protein; 281 AA.
DE Human PRO1096 protein.
PN WO200073348-A2.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 4; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1306
ID AAB67243 standard; protein; 281 AA.
DE Human Apo2 ligand.
PN WO200100832-A1.
PD 04-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 4; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1307
ID AAE11031 standard; protein; 281 AA.
DE Human TNF related apoptosis inducing ligand (TRAIL) protein.
PN US6284236-B1.
PD 04-SEP-2001.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 4; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1308
ID AAB48350 standard; protein; 281 AA.
DE Human TL2 polypeptide.
PN WO200077191-A1.
PD 21-DEC-2000.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 38.7%; Score 36; DB 4; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1309
ID ABB08133 standard; protein; 281 AA.
DE Human TRAIL polypeptide.
PN WO200236141-A2.
PD 10-MAY-2002.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 5; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1310
ID ABG31630 standard; protein; 281 AA.
DE Human TRAIL protein.
PN WO200266044-A2.
PD 29-AUG-2002.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 5; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1311
ID AAU75062 standard; protein; 281 AA.
DE Human TNF related apoptosis inducing ligand (TRAIL) protein.
PN US6329148-B1.
PD 11-DEC-2001.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 38.7%; Score 36; DB 5; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1312
ID ABG72257 standard; protein; 281 AA.

DE Human tumour related apoptosis inducing ligand (Trail).
PN CN1354183-A.
PD 19-JUN-2002.
PA (TWOM-) NO 2 MILITARY MEDICAL COLLEGE PLA.
Query Match 38.7%; Score 36; DB 5; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1313
ID AAMS1077 standard; protein; 281 AA.
DE Human Apo-2 ligand (TRAIL).
PN WO200209755-A2.
PD 07-FEB-2002.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 5; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1314
ID ABP51954 standard; protein; 281 AA.
DE Human Apo-2 ligand protein sequence SEQ ID NO:4.
PN WO200248376-A2.
PD 20-JUN-2002.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 5; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1315
ID AAO19095 standard; protein; 281 AA.
DE C neoformans antigen expressing dendritic cell related protein #4.
PN WO200266053-A2.
PD 29-AUG-2002.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 5; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1316
ID AAU79593 standard; protein; 281 AA.
DE Human TNF-related apoptosis inducing ligand (TRAIL) protein.
PN US2002061525-A1.
PD 23-MAY-2002.
PA (YELI/) YELIN R.
PA (KHOS/) KHOSRAVI R.
PA (SAVI/) SAVITZKY K.
Query Match 38.7%; Score 36; DB 5; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1317
ID ABG73861 standard; protein; 281 AA.
DE Human Apo-2 ligand protein.
PN US6462176-B1.
PD 08-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1318
ID ABU10205 standard; protein; 281 AA.
DE Human Apo-2 ligand.
PN US2003004313-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1319
ID ABU71443 standard; protein; 281 AA.
DE Human neoplasia inhibiting PRO polypeptide PRO1096.
PN US2002192209-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1320
ID AG72738 standard; protein; 281 AA.
DE Human TNF-related apoptosis inducing ligand (TRAIL) protein.
PN WO200283946-A1.
PD 24-OCT-2002.
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN AGENCY NATTON.
Query Match 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;

RESULT 1321
ID AAO29543 standard; protein; 281 AA.
DE Human TRAIL protein.
PN WO2003042367-A2.
PD 22-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1322
ID ASU08558 standard; protein; 281 AA.
DE Human TNF Related Apoptosis Inducing Ligand, TRAIL.
PN US6521228-B1.
PD 18-FEB-2003.
PA (IMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1323
ID ABR42313 standard; protein; 281 AA.
DE Human TRAIL protein.
PN WO2003040307-A2.
PD 15-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1324
ID ASG71905 standard; protein; 281 AA.
DE Human TRAIL receptor-associated protein.
PN WO200279377-A2.
PD 10-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1325
ID ABF60546 standard; protein; 281 AA.
DE Human tumour necrosis factor TRAIL.
PN WO200294192-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1326
ID AAE36258 standard; protein; 281 AA.
DE Human TR4 ligand, TRAIL protein.
PN WO200297033-A2.
PD 05-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1327
ID AAO31151 standard; protein; 281 AA.
DE Human TNF-related apoptosis-inducing ligand (TRAIL).
PN WO2003054216-A2.
PD 03-JUL-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1328
ID ABO25125 standard; protein; 281 AA.
DE Human TNF-related apoptosis inducing ligand TRAIL Incyte 059509CD1.
PN US2003013099-A1.
PD 16-JAN-2003.
PA (LASE) LASEK A K W.
PA (JONE) JONES D A.
PA (KARP) KARP A R.
Query Match 38.7%; Score 36; DB 6; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1329
ID ADB61480 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant R115C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;

Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1330
ID ADB61482 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant N134C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1331
ID ADB61484 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant E144C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1332
ID ADB61495 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant H264C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1333
ID ADB61478 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant S111C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1334
ID ADB61494 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant E263C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1335
ID ADB61481 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant E116C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1336
ID ADB61487 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant R170C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1337
ID ADB61485 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant N152C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1338
ID ADB61490 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant K179C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;

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RESULT 1339
ID ADB61471 standard; protein; 281 AA.
DE Native Human Apo-2 ligand protein.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1340
ID ADB61477 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant S101C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1341
ID ADB61479 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant V114C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1342
ID ADB61491 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant D234C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1343
ID ADB61493 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant R255C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1344
ID ADB61486 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant S153C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1345
ID ADB61488 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant R170K.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1346
ID ADB61483 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant N140C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1347
ID ADB61489 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant R170S.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1348
ID ADB61476 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant S96C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1349
ID ADB61492 standard; protein; 281 AA.
DE Human Apo-2 ligand protein mutant E249C.
PN WO2003029420-A2.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1350
ID ADC35202 standard; protein; 281 AA.
DE Human TNF ligand family member #10.
PN US2003100074-A1.
PD 29-MAY-2003.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (NARD/) NARDELLI B.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1351
ID ADD14080 standard; protein; 281 AA.
DE Human src biomarker polypeptide SEQ ID NO:269.
PN WO2003062395-A2.
PD 31-JUL-2003.
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1352
ID ADD19010 standard; protein; 281 AA.
DE Human disease related protein SeqID499.
PN WO2003018621-A2.
PD 06-MAR-2003.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1353
ID ABW02276 standard; protein; 281 AA.
DE Human TRAIL protein.
PN US2003198640-A1.
PD 23-OCT-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 7; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1354
ID ADE76953 standard; protein; 281 AA.
DE Human protein expressed in a liver disorder #32.
PN US2003108871-A1.
PD 12-JUN-2003.
PA (KASE/) KASER M R.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1355
ID ADK72311 standard; protein; 281 AA.
DE Human Apo-2 ligand with potential substitutions highlighted #4.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1356
ID ADK72306 standard; protein; 281 AA.
DE Human Apo-2 ligand variant #2.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
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Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1357
ID ADK72313 standard; protein; 281 AA.
DE Human Apo-2 ligand variant #7.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1358
ID ADK72305 standard; protein; 281 AA.
DE Human Apo-2 ligand variant #1.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1359
ID ADK72309 standard; protein; 281 AA.
DE Human Apo-2 ligand variant #5.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1360
ID ADK72303 standard; protein; 281 AA.
DE Human Apo-2 ligand with potential substitutions highlighted #1.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1361
ID ADK72304 standard; protein; 281 AA.
DE Human Apo-2 ligand with potential substitutions highlighted #2.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1362
ID ADK72308 standard; protein; 281 AA.
DE Human Apo-2 ligand variant #4.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1363
ID ADK72312 standard; protein; 281 AA.
DE Human Apo-2 ligand variant #6.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1364
ID ADK72307 standard; protein; 281 AA.
DE Human Apo-2 ligand variant #3.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1365
ID ADK72296 standard; protein; 281 AA.
DE Human wild-type Apo-2 ligand, seq id 1.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1366
ID ADK72310 standard; protein; 281 AA.
DE Human Apo-2 ligand with potential substitutions highlighted #3.
PN WO2004001009-A2.
PD 31-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1367
ID ADJ63976 standard; protein; 281 AA.
DE Human apoptosis inducing molecule 1, AIM-1.
PN US2004038347-A1.
PD 26-FEB-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1368
ID ADL71816 standard; protein; 281 AA.
DE Human apoptosis inducing molecule-1 (AIM-1) protein.
PN US2004047864-A1.
PD 11-MAR-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1369
ID ADK15498 standard; protein; 281 AA.
DE Human TRAIL protein.
PN US2004052788-A1.
PD 18-MAR-2004.
PA (IMMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1370
ID ADN07587 standard; protein; 281 AA.
DE Human apoptosis inducing molecule-1 protein.
PN US2004048340-A1.
PD 11-MAR-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1371
ID ADR14209 standard; protein; 281 AA.
DE Human NF-kappaB pathway-associated protein SeqID210.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1372
ID ADK82215 standard; protein; 281 AA.
DE Human TRAIL amino acid sequence SEQ ID NO:66.
PN WO2004016753-A2.
PD 26-FEB-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1373
ID ADS88000 standard; protein; 281 AA.
DE Tumour treatment-related human protein sequence SeqID336.
PN WO2004034995-A2.
PD 29-APR-2004.
PA (UVPI-) UNIV PITTSBURGH.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1374
ID ABO84415 standard; protein; 281 AA.
DE Human cancer-associated protein HP7-053.3.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1375

ID ADP23388 standard; protein; 281 AA.
DE PRO polypeptide SEQ ID NO:566.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1376
ID ADP55244 standard; protein; 281 AA.
DE Amino acid sequence of human TRAIL protein.
PN WO2004087930-A2.
PD 14-OCT-2004.
PA (UYSL-) UNIV SAINT LOUIS.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1377
ID ADU22883 standard; protein; 281 AA.
DE Human apoptosis inducing DR4/DR5 ligand (Apo2L) protein.
PN US2004224389-A1.
PD 11-NOV-2004.
PA (COLS) UNIV COLORADO.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1378
ID ADU22881 standard; protein; 281 AA.
DE Human apoptosis inducing DR4/DR5 ligand (TRAIL) protein.
PN US2004224389-A1.
PD 11-NOV-2004.
PA (COLS) UNIV COLORADO.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1379
ID ADU77157 standard; protein; 281 AA.
DE Human Apo-2 ligand.
PN WO2004101608-A2.
PD 25-NOV-2004.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1380
ID ADW02206 standard; protein; 281 AA.
DE Human membrane bound TRAIL protein.
PN WO2005000220-A2.
PD 06-JAN-2005.
PA (CELL-) CELL GENESYS INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1381
ID ADY34239 standard; protein; 281 AA.
DE Human TRAIL protein.
PN WO2005016236-A2.
PD 24-FEB-2005.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1382
ID ADY14868 standard; protein; 281 AA.
DE PRO polypeptide SEQ ID NO 674.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1383
ID ADY14870 standard; protein; 281 AA.
DE PRO polypeptide SEQ ID NO 676.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1384
ID ADY19766 standard; protein; 281 AA.

DE PRO polypeptide SEQ ID NO 5572.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1385
ID ADZ72350 standard; protein; 281 AA.
DE Human Apo-2 ligand protein, SEQ ID NO: 1.
PN US2005089958-A1.
PD 28-APR-2005.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1386
ID AEA21853 standard; protein; 281 AA.
DE Human kininogen D5-TRAIL related protein SEQ ID NO 4.
PN CN1546528-A.
PD 17-NOV-2004.
PA (UYPL-) UNIV PLA SECOND MILITARY MEDICAL.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1387
ID AEA23811 standard; protein; 281 AA.
DE Human PRO polypeptide SEQ ID NO 353.
PN WO2005051988-A2.
PD 09-JUN-2005.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1388
ID AEA23728 standard; protein; 281 AA.
DE Human PRO polypeptide SEQ ID NO 270.
PN WO2005051988-A2.
PD 09-JUN-2005.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1389
ID AEA27598 standard; protein; 281 AA.
DE Human TRAIL protein SEQ ID NO:66.
PN US2005129616-A1.
PD 16-JUN-2005.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1390
ID AEA55214 standard; protein; 281 AA.
DE Human TRAIL protein, SEQ ID NO:66.
PN US2005129699-A1.
PD 16-JUN-2005.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1391
ID AEB16293 standard; protein; 281 AA.
DE Trail cytokine.
PN WO2005056596-A1.
PD 23-JUN-2005.
PA (UYGR-) RIJKSUNIV GRONINGEN.
PA (EUMO-) EURO MOLECULAR BIOLOGY LAB.
PA (UYNA-) UNIV NAT IRELAND.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1392
ID AEA81246 standard; protein; 281 AA.
DE Human tumor necrosis factor superfamily-10 protein.
PN US2005136465-A1.
PD 23-JUN-2005.
PA (CLER/) CLERC R G.
PA (DUCH/) DUCHATEAU-NGUYEN G.
PA (GARD/) GARDES C.
PA (MIZR/) MIZRAHI J.

PA (OSTE/) OSTENSON C.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1393
ID AEB92344 standard; protein; 281 AA.
DE Human TRAIL, SEQ ID 2.
PN US2005158823-A1.
PD 21-JUL-2005.
PA (IMV) IMMUNEX CORP.
Query Match 38.7%; Score 36; DB 9; Length 281;
Best Local Similarity 41.7%; Pred. No. 1.5e+03;
RESULT 1394
ID AEM67549 standard; protein; 283 AA.
DE Photorhabdus luminescens protein sequence #646.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
Query Match 38.7%; Score 36; DB 6; Length 283;
Best Local Similarity 47.1%; Pred. No. 1.6e+03;
RESULT 1395
ID ADH71894 standard; protein; 284 AA.
DE Human protein of the invention NOV31k SEQ ID NO:790.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 8; Length 284;
Best Local Similarity 42.9%; Pred. No. 1.6e+03;
RESULT 1396
ID AAB08727 standard; protein; 288 AA.
DE Amino acid sequence of a human B7RP1 polypeptide.
PN WO200046240-A2.
PD 10-AUG-2000.
PA (AMGE-) AMGEN INC.
Query Match 38.7%; Score 36; DB 3; Length 288;
Best Local Similarity 42.9%; Pred. No. 1.6e+03;
RESULT 1397
ID AAU99785 standard; protein; 288 AA.
DE Human B7 related protein-1 (B7RP1) #1.
PN WO200244364-A2.
PD 06-JUN-2002.
PA (AMGE-) AMGEN INC.
PA (AMGE-) AMGEN CANADA INC.
Query Match 38.7%; Score 36; DB 5; Length 288;
Best Local Similarity 42.9%; Pred. No. 1.6e+03;
RESULT 1398
ID ADH71880 standard; protein; 290 AA.
DE Human protein of the invention NOV31d SEQ ID NO:776.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 8; Length 290;
Best Local Similarity 42.9%; Pred. No. 1.6e+03;
RESULT 1399
ID AAB08729 standard; protein; 302 AA.
DE Amino acid sequence of a human B7RP1 polypeptide.
PN WO200046240-A2.
PD 10-AUG-2000.
PA (AMGE-) AMGEN INC.
Query Match 38.7%; Score 36; DB 3; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1400
ID AAB87395 standard; protein; 302 AA.
DE Human gene 2 encoded secreted protein HMWDB84, SEQ ID NO:136.
PN WO200118022-A1.
PD 15-MAR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 4; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1401
ID AAG67292 standard; protein; 302 AA.
DE Amino acid sequence of a human hB7-H2 polypeptide.
PN WO200164704-A1.

PD 07-SEP-2001.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 38.7%; Score 36; DB 4; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1402
ID AEG65402 standard; protein; 302 AA.
DE Human albumin fusion protein #2077.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 5; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1403
ID AAU99789 standard; protein; 302 AA.
DE Human B7 related protein-1 (B7RP1) #2.
PN WO200244364-A2.
PD 06-JUN-2002.
PA (AMGE-) AMGEN INC.
PA (AMGE-) AMGEN CANADA INC.
Query Match 38.7%; Score 36; DB 5; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1404
ID ADH47719 standard; protein; 302 AA.
DE NOV3a protein, SEQ ID 16.
PN WO200268647-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 5; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1405
ID ADA41234 standard; protein; 302 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 6; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1406
ID ADC74429 standard; protein; 302 AA.
DE Human secreted protein - SEQ ID 1062.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 7; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1407
ID AD25558 standard; protein; 302 AA.
DE , Binding domain-immunoglobulin fusion protein-associated protein #56.
PN US2003118592-A1.
PD 26-JUN-2003.
PA (GENE-) GENE-CRAFT INC.
Query Match 38.7%; Score 36; DB 7; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1408
ID ADF68255 standard; protein; 302 AA.
DE Human NOV3a protein, a B7-H2 like protein SeqID 16.
PN WO200281510-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 7; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1409
ID ADH71892 standard; protein; 302 AA.
DE Human protein of the invention NOV31j SEQ ID NO:788.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 8; Length 302;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1410
ID ADH71886 standard; protein; 302 AA.
DE Human protein of the invention NOV31g SEQ ID NO:782.
PN WO2003102155-A2.

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PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP. 38.7%; Score 36; DB 8; Length 302;
Query Match
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1411
ID ADH71884 standard; protein; 302 AA.
DE Human protein of the invention NOV31f SEQ ID NO:780.
PN W02003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP. 38.7%; Score 36; DB 8; Length 302;
Query Match
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1412
ID ADH71896 standard; protein; 302 AA.
DE Human protein of the invention NOV31l SEQ ID NO:792.
PN W02003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP. 38.7%; Score 36; DB 8; Length 302;
Query Match
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1413
ID ADH73010 standard; protein; 302 AA.
DE Human B7-related protein-1, B7RP-1.
PN US2004001831-A1.
PD 01-JAN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
PA (KOCH-) KOCH INST ROBERT.
Query Match
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1414
ID ADL78669 standard; protein; 302 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 2151.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1415
ID ADL25602 standard; protein; 302 AA.
DE Human diagnostic protein, NOV3a.
PN US2004005557-A1.
PD 08-JAN-2004.
PA (PADI/) PADIGARU M.
PA (ALSO/) ALSOBROOK J P.
PA (COLM/) COLMAN S D.
PA (SPYT/) SPYTEK K A.
PA (BOLD/) BOLDOG F L.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (SHEN/) SHENOY S G.
PA (CASM/) CASMAN S J.
PA (GUOX/) GUO X.
PA (EDIN/) EDINGER S R.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (PATT/) PATTURAJAN M.
PA (SHIM/) SHIMKETS R A.
PA (PENA/) PENA C E A.
PA (TCHE/) TCHERNEV V T.
PA (ZERH/) ZERHUSEN B D.
PA (MILL/) MILLET I.
PA (LEPL/) MILLER C E.
PA (LEPL/) LEPLEY D M.
PA (SMIT/) SMITHSON G.
PA (BAUM/) BAUMGARTNER J C.
PA (HERR/) HERRMANN J L.
PA (PEYM/) PEYMAN J A.
PA (GORM/) GORMAN L.
PA (MEZE/) MEZES P D.
PA (KEKU/) KEKUDA R.
PA (TAUP/) TAUFIER R J.
PA (GERL/) GERLACH V.

PA (GROS/) GROSSE W M.
PA (LIUX/) LIU X.
PA (ELLE/) ELLERMAN K.
PA (ROTH/) ROTHENBERG M.
PA (STON/) STONE D J.
PA (BURG/) BURGESS C B.
Query Match
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1416
ID ADN59025 standard; protein; 302 AA.
DE Human B7H protein #3.
PN US2004102398-A1.
PD 27-MAY-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1417
ID ADN59021 standard; protein; 302 AA.
DE Human B7H protein #1.
PN US2004102398-A1.
PD 27-MAY-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1418
ID ADR89355 standard; protein; 302 AA.
DE Human ICOS Ligand protein for immunotherapy method.
PN WO2004073732-A1.
PD 02-SRP-2004.
PA (LORA-) LORANTIS LTD.
Query Match
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1419
ID AEA18914 standard; protein; 302 AA.
DE Amino acid sequence of the human B7-like protein.
PN WO2005044999-A2.
PD 19-MAY-2005.
PA (NEWS-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
Query Match
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1420
ID ADX76510 standard; protein; 303 AA.
DE Plant full length insert polypeptide seqid 45876.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
RESULT 1421
ID ASG30730 standard; protein; 304 AA.
DE Human B7-H2 transcript 1 (B7-H2 V1) polypeptide.
PN WO200253733-A2.
PD 11-JUL-2002.
PA (FARB ) BAYER AG.
Query Match
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1422
ID AAB67713 standard; protein; 309 AA.
DE Amino acid sequence of a human GL50 polypeptide.
PN WO200121796-A2.
PD 29-MAR-2001.
PA (GEMY ) GENETICS INST INC.
Query Match
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
RESULT 1423
ID AAO15802 standard; protein; 309 AA.
DE Human B7RP-1 protein.
PN US2002106730-A1.

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PD 08-AUG-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 38.7%; Score 36; DB 5; Length 309;
 Best Local Similarity 42.9%; Pred. No. 1.7e+03;
 RESULT 1424
 ID ADH71882 standard; protein; 309 AA.
 DE Human protein of the invention NOV31e SEQ ID NO:778.
 PN W02003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 38.7%; Score 36; DB 8; Length 309;
 Best Local Similarity 42.9%; Pred. No. 1.7e+03;
 RESULT 1425
 ID ADN59023 standard; protein; 309 AA.
 DE Human B7H protein #2.
 PN US2004102398-A1.
 PD 27-MAY-2004.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 38.7%; Score 36; DB 8; Length 309;
 Best Local Similarity 42.9%; Pred. No. 1.7e+03;
 RESULT 1426
 ID ADQ76299 standard; protein; 309 AA.
 DE Human B7RP-1 protein.
 PN US2004137577-A1.
 PD 15-JUL-2004.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 38.7%; Score 36; DB 8; Length 309;
 Best Local Similarity 42.9%; Pred. No. 1.7e+03;
 RESULT 1427
 ID ADN42318 standard; protein; 310 AA.
 DE Human novel protein NOV 54b.
 PN US2004033493-A1.
 PD 19-FEB-2004.
 PA (TCHE-) TCHERNEV V T.
 PA (SPYT-) SPYTEK K A.
 PA (ZERH-) ZERHUSEN B D.
 PA (PATT-) PATTURAJAN M.
 PA (SHIM-) SHINKETS R A.
 PA (LILL-) LI L.
 PA (GANG-) GANGOLLI E A.
 PA (PADI-) PADIGARU M.
 PA (ANDE-) ANDERSON D W.
 PA (RAST-) RASTELLI L.
 PA (MILL-) MILLER C E.
 PA (GERL-) GERLACH V.
 PA (TAUP-) TAUPIER R J.
 PA (GUSE-) GUSEV V Y.
 PA (COLM-) COLMAN S D.
 PA (WOLE-) WOLENC A R.
 PA (PENA-) PENNA C E A.
 PA (FURT-) FURTAK K.
 PA (GROS-) GROSSE W M.
 PA (ALSO-) ALSOBROOK J P.
 PA (LEPL-) LEPLEY D M.
 PA (RIEG-) RIEGER D K.
 PA (BURG-) BURGESS C E.
 Query Match 38.7%; Score 36; DB 8; Length 310;
 Best Local Similarity 50.0%; Pred. No. 1.7e+03;
 RESULT 1428
 ID AAB93542 standard; protein; 314 AA.
 DE Human protein sequence SEQ ID NO:12910.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 38.7%; Score 36; DB 4; Length 314;
 Best Local Similarity 50.0%; Pred. No. 1.7e+03;
 RESULT 1429
 ID AAB94208 standard; protein; 314 AA.
 DE Human protein sequence SEQ ID NO:14557.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 38.7%; Score 36; DB 4; Length 314;

Best Local Similarity 50.0%; Pred. No. 1.7e+03;
 RESULT 1430
 ID AAB36628 standard; protein; 314 AA.
 DE Human FLEXHT-50 protein sequence SEQ ID NO:50.
 PN W0200070047-A2.
 PD 23-NOV-2000.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 38.7%; Score 36; DB 4; Length 314;
 Best Local Similarity 50.0%; Pred. No. 1.7e+03;
 RESULT 1431
 ID AAE14787 standard; protein; 314 AA.
 DE Human purple acid phosphatase.
 PN W0200240684-A2.
 PD 23-MAY-2002.
 PA (FARB-) BAYER AG.
 Query Match 38.7%; Score 36; DB 5; Length 314;
 Best Local Similarity 50.0%; Pred. No. 1.7e+03;
 RESULT 1432
 ID ADM07261 standard; protein; 314 AA.
 DE Human hepatotoxicity biomarker protein BMS-PTX-062 SeqID13.
 PN US2004265889-A1.
 PD 30-DEC-2004.
 PA (DURH-) DURHAM S K.
 PA (DAMB-) DAMEBACH D.
 PA (HEFT-) HEFTA S.
 PA (MOUL-) MOULIN F.
 PA (GAOJ-) GAO J.
 PA (OPIT-) OPITECK G.
 PA (STOR-) STORM S M.
 PA (GARU-) GARULACAN L A.
 PA (LINJ-) LIN J.
 Query Match 38.7%; Score 36; DB 9; Length 314;
 Best Local Similarity 50.0%; Pred. No. 1.7e+03;
 RESULT 1433
 ID ADY17085 standard; protein; 321 AA.
 DE PRO polypeptide SEQ ID NO 2891.
 PN W02005016962-A2.
 PD 24-FEB-2005.
 PA (GETH-) GENENTECH INC.
 Query Match 38.7%; Score 36; DB 9; Length 321;
 Best Local Similarity 41.7%; Pred. No. 1.8e+03;
 RESULT 1434
 ID AAY74886 standard; protein; 327 AA.
 DE Neisseria meningitidis ORF 298 protein sequence SEQ ID NO:1246.
 PN W0957280-A2.
 PD 11-NOV-1999.
 PA (CHIR-) CHIRON CORP.
 PA (GENO-) INST GENOMIC RES.
 Query Match 38.7%; Score 36; DB 3; Length 327;
 Best Local Similarity 66.7%; Pred. No. 1.8e+03;
 RESULT 1435
 ID AAY74884 standard; protein; 327 AA.
 DE Neisseria gonorrhoeae ORF 298 protein sequence SEQ ID NO:1242.
 PN W0957280-A2.
 PD 11-NOV-1999.
 PA (CHIR-) CHIRON CORP.
 PA (GENO-) INST GENOMIC RES.
 Query Match 38.7%; Score 36; DB 3; Length 327;
 Best Local Similarity 66.7%; Pred. No. 1.8e+03;
 RESULT 1436
 ID AAY74885 standard; protein; 327 AA.
 DE Neisseria meningitidis ORF 298 protein sequence SEQ ID NO:1244.
 PN W0957280-A2.
 PD 11-NOV-1999.
 PA (CHIR-) CHIRON CORP.
 PA (GENO-) INST GENOMIC RES.
 Query Match 38.7%; Score 36; DB 3; Length 327;
 Best Local Similarity 66.7%; Pred. No. 1.8e+03;
 RESULT 1437
 ID ADM17396 standard; protein; 328 AA.
 DE Eucalyptus grandis transcription factor protein MYB family Seq 1152.
 PN W02005001050-A2.
 PD 06-JAN-2005.

PA (ARBO-) ARBORGEN LLC.
Query Match 38.7%; Score 36; DB 9; Length 328;
Best Local Similarity 58.3%; Pred. No. 1.8e+03;
RESULT 1438
ID ADQ94415 standard; protein; 332 AA.
DE Rat lactate dehydrogenase A.
PN W02004065552-A2.
PD 05-AUG-2004.
PA (UYDU-) UNIV DUKE.
PA (TEXA-) UNIV TEXAS SYSTEM.
Query Match 38.7%; Score 36; DB 8; Length 332;
Best Local Similarity 46.7%; Pred. No. 1.9e+03;
RESULT 1439
ID ADR89010 standard; protein; 332 AA.
DE Rat lactate dehydrogenase A (LDH-A) polypeptide.
PN W02004071405-A2.
PD 26-AUG-2004.
PA (UYDU-) UNIV DUKE.
PA (TEXA-) UNIV TEXAS SYSTEM.
Query Match 38.7%; Score 36; DB 8; Length 332;
Best Local Similarity 46.7%; Pred. No. 1.9e+03;
RESULT 1440
ID ABP78644 standard; protein; 335 AA.
DE N. Gonorrhoae amino acid sequence SEQ ID 3818.
PN W0200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Query Match 38.7%; Score 36; DB 6; Length 335;
Best Local Similarity 66.7%; Pred. No. 1.9e+03;
RESULT 1441
ID ADB08318 standard; protein; 336 AA.
DE Allostococcus otitis antigenic protein SEQ ID NO:2258.
PN W02003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match 38.7%; Score 36; DB 6; Length 336;
Best Local Similarity 63.6%; Pred. No. 1.9e+03;
RESULT 1442
ID ABB10322 standard; protein; 343 AA.
DE Human cDNA SEQ ID NO: 630.
PN W0200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 4; Length 343;
Best Local Similarity 42.9%; Pred. No. 1.9e+03;
RESULT 1443
ID ABP66909 standard; protein; 343 AA.
DE Human polypeptide SEQ ID NO 630.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 38.7%; Score 36; DB 5; Length 343;
Best Local Similarity 42.9%; Pred. No. 1.9e+03;
RESULT 1444
ID AAU18067 standard; protein; 344 AA.
DE Human immunoglobulin polypeptide SEQ ID NO 212.
PN W0200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 4; Length 344;
Best Local Similarity 42.9%; Pred. No. 1.9e+03;
RESULT 1445
ID ABB10504 standard; protein; 344 AA.
DE Human cDNA SEQ ID NO: 812.
PN W0200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 4; Length 344;
Best Local Similarity 42.9%; Pred. No. 1.9e+03;
RESULT 1446
ID ABP67091 standard; protein; 344 AA.

DE Human polypeptide SEQ ID NO 812.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 38.7%; Score 36; DB 5; Length 344;
Best Local Similarity 42.9%; Pred. No. 1.9e+03;
RESULT 1447
ID ADB31691 standard; protein; 344 AA.
DE Human novel protein SEQ ID NO 212.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 7; Length 344;
Best Local Similarity 42.9%; Pred. No. 1.9e+03;
RESULT 1448
ID AAU18065 standard; protein; 345 AA.
DE Human immunoglobulin polypeptide SEQ ID NO 210.
PN W0200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 4; Length 345;
Best Local Similarity 42.9%; Pred. No. 1.9e+03;
RESULT 1449
ID ABB10502 standard; protein; 345 AA.
DE Human cDNA SEQ ID NO: 810.
PN W0200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 4; Length 345;
Best Local Similarity 42.9%; Pred. No. 1.9e+03;
RESULT 1450
ID ABP67089 standard; protein; 345 AA.
DE Human polypeptide SEQ ID NO 810.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 38.7%; Score 36; DB 5; Length 345;
Best Local Similarity 42.9%; Pred. No. 1.9e+03;
RESULT 1451
ID ADB31689 standard; protein; 345 AA.
DE Human novel protein SEQ ID NO 210.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 7; Length 345;
Best Local Similarity 42.9%; Pred. No. 1.9e+03;
RESULT 1452
ID AAU15973 standard; protein; 351 AA.
DE Human novel secreted protein, Seq ID 926.
PN W0200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 4; Length 351;
Best Local Similarity 38.7%; Pred. No. 2e+03;
RESULT 1453
ID ABU55042 standard; protein; 351 AA.
DE Human novel polypeptide #129.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 38.7%; Score 36; DB 6; Length 351;
Best Local Similarity 38.9%; Pred. No. 2e+03;
RESULT 1454
ID AAG81561 standard; protein; 352 AA.
DE S. epidermidis open reading frame protein sequence SEQ ID NO:216.
PN W0200134809-A2.
PD 17-MAY-2001.

PA (GLAX) GLAXO GROUP LTD.
Query Match 38.7%; Score 36; DB 4; Length 352;
Best Local Similarity 61.5%; Pred. No. 2e+03;
RESULT 1455
ID ADB80938 standard; protein; 359 AA.
DE RING-SH complex related protein, SEQ ID NO 12.
PN WO2003033646-A2.
PD 24-APR-2003.
PA (PROT-) PROTEOLOGICS INC.
Query Match 38.7%; Score 36; DB 7; Length 359;
Best Local Similarity 57.1%; Pred. No. 2e+03;
RESULT 1456
ID ADE54266 standard; protein; 359 AA.
DE Human Protein O00623, SEQ ID NO 69.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 38.7%; Score 36; DB 7; Length 359;
Best Local Similarity 57.1%; Pred. No. 2e+03;
RESULT 1457
ID AAU36115 standard; protein; 361 AA.
DE Klebsiella pneumoniae cellular proliferation protein #103.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 38.7%; Score 36; DB 4; Length 361;
Best Local Similarity 37.5%; Pred. No. 2e+03;
RESULT 1458
ID ABU28113 standard; protein; 361 AA.
DE Protein encoded by Prokaryotic essential gene #13640.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 38.7%; Score 36; DB 6; Length 361;
Best Local Similarity 37.5%; Pred. No. 2e+03;
RESULT 1459
ID ABU31873 standard; protein; 361 AA.
DE Protein encoded by Prokaryotic essential gene #17400.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 38.7%; Score 36; DB 6; Length 361;
Best Local Similarity 37.5%; Pred. No. 2e+03;
RESULT 1460
ID ADO94417 standard; protein; 361 AA.
DE Rat mitochondrial lactate dehydrogenase A.
PN WO2004065552-A2.
PD 05-AUG-2004.
PA (UYDU-) UNIV DUKE.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 38.7%; Score 36; DB 8; Length 361;
Best Local Similarity 46.7%; Pred. No. 2e+03;
RESULT 1461
ID ADR89012 standard; protein; 361 AA.
DE Rat mitochondrial form of LDH-A polypeptide.
PN WO2004071405-A2.
PD 26-AUG-2004.
PA (UYDU-) UNIV DUKE.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 38.7%; Score 36; DB 8; Length 361;
Best Local Similarity 46.7%; Pred. No. 2e+03;
RESULT 1462
ID AEG22417 standard; protein; 362 AA.
DE Novel human diagnostic protein #22408.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 38.7%; Score 36; DB 4; Length 362;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
RESULT 1463
ID AAU18005 standard; protein; 370 AA.
DE Human immunoglobulin polypeptide SEQ ID NO 150.

PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 4; Length 370;
Best Local Similarity 42.9%; Pred. No. 2.1e+03;
RESULT 1464
ID ADB31629 standard; protein; 370 AA.
DE Human novel protein SEQ ID NO 150.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 7; Length 370;
Best Local Similarity 42.9%; Pred. No. 2.1e+03;
RESULT 1465
ID ADC31206 standard; protein; 374 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1288.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 38.7%; Score 36; DB 7; Length 374;
Best Local Similarity 50.0%; Pred. No. 2.1e+03;
RESULT 1466
ID ADH52744 standard; protein; 375 AA.
DE Porphyromonas gulae B69 OprF protein.
PN WO2003054755-A2.
PD 03-JUL-2003.
PA (PFIZ) PFIZER PROD INC.
Query Match 38.7%; Score 36; DB 7; Length 375;
Best Local Similarity 42.9%; Pred. No. 2.1e+03;
RESULT 1467
ID ADH52741 standard; protein; 375 AA.
DE Porphyromonas gulae B43 OprF protein.
PN WO2003054755-A2.
PD 03-JUL-2003.
PA (PFIZ) PFIZER PROD INC.
Query Match 38.7%; Score 36; DB 7; Length 375;
Best Local Similarity 42.9%; Pred. No. 2.1e+03;
RESULT 1468
ID ABO66029 standard; protein; 377 AA.
DE Klebsiella pneumoniae polypeptide seqid 12546.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 38.7%; Score 36; DB 7; Length 377;
Best Local Similarity 37.5%; Pred. No. 2.2e+03;
RESULT 1469
ID ADI16664 standard; protein; 382 AA.
DE Human NOVX protein to treat human pathological conditions SeqID200.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 38.7%; Score 36; DB 5; Length 382;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
RESULT 1470
ID AAU23676 standard; protein; 387 AA.
DE Novel human enzyme polypeptide #762.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 38.7%; Score 36; DB 4; Length 387;
Best Local Similarity 66.7%; Pred. No. 2.2e+03;
RESULT 1471
ID ABR53859 standard; protein; 387 AA.
DE Protein sequence #SEQ ID 2583.
PN EPI258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 38.7%; Score 36; DB 6; Length 387;
Best Local Similarity 77.8%; Pred. No. 2.2e+03;
RESULT 1472
ID ADK64914 standard; protein; 387 AA.
DE Disease treating protein complex-derived protein #1559.
PN EPI338608-A2.

PD 27-AUG-2003.
 PA (CELL-) CELLZOME AG. 38.7%; Score 36; DB 7; Length 387;
 Query Match 77.8%; Pred. No. 2.2e+03;
 RESULT 1473
 ID AAO19905 standard; protein; 388 AA.
 DE Human TA4 receptor associated protein swissnew/070528/5H4_CAVPO.
 PN WO2002101043-A2.
 PD 19-DEC-2002.
 PA (FARB) BAYER AG. 38.7%; Score 36; DB 6; Length 388;
 Query Match 41.2%; Pred. No. 2.2e+03;
 RESULT 1474
 ID AAU09397 standard; protein; 390 AA.
 DE Soluble Porphyromonas gingivalis polypeptide from PG32.
 PN WO200183530-A1.
 PD 08-NOV-2001.
 PA (CSLC-) CSL LTD. 38.7%; Score 36; DB 5; Length 390;
 Query Match 42.9%; Pred. No. 2.2e+03;
 RESULT 1475
 ID AAY34490 standard; protein; 391 AA.
 DE Porphyromonas gingivalis protein PG32.
 PN WO9929870-A1.
 PD 17-JUN-1999.
 PA (CSLC-) CSL LTD. 38.7%; Score 36; DB 2; Length 391;
 Query Match 42.9%; Pred. No. 2.2e+03;
 RESULT 1476
 ID AAY34365 standard; protein; 395 AA.
 DE Porphyromonas gingivalis protein PG32.
 PN WO9929870-A1.
 PD 17-JUN-1999.
 PA (CSLC-) CSL LTD. 38.7%; Score 36; DB 2; Length 395;
 Query Match 42.9%; Pred. No. 2.3e+03;
 RESULT 1477
 ID ABG12815 standard; protein; 400 AA.
 DE Novel human diagnostic protein #12806.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC. 38.7%; Score 36; DB 4; Length 400;
 Query Match 50.0%; Pred. No. 2.3e+03;
 RESULT 1478
 ID ASU65118 standard; protein; 403 AA.
 DE Human NOV51a protein.
 PN WO200272757-A2.
 PD 19-SEP-2002.
 PA (CURA-) CURAGEN CORP. 38.7%; Score 36; DB 5; Length 403;
 Query Match 66.7%; Pred. No. 2.3e+03;
 RESULT 1479
 ID ADL04887 standard; protein; 403 AA.
 DE M. catarrhalis protein #653.
 PN US6673910-B1.
 PD 06-JAN-2004.
 PA (GENO-) GENOME THERAPEUTICS CORP. 38.7%; Score 36; DB 8; Length 403;
 Query Match 71.4%; Pred. No. 2.3e+03;
 RESULT 1480
 ID ADN61987 standard; protein; 404 AA.
 DE Human novel protein NOV51a.
 PN US2004043382-A1.
 PD 04-MAR-2004.
 PA (PADI-) PADIGARU M. 38.7%; Score 36; DB 8; Length 409;
 PA (SPYT-) SPYTEK K A. 38.7%; Score 36; DB 8; Length 409;
 PA (SHEN/) SHENOY S G. 38.7%; Score 36; DB 8; Length 409;
 PA (TAUP/) TAUPIER R J. 38.7%; Score 36; DB 8; Length 409;
 PA (PENA/) PENA C B A. 38.7%; Score 36; DB 8; Length 409;
 PA (LILL/) LI L. 38.7%; Score 36; DB 8; Length 409;
 PA (ZERH/) ZERHUSEN B D. 38.7%; Score 36; DB 8; Length 409;
 PA (GUSE/) GUSEV V Y. 38.7%; Score 36; DB 8; Length 409;
 PA (GENE-) GENESIS RES & DEV CORP LTD. 38.7%; Score 36; DB 8; Length 409;
 PA (JIWV/) JI W. 38.7%; Score 36; DB 8; Length 404;
 PA (GORM/) GORMAN L. 38.7%; Score 36; DB 8; Length 404;
 PA (MILL/) MILLER C E. 38.7%; Score 36; DB 8; Length 404;
 PA (KEKU/) KEKUDA R. 38.7%; Score 36; DB 8; Length 404;
 PA (PATT/) PATTURAJAN M. 38.7%; Score 36; DB 8; Length 404;
 PA (GANG/) GANGOLLI E A. 38.7%; Score 36; DB 8; Length 404;
 PA (VERN/) VERNET C A M. 38.7%; Score 36; DB 8; Length 404;
 PA (GUOX/) GUO X S. 38.7%; Score 36; DB 8; Length 404;
 PA (TCHE/) TCHERNEV V T. 38.7%; Score 36; DB 8; Length 404;
 PA (FERN/) FERNANDES E R. 38.7%; Score 36; DB 8; Length 404;
 PA (CASM/) CASMAN S J. 38.7%; Score 36; DB 8; Length 404;
 PA (MALY/) MALYANKAR U M. 38.7%; Score 36; DB 8; Length 404;
 PA (GERL/) GERLACH V. 38.7%; Score 36; DB 8; Length 404;
 PA (LIUY/) LIU Y. 38.7%; Score 36; DB 8; Length 404;
 PA (ANDE/) ANDERSON D W. 38.7%; Score 36; DB 8; Length 404;
 PA (SPAD/) SPADERNA S K. 38.7%; Score 36; DB 8; Length 404;
 PA (CATT/) CATTERTON E. 38.7%; Score 36; DB 8; Length 404;
 PA (LEIT/) LEITE M W. 38.7%; Score 36; DB 8; Length 404;
 PA (ZHON/) ZHONG H. 38.7%; Score 36; DB 8; Length 404;
 PA (ALSO/) ALSOBROOK J P. 38.7%; Score 36; DB 8; Length 404;
 PA (LEPL/) LEPLLEY D M. 38.7%; Score 36; DB 8; Length 404;
 PA (RIEG/) RIEGER D K. 38.7%; Score 36; DB 8; Length 404;
 PA (BURG/) BURGESS C E. 38.7%; Score 36; DB 8; Length 404;
 Query Match 66.7%; Pred. No. 2.3e+03;
 RESULT 1481
 ID AAY96727 standard; protein; 409 AA.
 DE Casein kinase II interacting protein 1 (CKIP-1).
 PN WO200036100-A1.
 PD 22-JUN-2000.
 PA (UYWO-) UNIV WESTERN ONTARIO. 38.7%; Score 36; DB 3; Length 409;
 PA (UYMA-) UNIV MANITOBA. 38.7%; Score 36; DB 3; Length 409;
 PA (MANI-) MANITOBA CANCER TREATMENT & RES FOUND. 38.7%; Score 36; DB 3; Length 409;
 Query Match 50.0%; Pred. No. 2.4e+03;
 RESULT 1482
 ID AAW51211 standard; protein; 409 AA.
 DE Human osteoclast expressed polypeptide SEQ ID NO 8.
 PN JP2001231573-A.
 PD 28-AUG-2001.
 PA (SHIO) SHIONOGI & CO LTD. 38.7%; Score 36; DB 4; Length 409;
 Query Match 50.0%; Pred. No. 2.4e+03;
 RESULT 1483
 ID ADQ19480 standard; protein; 409 AA.
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2299.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC. 38.7%; Score 36; DB 8; Length 409;
 Query Match 50.0%; Pred. No. 2.4e+03;
 RESULT 1484
 ID ADR14341 standard; protein; 409 AA.
 DE Human NF-kappaB pathway-associated protein SeqID342.
 PN WO2004065577-A2.
 PD 05-AUG-2004.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO. 38.7%; Score 36; DB 8; Length 409;
 Query Match 50.0%; Pred. No. 2.4e+03;
 RESULT 1485
 ID ADP55230 standard; protein; 409 AA.
 DE Human PRO protein sequence SEQ ID NO:1206.
 PN WO2004039956-A2.
 PD 13-MAY-2004.
 PA (GETH) GENENTECH INC. 38.7%; Score 36; DB 8; Length 409;
 Query Match 50.0%; Pred. No. 2.4e+03;
 RESULT 1486
 ID AAY76047 standard; protein; 411 AA.
 DE Rat skin cell protein, SEQ ID NO:302.
 PN WO955865-A1.
 PD 04-NOV-1999.
 PA (GENE-) GENESIS RES & DEV CORP LTD. 38.7%; Score 36; DB 8; Length 409;

Query Match
Best Local Similarity 38.7%; Score 36; DB 3; Length 411;
RESULT 1487
ID AAB55986 standard; protein; 411 AA.
DE Skin cell protein, SEQ ID NO: 302.
PN WO200069884-A2.
PD 23-NOV-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 38.7%; Score 36; DB 4; Length 411;
Best Local Similarity 46.2%; Pred. No. 2.4e+03;
RESULT 1488
ID ABB72186 standard; protein; 411 AA.
DE Rat protein isolated from skin cells SEQ ID NO: 302.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 38.7%; Score 36; DB 5; Length 411;
Best Local Similarity 46.2%; Pred. No. 2.4e+03;
RESULT 1489
ID ABG00248 standard; protein; 418 AA.
DE Novel human diagnostic protein #239.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 38.7%; Score 36; DB 4; Length 418;
Best Local Similarity 50.0%; Pred. No. 2.4e+03;
RESULT 1490
ID AAM39789 standard; protein; 419 AA.
DE Human polypeptide SEQ ID NO 2934.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 38.7%; Score 36; DB 4; Length 419;
Best Local Similarity 42.9%; Pred. No. 2.4e+03;
RESULT 1491
ID AAB93457 standard; protein; 419 AA.
DE Human protein sequence SEQ ID NO:12716.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 38.7%; Score 36; DB 4; Length 419;
Best Local Similarity 42.9%; Pred. No. 2.4e+03;
RESULT 1492
ID AAM80981 standard; protein; 419 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO81664, SEQ:2528.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 38.7%; Score 36; DB 8; Length 419;
Best Local Similarity 42.9%; Pred. No. 2.4e+03;
RESULT 1493
ID ADU60360 standard; protein; 419 AA.
DE Housekeeping gene protein, SEQ ID 321.
PN US2004229233-A1.
PD 18-NOV-2004.
PA (NIGA) NGK INSULATORS LTD.
Query Match 38.7%; Score 36; DB 8; Length 419;
Best Local Similarity 42.9%; Pred. No. 2.4e+03;
RESULT 1494
ID AAR88131 standard; protein; 422 AA.
DE Aureobasidin sensitivity gene spauris product.
PN EP692534-A2.
PD 17-JAN-1996.
PA (TAKI) TAKARA SHUZO CO LTD.
Query Match 38.7%; Score 36; DB 2; Length 422;
Best Local Similarity 54.5%; Pred. No. 2.4e+03;
RESULT 1495
ID AAR88130 standard; protein; 422 AA.
DE Aureobasidin resistance gene spaurir product.
PN EP692534-A2.
PD 17-JAN-1996.
PA (TAKI) TAKARA SHUZO CO LTD.
Query Match 38.7%; Score 36; DB 2; Length 422;
Best Local Similarity 54.5%; Pred. No. 2.4e+03;
RESULT 1496
ID ABU20958 standard; protein; 431 AA.
DE Protein encoded by Prokaryotic essential gene #6485.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 38.7%; Score 36; DB 6; Length 431;
Best Local Similarity 58.3%; Pred. No. 2.5e+03;
RESULT 1497
ID ADZ68028 standard; protein; 440 AA.
DE Escherichia coli HipA7 protein.
PN WO2005038003-A2.
PD 28-APR-2005.
PA (INVI-) INVITROGEN CORP.
Query Match 38.7%; Score 36; DB 9; Length 440;
Best Local Similarity 38.9%; Pred. No. 2.6e+03;
RESULT 1498
ID ADZ68026 standard; protein; 440 AA.
DE Escherichia coli HipA protein.
PN WO2005038003-A2.
PD 28-APR-2005.
PA (INVI-) INVITROGEN CORP.
Query Match 38.7%; Score 36; DB 9; Length 440;
Best Local Similarity 38.9%; Pred. No. 2.6e+03;
RESULT 1499
ID ADZ68032 standard; protein; 440 AA.
DE Escherichia coli HipAD291A protein.
PN WO2005038003-A2.
PD 28-APR-2005.
PA (INVI-) INVITROGEN CORP.
Query Match 38.7%; Score 36; DB 9; Length 440;
Best Local Similarity 38.9%; Pred. No. 2.6e+03;
RESULT 1500
ID ADZ68030 standard; protein; 440 AA.
DE Escherichia coli HipAD88N protein.
PN WO2005038003-A2.
PD 28-APR-2005.
PA (INVI-) INVITROGEN CORP.
Query Match 38.7%; Score 36; DB 9; Length 440;
Best Local Similarity 38.9%; Pred. No. 2.6e+03;

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OM protein - protein search, using sw model

Run on: December 22, 2005, 02:54:14 ; Search time 8.81633 Seconds
(without alignments)
196.443 Million cell updates/sec

Title: US-10-063-553-48_COPY_32_49
Perfect score: 93
Sequence: 1 VSLVEDQFSQNPISCFE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1500 summaries

Database :

PIR_80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	47.3	1249	2 F86909	probable DNA gyrase
2	44	47.3	1273	2 T10006	DNA topoisomerase
3	43	46.2	221	2 T29509	hypothetical prote
4	43	46.2	518	2 E84536	hypothetical prote
5	43	46.2	601	2 S38171	peptide transport
6	42	45.2	316	2 T38754	transcription fact
7	42	45.2	420	2 T45592	hypothetical prote
8	42	45.2	478	2 A49238	trypsin-like prote
9	42	45.2	681	2 T38755	transcription fact
10	42	45.2	1097	2 A56138	transcription fact
11	42	45.2	1356	2 T16754	hypothetical prote
12	42	45.2	1464	2 S47555	N-methyl-D-asparta
13	41.5	44.6	353	2 S37138	protoporphyrin IX
14	41.5	44.6	355	2 A89858	hypothetical prote
15	41.5	44.6	632	2 T16128	hypothetical prote
16	41	44.1	449	2 H84870	probable glucosylt
17	41	44.1	502	2 T29729	hypothetical prote
18	41	44.1	766	1 WZBEC5	infected cell prot
19	41	44.1	925	2 T37831	hypothetical prote
20	40.5	43.5	792	2 G86564	phenylalanine tRNA
21	40.5	43.5	792	2 H72058	phenylalanine tRNA
22	40.5	43.5	792	2 D81608	phenylalanine-tRNA
23	40	43.0	235	2 S73609	MG381 homolog H03
24	40	43.0	317	2 A47336	R-phycocoeythrin ga
25	40	43.0	574	2 T29615	hypothetical prote
26	40	43.0	1491	1 S43793	copper-transportin
27	40	43.0	1500	2 S36149	copper-transportin
28	39.5	42.5	1985	2 T40570	Munc13-2 - rat
29	39.5	42.5	778	2 T40570	probable nuclear p

30	39	5	42	5	1137	2	G84581	copia-like retroel
31	39	41.9	70	2	T32770	2	T32770	hypothetical prote
32	39	41.9	71	2	T17765	2	T17765	hypothetical prote
33	39	41.9	165	2	C95036	2	C95036	PTS system, IIA co
34	39	41.9	214	2	A81697	2	A81697	hypothetical prote
35	39	41.9	277	2	S65014	2	S65014	xanthosine phospho
36	39	41.9	324	2	S73000	2	S73000	hypothetical prote
37	39	41.9	428	2	AD3593	2	AD3593	dihydroorotase (EC
38	39	41.9	450	2	JC7266	2	JC7266	3',5'-cyclic-nucle
39	39	41.9	505	2	T51403	2	T51403	hypothetical prote
40	39	41.9	659	2	G97906	2	G97906	transcription anti
41	39	41.9	929	2	T17392	2	T17392	vrlL protein - Dic
42	39	41.9	1411	2	S40525	2	S40525	copper-transportin
43	39	41.9	1451	1	I58124	1	I58124	copper-transportin
44	39	41.9	1465	1	S78555	1	S78555	copper-transportin
45	39	41.9	1743	2	T26859	2	T26859	hypothetical prote
46	38	40.9	100	2	G71950	2	G71950	hypothetical prote
47	38	40.9	225	2	C86563	2	C86563	CT465 hypothetical
48	38	40.9	225	2	C72062	2	C72062	conserved hypotet
49	38	40.9	287	2	H90314	2	H90314	conserved hypotet
50	38	40.9	288	2	H81309	2	H81309	hypothetical prote
51	38	40.9	339	2	I58295	2	I58295	RAD51 protein homo
52	38	40.9	339	2	A48221	2	A48221	RAD51 protein homo
53	38	40.9	345	2	S64151	2	S64151	hypothetical prote
54	38	40.9	361	2	A95089	2	A95089	conserved hypotet
55	38	40.9	385	2	T22666	2	T22666	hypothetical prote
56	38	40.9	395	2	S44454	2	S44454	transcription fact
57	38	40.9	414	2	S62462	2	S62462	protein phosphatas
58	38	40.9	430	2	T44851	2	T44851	molybdopterin co-f
59	38	40.9	436	2	T39837	2	T39837	MAD box transcript
60	38	40.9	446	2	C86459	2	C86459	probable serine ca
61	38	40.9	448	2	I50730	2	I50730	yes-associated pro
62	38	40.9	498	2	A47286	2	A47286	3',5'-cyclic-AMP p
63	38	40.9	503	2	G85432	2	G85432	transcription init
64	38	40.9	551	2	T05667	2	T05667	aspartate-tRNA lig
65	38	40.9	558	2	T10672	2	T10672	probable growth re
66	38	40.9	653	2	A39922	2	A39922	potassium channel
67	38	40.9	654	2	S11049	2	S11049	potassium channel
68	38	40.9	660	2	S24125	2	S24125	potassium channel
69	38	40.9	757	1	S64742	1	S64742	dynamitin-related pr
70	38	40.9	772	2	S22660	2	S22660	excision repair pr
71	38	40.9	844	2	T38730	2	T38730	probable helicase
72	38	40.9	913	2	T15474	2	T15474	hypothetical prote
73	38	40.9	937	2	JC6067	2	JC6067	CCAT-binding fact
74	38	40.9	998	2	A36368	2	A36368	transcription fact
75	38	40.9	1068	1	A43322	1	A43322	1-phosphatidylinos
76	38	40.9	1068	1	I38110	1	I38110	1-phosphatidylinos
77	38	40.9	1276	2	S69048	2	S69048	probable membrane
78	38	40.9	1364	2	T40839	2	T40839	hypothetical prote
79	38	40.9	2201	2	AH0095	2	AH0095	probable sideropho
80	37.5	40.3	372	2	B84262	2	B84262	hypothetical prote
81	37.5	40.3	838	2	A96557	2	A96557	probable receptor
82	37	39.8	193	2	H86404	2	H86404	probable lipid tra
83	37	39.8	194	2	C82244	2	C82244	hypothetical prote
84	37	39.8	249	2	A97227	2	A97227	polyferredoxin lim
85	37	39.8	256	2	T03932	2	T03932	hypothetical prote
86	37	39.8	265	2	T31245	2	T31245	transglucosylase h
87	37	39.8	271	2	C75060	2	C75060	hydrogenase (EC 1.
88	37	39.8	341	2	T48958	2	T48958	acetylpolylamine an
89	37	39.8	365	2	C86700	2	C86700	mannosyltransferas
90	37	39.8	377	2	AC3426	2	AC3426	mannosyltransferas
91	37	39.8	386	2	T18890	2	T18890	hypothetical prote
92	37	39.8	404	2	G87757	2	G87757	protein Di007.8 [i
93	37	39.8	420	2	S62541	2	S62541	hypothetical prote
94	37	39.8	425	2	T33111	2	T33111	hypothetical prote
95	37	39.8	445	2	D83932	2	D83932	aminotransferase (
96	37	39.8	447	2	I49126	2	I49126	protein-tyrosine-p
97	37	39.8	463	2	S43787	2	S43787	glutamate-1-semial
98	37	39.8	465	2	T02698	2	T02698	Nicotiana tabacum
99	37	39.8	505	2	T41303	2	T41303	hypothetical prote
100	37	39.8	509	2	E86273	2	E86273	hypothetical prote
101	37	39.8	510	1	F0LJTM	1	F0LJTM	glyc polypeptide -
102	37	39.8	529	2	B49993	2	B49993	glycylpeptide N-te

103	37	39.8	608	1	ABXL68	68K serum albumin	176	36	38.7	1072	2	AD1280	SNF2-type helicase
104	37	39.8	647	2	S48471	probable membrane	177	36	38.7	1072	2	AD1643	SNF2-type helicase
105	37	39.8	652	2	T16582	hypothetical prote	178	36	38.7	1144	2	T13749	dof protein - frui
106	37	39.8	731	1	A32821	gelsolin, cytosoli	179	36	38.7	1181	2	A41052	paraporal crystal
107	37	39.8	870	2	T25338	hypothetical prote	180	36	38.7	1204	2	A96876	hypothetical prote
108	37	39.8	930	2	T20817	hypothetical prote	181	36	38.7	1210	2	A53183	epidermal growth f
109	37	39.8	989	2	T46659	period clock prote	182	36	38.7	1320	2	G81961	phosphoribosylform
110	37	39.8	1047	2	B71452	hypothetical prote	183	36	38.7	1645	2	AG1897	two-component hybr
111	37	39.8	1064	2	F86182	hypothetical prote	184	36	38.7	1722	2	R89753	protein F11C7.4 [i
112	37	39.8	1082	2	T15269	hypothetical prote	185	36	38.7	2156	1	RRVUNE	genome polypeptid
113	37	39.8	1170	2	T45914	integrin alpha 2 s	186	36	38.7	2195	2	S61103	SEC16 protein - ye
114	37	39.8	1735	2	A57607	Munc13-1 - rat	187	36	38.7	4753	1	A47437	LDL-receptor-relat
115	37	39.8	13055	2	T16580	hypothetical prote	188	35.5	38.2	278	2	B82388	probable maltose o
116	36.5	39.2	78	2	F97852	hypothetical prote	189	35.5	38.2	349	2	T00526	probable GDSL-moti
117	36.5	39.2	238	2	T15817	hypothetical prote	190	35.5	38.2	356	2	S73315	protoporphyrin IX
118	36.5	39.2	657	2	A53545	protein p84 - huma	191	35.5	38.2	401	2	F86754	prophage pi2 prote
119	36.5	39.2	804	2	AD0958	DNA gyrase chain B	192	35.5	38.2	591	2	B81687	ATP synthase, chai
120	36.5	39.2	832	1	S71768	PA/CAF protein - hu	193	35.5	38.2	591	2	B71531	probable ATP synth
121	36.5	39.2	1756	2	T07566	hypothetical prote	194	35.5	38.2	742	1	S47018	cdcH protein - Hal
122	36.5	39.2	1889	2	T50069	dynein heavy chain	195	35.5	38.2	742	2	C84319	cell division cycl
123	36.5	39.2	4196	2	T43274	dynein heavy chain	196	35.5	38.2	1258	2	F96753	similar to downy m
124	36	38.7	15	2	A61612	allatostatin - tob	197	35	37.6	42	2	L48240	LDH-A - mouse (fra
125	36	38.7	68	2	A81968	hypothetical prote	198	35	37.6	89	2	S78744	protein YDR363w-a
126	36	38.7	108	2	C64516	hypothetical prote	199	35	37.6	130	2	H72642	hypothetical prote
127	36	38.7	121	2	JC7630	C-type allatostati	200	35	37.6	144	2	S66493	serotonin receptor
128	36	38.7	166	2	F59091	hypothetical prote	201	35	37.6	147	2	D27733	hypothetical prote
129	36	38.7	168	2	AG2198	hypothetical prote	202	35	37.6	157	2	H64965	DNA gyrase inhibit
130	36	38.7	176	2	T48238	hypothetical prote	203	35	37.6	157	2	C90980	ShmC protein [impo
131	36	38.7	218	2	D71693	hypothetical prote	204	35	37.6	157	2	H85825	ShmC protein [impo
132	36	38.7	227	2	T00671	probable methyl ch	205	35	37.6	161	2	T22222	hypothetical prote
133	36	38.7	246	2	AB1345	hypothetical prote	206	35	37.6	161	2	T41833	ACMNPV orf93 - Bom
134	36	38.7	268	2	T40101	hypothetical prote	207	35	37.6	219	2	T08083	H+-transporting tw
135	36	38.7	271	2	AG0757	probable cobalt tr	208	35	37.6	223	2	I59173	glutamate decarbox
136	36	38.7	282	2	S39972	leucine-rich prote	209	35	37.6	245	2	T28148	class II histocomp
137	36	38.7	297	2	S66102	protein secretion	210	35	37.6	245	2	S09666	pbG protein - whe
138	36	38.7	327	2	AB1839	probable periplasm	211	35	37.6	254	2	C70682	probable cydH - My
139	36	38.7	327	2	D81103	hypothetical prote	212	35	37.6	259	2	T28147	class II histocomp
140	36	38.7	332	2	A23083	L-lactate dehydrog	213	35	37.6	266	2	C71531	hypothetical prote
141	36	38.7	361	2	T49337	hypothetical prote	214	35	37.6	267	1	JQ1324	DNA excision repai
142	36	38.7	363	2	T22594	hypothetical prote	215	35	37.6	267	2	JG0191	XPA protein - Afri
143	36	38.7	387	2	S12773	mitochondrial impo	216	35	37.6	278	2	B81426	parB family protei
144	36	38.7	393	2	A49008	paired box transcr	217	35	37.6	281	2	JC4295	heat-shock protein
145	36	38.7	403	2	T38078	hipA protein - Esc	218	35	37.6	284	2	G82234	conserved hypotet
146	36	38.7	440	2	F64904	probable glucosylt	219	35	37.6	296	2	G90063	hypothetical prote
147	36	38.7	449	2	B84871	tagaturonate reduc	220	35	37.6	297	2	G88035	protein M01D1.8 [i
148	36	38.7	483	2	AB0072	gag polyprotein -	221	35	37.6	309	2	T41494	zinc finger, ADP-x
149	36	38.7	506	1	FOLJ03	WD repeat protein	222	35	37.6	313	2	T48439	probable RNA-bindi
150	36	38.7	543	2	T37570	glutaminyl-tRNA sy	223	35	37.6	324	2	T05273	hypothetical prote
151	36	38.7	562	2	B81069	hypothetical prote	224	35	37.6	342	2	T18474	hypothetical prote
152	36	38.7	562	2	T27807	glutamine-tRNA lig	225	35	37.6	344	2	F69272	hypothetical prote
153	36	38.7	573	2	D81799	hypothetical prote	226	35	37.6	344	2	C70208	conserved hypotet
154	36	38.7	579	2	AB4237	hypothetical prote	227	35	37.6	344	2	T50895	prephytoene pyroph
155	36	38.7	581	2	T41210	hypothetical prote	228	35	37.6	349	2	D64134	peptide transport
156	36	38.7	593	2	S48135	glutamate decarbox	229	35	37.6	351	2	A86045	type III secretion
157	36	38.7	593	2	S51776	glutamate decarbox	230	35	37.6	351	2	A91198	G protein-coupled
158	36	38.7	594	1	A46758	glutamate decarbox	231	35	37.6	362	2	A39714	G protein-coupled
159	36	38.7	594	2	S51775	glutamate decarbox	232	35	37.6	362	2	A30341	G protein-coupled
160	36	38.7	594	2	JC4085	glutamate decarbox	233	35	37.6	364	2	G69377	bacteriochlorophyl
161	36	38.7	622	2	E97126	DNA mismatch repai	234	35	37.6	365	2	AD2669	chorismate synthas
162	36	38.7	644	2	A36325	epidermal growth f	235	35	37.6	368	2	B97451	chorismate synthas
163	36	38.7	644	2	C86747	topoisomerase IV s	236	35	37.6	376	2	T16147	hypothetical prote
164	36	38.7	645	2	S47929	signal recognition	237	35	37.6	380	2	B81302	probable type I re
165	36	38.7	654	2	B75587	probable N-glycosi	238	35	37.6	391	2	T23227	hypothetical prote
166	36	38.7	695	2	T39242	hypothetical prote	239	35	37.6	405	1	F69611	cytochrome P450 cy
167	36	38.7	725	2	T19994	hypothetical prote	240	35	37.6	408	2	T42850	hypothetical prote
168	36	38.7	741	2	A45771	2-5A-dependent RNA	241	35	37.6	411	2	B91220	probable arylsulfa
169	36	38.7	792	2	AB0038	probable outer mem	242	35	37.6	411	2	D86066	probable arylsulfa
170	36	38.7	817	2	T24063	hypothetical prote	243	35	37.6	411	2	A65184	arylsulfatase acti
171	36	38.7	852	2	S57984	probable membrane	244	35	37.6	411	2	D88037	protein K02E7.2 [i
172	36	38.7	912	2	T02892	hypothetical prote	245	35	37.6	411	2	T03897	hypothetical prote
173	36	38.7	967	2	D72308	conserved hypotet	246	35	37.6	411	2	B89024	protein K02D1.1 [i
174	36	38.7	1003	2	T24545	hypothetical prote	247	35	37.6	414	2	T34000	hypothetical prote
175	36	38.7	1012	2	T13712	dof protein - frui	248	35	37.6	414	2	G82174	hypothetical prote

249	35	37.6	421	2	T35205	citrate synthase-1	322	34	36.6	63	1	FEDV2V
250	35	37.6	426	2	T70343	enolase - Aquifex	323	34	36.6	96	2	T04223
251	35	37.6	431	2	G81179	oxidoreductase, pr	324	34	36.6	101	2	B86645
252	35	37.6	440	2	T01115	probable protein d	325	34	36.6	107	2	A82815
253	35	37.6	440	2	T49624	gap junction prote	326	34	36.6	114	2	AE1349
254	35	37.6	441	2	T20840	hypothetical prote	327	34	36.6	133	2	T08447
255	35	37.6	441	2	A46248	dihydroorotate oxi	328	34	36.6	145	2	S34574
256	35	37.6	443	1	A46248	probable membrane	329	34	36.6	176	2	A97808
257	35	37.6	451	2	S57989	GDP dissociation i	330	34	36.6	179	2	A13477
258	35	37.6	451	2	S44446	hypothetical prote	331	34	36.6	224	2	D64454
259	35	37.6	454	2	H85293	yes-associated pro	332	34	36.6	224	2	G70119
260	35	37.6	454	2	A56954	hypothetical prote	333	34	36.6	227	2	T00672
261	35	37.6	455	2	T05804	hypothetical prote	334	34	36.6	230	2	AF3113
262	35	37.6	458	2	T19941	ornithine decarbox	335	34	36.6	234	2	G98173
263	35	37.6	461	1	DUHO0	glutamate-ammonia	336	34	36.6	237	2	JU0176
264	35	37.6	472	2	T64098	hypothetical prote	337	34	36.6	238	2	T30945
265	35	37.6	505	2	S50567	DNA nucleotidyllexo	338	34	36.6	241	2	T33932
266	35	37.6	506	2	S55786	t-complex protein1	339	34	36.6	257	2	T28946
267	35	37.6	511	2	B90083	periplasmic oligop	340	34	36.6	266	2	F81687
268	35	37.6	514	2	B64055	conserved hypothet	341	34	36.6	273	2	T51512
269	35	37.6	541	2	G90132	type I restriction	342	34	36.6	285	1	QOECHP
270	35	37.6	543	2	S73820	CO2FS.9 protein -	343	34	36.6	285	2	E90770
271	35	37.6	564	2	S44611	interleukin-1 rece	344	34	36.6	285	2	A85633
272	35	37.6	569	2	A36187	glycerone kinase (345	34	36.6	287	2	B84039
273	35	37.6	580	2	T43310	hypothetical prote	346	34	36.6	289	2	A84058
274	35	37.6	585	2	S61534	glutamate decarbox	347	34	36.6	303	2	B83096
275	35	37.6	593	1	A41367	glutamate decarbox	348	34	36.6	309	2	A36064
276	35	37.6	594	1	B41935	glutamate decarbox	349	34	36.6	313	2	F96493
277	35	37.6	599	2	S47928	signal recognition	350	34	36.6	314	2	G85575
278	35	37.6	611	1	W1WLP	El protein - Europ	351	34	36.6	314	2	G90724
279	35	37.6	613	1	W1WLP	El protein - deer	352	34	36.6	317	2	S77827
280	35	37.6	616	1	A40457	replication protei	353	34	36.6	322	2	B81336
281	35	37.6	618	2	T39985	probable arginyl-t	354	34	36.6	323	2	S43850
282	35	37.6	622	2	T37257	hypothetical prote	355	34	36.6	323	2	S36636
283	35	37.6	643	2	T19199	hypothetical prote	356	34	36.6	325	2	T40264
284	35	37.6	649	2	S74823	N-acetylmuramoyl-L	357	34	36.6	330	2	T51834
285	35	37.6	702	2	C86268	P13B4.2 protein -	358	34	36.6	334	2	C69148
286	35	37.6	711	2	T05148	protein kinase hom	359	34	36.6	334	2	T19519
287	35	37.6	716	2	G01637	androgen receptor	360	34	36.6	339	2	S35642
288	35	37.6	723	2	S70098	probable membrane	361	34	36.6	341	2	E83779
289	35	37.6	728	2	A86453	CPS protein F9L11.	362	34	36.6	347	2	H86743
290	35	37.6	749	2	B86606	primosomal protein	363	34	36.6	348	2	T39358
291	35	37.6	749	2	T72018	primosomal protein	364	34	36.6	351	2	AC2289
292	35	37.6	773	2	T42575	infected cell prot	365	34	36.6	359	2	A48857
293	35	37.6	781	2	B64135	ribonucleoside-dip	366	34	36.6	367	2	JC6087
294	35	37.6	802	2	B84560	hypothetical prote	367	34	36.6	380	2	T19280
295	35	37.6	831	2	G91036	probable PTS svste	368	34	36.6	382	2	S74947
296	35	37.6	831	2	A95821	hypothetical prote	369	34	36.6	387	2	A11567
297	35	37.6	831	2	D85012	probable phosphoen	370	34	36.6	388	2	D82023
298	35	37.6	916	2	G81797	preprotein translo	371	34	36.6	388	2	E81244
299	35	37.6	916	2	D81072	preprotein translo	372	34	36.6	411	1	OXRTL
300	35	37.6	958	2	T51148	hypothetical prote	373	34	36.6	422	2	T38764
301	35	37.6	993	2	S21964	mating-type switch	374	34	36.6	424	1	G69641
302	35	37.6	1081	2	T31329	receptor tyrosine	375	34	36.6	424	2	AH0301
303	35	37.6	1135	2	J50605	M polyprotein - Ha	376	34	36.6	425	2	D64542
304	35	37.6	1155	2	A26513	parasporeal crystal	377	34	36.6	425	2	D71965
305	35	37.6	1181	2	C82500	ICMf-related prote	378	34	36.6	428	2	JQ1864
306	35	37.6	1190	2	P96677	pyruvate-flavodoxi	379	34	36.6	431	2	T24597
307	35	37.6	1217	2	D89896	protein C17B7.7 [i	380	34	36.6	435	2	E72342
308	35	37.6	1464	1	S29159	Glutamate receptor	381	34	36.6	449	2	T47950
309	35	37.6	1464	2	A43274	N-methyl D-asparta	382	34	36.6	450	2	T38465
310	35	37.6	1704	2	T43141	vitellinogen 1 - m	383	34	36.6	465	2	B69788
311	35	37.6	1704	2	T13937	plexin A - fruit f	384	34	36.6	467	2	D83055
312	35	37.6	1945	2	T33937	ESR1 protein - yea	385	34	36.6	472	2	A33312
313	35	37.6	2368	2	S46005	hypothetical prote	386	34	36.6	474	2	T27566
314	34.5	37.1	4767	2	T31345	hypothetical prote	387	34	36.6	479	2	B69613
315	34.5	37.1	145	2	S58628	hypothetical prote	388	34	36.6	480	2	S46153
316	34.5	37.1	189	2	E82618	DNA-directed RNA p	389	34	36.6	481	2	A89102
317	34.5	37.1	537	2	D89899	hypothetical prote	390	34	36.6	498	2	T51430
318	34.5	37.1	804	1	I5ECTB	conserved hypothet	391	34	36.6	503	2	A28415
319	34.5	37.1	804	2	B91208	DNA topoisomerase	392	34	36.6	503	2	JK0151
320	34.5	37.1	804	2	D86034	DNA gyrase subunit	393	34	36.6	503	2	JK0071
321	34.5	37.1	1297	2	S25714	hypothetical prote	394	34	36.6	503	2	S52085
					son-of-sevenless-2							

ferredoxin [4Fe-4S]
hypothetical prote
Glu-tRNA amidotran
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
gene 70 protein -
hypothetical prote
hypothetical cytos
proteasome beta su
hypothetical prote
hypothetical prote
transcription regu
probable transcript
lectin alpha chain
hypothetical prote
hypothetical prote
hypothetical prote
conserved hypothet
hypothetical prote
hydrogenase-1 cofa
hypothetical prote
hypothetical prote
hypothetical prote
ketomyltetrahydrof
ketopantoate reduc
basic fibroblast g
probable transposo
hypothetical prote
hypothetical prote
hypothetical prote
probable DNA-direc
pseudouridyate sy
melanocortin 3 rec
melanocortin recep
zinc-binding dehyd
transcription fact
dPPP-glucose 4,6-d
hypothetical prote
RAD51 protein homo
iron (III) dicitra
heat-inducible tra
DNA-directed RNA p
hypothetical prote
hypothetical prote
hypothetical prote
helix-loop-helix t
hypothetical prote
probable lipoprote
conserved hypothet
protein-lysine 6-o
aureobasidin A res
histidine-tRNA lig
probable exported
apolipoprotein N-a
apolipoprotein n-a
hypothetical 47.0K
hypothetical prote
pmbA-related prote
delta-8 sphingolip
probable dolichyl-
hypothetical prote
poly(A) polymerase
sarcoplasmic retic
hypothetical prote
ATP-dependent RNA
probable membrane
protein F25B5.4 [i
dolichyl-phosphate
steroid 11beta-mon
steroid 11beta-mon
steroid 11-beta-hy

395	34	36.6	516	2	G95406	probable ABC trans	468	34	36.6	1212	2	T13804	shs protein - frui
396	34	36.6	520	2	T20007	hypothetical prote	469	34	36.6	1214	2	T18549	DNA polymerase hom
397	34	36.6	520	2	D82412	chaperonin, 60 kD	470	34	36.6	1214	2	T30941	DNA polymerase - c
398	34	36.6	533	2	A72292	hypothetical prote	471	34	36.6	1239	2	G71266	probable ATP-depen
399	34	36.6	544	2	S62527	probable amino-acl	472	34	36.6	1263	2	T13805	spalt-related prot
400	34	36.6	544	2	H86828	fructuronate reduc	473	34	36.6	1299	2	A86366	fr26j12.6 protein -
401	34	36.6	554	2	T43211	cytoplasmic signal	474	34	36.6	1328	2	T23007	hypothetical prote
402	34	36.6	557	1	WZBYI	isocitrate lyase (475	34	36.6	1345	2	T44204	capsid protein U57
403	34	36.6	560	1	RGNVPM	trans-activating t	476	34	36.6	1345	2	T44017	major capsid prote
404	34	36.6	560	2	T10414	immediate early pr	477	34	36.6	1397	2	T10466	DNA topoisomerase
405	34	36.6	564	2	B64241	threonine-tRNA lig	478	34	36.6	1536	1	RGBYS3	regulatory protein
406	34	36.6	578	2	AF1958	L-aspartate oxidas	479	34	36.6	1557	2	T28811	hypothetical prote
407	34	36.6	584	2	T18908	hypothetical prote	480	34	36.6	1658	2	S55101	hypothetical prote
408	34	36.6	594	2	D4676	oligopeptide ABC t	481	34	36.6	1787	2	F84528	probable retroelem
409	34	36.6	607	2	H64041	probable long-chai	482	34	36.6	1919	2	T40032	hypothetical prote
410	34	36.6	608	2	A53195	afamin precursor -	483	34	36.6	2049	2	T43161	sodium channel pro
411	34	36.6	615	2	T15423	hypothetical prote	484	34	36.6	2180	2	A47651	zinc-finger protei
412	34	36.6	616	2	T38717	probable GRP-bindi	485	34	36.6	2761	2	T29285	hypothetical prote
413	34	36.6	623	2	D71435	hypothetical prote	486	34	36.6	2907	2	A57278	fibrillin-2 precu
414	34	36.6	623	2	T28051	hypothetical prote	487	34	36.6	3507	2	T34513	hypothetical prote
415	34	36.6	632	2	G88109	protein T24E12.10	488	34	36.6	3724	2	T18427	hypothetical prote
416	34	36.6	638	1	YSBS72	threonine-tRNA lig	489	33.5	36.0	78	2	T17963	hypothetical prote
417	34	36.6	638	2	T21321	hypothetical prote	490	33.5	36.0	168	2	A28476	myosin heavy chain
418	34	36.6	640	1	UZADP7	terminal protein p	491	33.5	36.0	168	2	B25217	myosin heavy chain
419	34	36.6	658	2	A86231	hypothetical prote	492	33.5	36.0	169	2	A25217	myosin heavy chain
420	34	36.6	660	2	T38294	sec-7 cytohesin-li	493	33.5	36.0	258	2	T35147	glutamate uptake s
421	34	36.6	666	2	T43171	cytoplasmic signal	494	33.5	36.0	294	2	C75574	conserved hypothet
422	34	36.6	670	2	H96707	probable receptor	495	33.5	36.0	359	2	D81711	phospholipase D fa
423	34	36.6	672	2	T24507	hypothetical prote	496	33.5	36.0	374	2	AH1825	protoporphyrin IX
424	34	36.6	715	2	JC4560	methyilmalonyl-CoA	497	33.5	36.0	493	2	T05105	hypothetical prote
425	34	36.6	716	2	A86181	hypothetical prote	498	33.5	36.0	508	2	A22206	serine/threonine k
426	34	36.6	739	2	T15215	hypothetical prote	499	33.5	36.0	523	2	H90529	potassium uptake p
427	34	36.6	755	2	G84791	probable ABC trans	500	33.5	36.0	838	2	S38156	hypothetical prote
428	34	36.6	757	2	C70034	conserved hypothet	501	33.5	36.0	953	2	F96498	hypothetical prote
429	34	36.6	764	2	I39934	protective antigen	502	33.5	36.0	1776	2	G86280	protein T521.13 l
430	34	36.6	764	2	S64951	hypothetical prote	503	33.5	36.0	1804	2	AF2250	serine/threonine k
431	34	36.6	804	2	T18014	hypothetical prote	504	33.5	36.0	1938	1	JX0178	myosin heavy chain
432	34	36.6	818	2	F97348	heavy-metal transp	505	33.5	36.0	1940	2	A29320	myosin heavy chain
433	34	36.6	857	2	S33821	median body protei	506	33	35.5	74	2	AF3436	hypothetical prote
434	34	36.6	861	2	B84885	probable transcrip	507	33	35.5	75	2	C90601	hypothetical prote
435	34	36.6	876	2	T33176	hypothetical prote	508	33	35.5	76	2	AD1442	gp37-1 (Bacterioph
436	34	36.6	908	2	A33280	sarcosulmenin precu	509	33	35.5	103	2	T13589	probable small nuc
437	34	36.6	957	2	A49847	nitrite reductase	510	33	35.5	108	2	T00420	hypothetical prote
438	34	36.6	962	2	D70661	probable membranep	511	33	35.5	110	2	H64512	hypothetical prote
439	34	36.6	967	2	G96637	hypothetical prote	512	33	35.5	113	2	AH3438	hypothetical prote
440	34	36.6	981	2	T51921	hypothetical prote	513	33	35.5	115	2	T38514	small nuclear ribo
441	34	36.6	997	2	S44457	period clock prote	514	33	35.5	118	2	I38861	small nuclear ribo
442	34	36.6	1010	2	S45389	probable membrane	515	33	35.5	128	2	AF2143	hypothetical prote
443	34	36.6	1014	2	H71602	protein with DnaJ	516	33	35.5	135	2	C69446	hypothetical prote
444	34	36.6	1036	2	S73601	protein P200 - Myc	517	33	35.5	137	2	A11375	hypothetical prote
445	34	36.6	1058	2	AG2541	cation efflux avst	518	33	35.5	152	2	T07858	glycine-rich prote
446	34	36.6	1075	2	C59434	XtAA0411 protein [519	33	35.5	155	2	S75888	hypothetical prote
447	34	36.6	1075	2	C96682	protein F1822.16 [520	33	35.5	161	2	T00729	hypothetical prote
448	34	36.6	1133	2	S54496	probable membrane	521	33	35.5	161	2	F72861	hypothetical prote
449	34	36.6	1135	1	GNVUH7	M polypeptide - Ha	522	33	35.5	162	2	D84959	small protein B [i
450	34	36.6	1135	1	GNVUH7	M polypeptide - Ha	523	33	35.5	164	2	S73814	small 5-formyl
451	34	36.6	1155	2	S02134	parasporeal crystal	524	33	35.5	167	2	T12580	GTP-binding protei
452	34	36.6	1155	2	S02134	parasporeal crystal	525	33	35.5	177	2	A86610	frame-shift with C
453	34	36.6	1155	2	JD0002	parasporeal crystal	526	33	35.5	188	2	F81808	hypothetical prote
454	34	36.6	1156	2	A29125	parasporeal crystal	527	33	35.5	188	2	AC3613	probable s-adenosy
455	34	36.6	1156	2	A29838	parasporeal crystal	528	33	35.5	195	2	I46272	trophoblast interf
456	34	36.6	1165	2	S11446	parasporeal crystal	529	33	35.5	195	2	A96731	unknown protein F5
457	34	36.6	1166	2	S32645	parasporeal crystal	530	33	35.5	195	2	S55609	hypothetical prote
458	34	36.6	1171	2	A37859	parasporeal crystal	531	33	35.5	200	2	T05541	heat shock protein
459	34	36.6	1171	2	I40572	parasporeal crystal	532	33	35.5	216	1	TLBPX2	tail fiber protein
460	34	36.6	1172	2	S32689	parasporeal crystal	533	33	35.5	220	2	A41662	hypothetical prote
461	34	36.6	1174	2	A42459	parasporeal crystal	534	33	35.5	223	2	S06576	finger protein (cl
462	34	36.6	1176	2	A48970	parasporeal crystal	535	33	35.5	237	2	A45587	lectin - Dioclea l
463	34	36.6	1182	2	T30189	myelin transcripti	536	33	35.5	237	2	T27145	hypothetical prote
464	34	36.6	1187	2	T46637	transcription fact	537	33	35.5	243	2	C64124	molybdopterin bios
465	34	36.6	1188	2	T46608	zinc finger protei	538	33	35.5	247	1	D24706	modulation protein
466	34	36.6	1189	2	S00944	parasporeal crystal	539	33	35.5	247	2	H95319	phosphoadenylyl-su
467	34	36.6	1190	2	T38636	tat binding homolo	540	33	35.5	249	2	C85592	molybdopterin bios

541	33	35.5	249	2	H90741	molybdopterin bios	614	33	35.5	469	2	A71369	probable sugar ABC
542	33	35.5	257	2	D81086	FrpC operon protei	615	33	35.5	470	2	C70641	hypothetical prote
543	33	35.5	258	2	G36798	hypothetical prote	616	33	35.5	475	2	T20706	hypothetical prote
544	33	35.5	263	2	AF2534	hypothetical prote	617	33	35.5	477	2	S74716	hypothetical prote
545	33	35.5	267	2	T00114	exodeoxyribonuclea	618	33	35.5	480	2	A86371	hypothetical prote
546	33	35.5	271	2	B81182	FrpC operon protei	619	33	35.5	498	2	A97061	uncharacterized pr
547	33	35.5	275	2	A82257	oxidoreductase, sh	620	33	35.5	505	2	AC2107	hypothetical prote
548	33	35.5	284	2	S52672	hypothetical prote	621	33	35.5	514	2	S72847	hypothetical prote
549	33	35.5	287	2	S42259	streptomycin resis	622	33	35.5	516	2	B84145	transposase (22) B
550	33	35.5	289	2	A84790	probable RNA-bindi	623	33	35.5	534	2	S06548	finger protein (cl
551	33	35.5	294	2	T24776	hypothetical prote	624	33	35.5	541	2	T13162	cytosolic phosphol
552	33	35.5	298	2	C82073	signal peptidase I	625	33	35.5	554	2	C70512	hypothetical prote
553	33	35.5	299	2	T25596	hypothetical prote	626	33	35.5	556	2	T49501	hypothetical prote
554	33	35.5	301	2	B89815	CDP-glucose 4,6-de	627	33	35.5	565	1	HMIW55	hemagglutinin prec
555	33	35.5	304	2	T09357	hypothetical prote	628	33	35.5	565	2	A25226	RAD7 protein - yea
556	33	35.5	305	2	C89915	hypothetical prote	629	33	35.5	584	2	F75090	archaeosine trna-r
557	33	35.5	305	2	A89721	protein T10B10.4 [630	33	35.5	591	2	T43443	hypothetical prote
558	33	35.5	307	2	T16457	hypothetical prote	631	33	35.5	615	2	S06546	finger protein (cl
559	33	35.5	309	2	I48125	syndecan-1 - Chine	632	33	35.5	618	2	T44595	alcaligin synthesi
560	33	35.5	310	2	S43101	SED5 protein - fru	633	33	35.5	643	1	FOV22W	major core protein
561	33	35.5	314	2	B95034	dihydropteroate sy	634	33	35.5	643	2	G89008	protein T27C4.2 [1
562	33	35.5	314	2	B97905	dihydropteroate sy	635	33	35.5	644	1	FOV25R	major core protein
563	33	35.5	316	1	A43661	dihydropteroate sy	636	33	35.5	644	2	T37390	major core protein
564	33	35.5	326	2	A54497	surface membrane p	637	33	35.5	644	2	A72164	A4L protein - vari
565	33	35.5	330	2	AD2854	conserved hypotet	638	33	35.5	644	2	D36848	major core protein
566	33	35.5	336	2	H70328	hypothetical prote	639	33	35.5	644	2	T28545	hypothetical prote
567	33	35.5	338	2	E95251	ornithine carbamoy	640	33	35.5	649	2	B75317	threonyl-tRNA synt
568	33	35.5	338	2	B98116	ornithine carbamoy	641	33	35.5	651	2	C86333	hypothetical prote
569	33	35.5	349	2	T23931	hypothetical prote	642	33	35.5	660	2	AB0794	probable lipopolys
570	33	35.5	356	2	A82729	cytochrome oxidase	643	33	35.5	660	2	F85965	probable transform
571	33	35.5	363	2	A85700	probable GTP-bindi	644	33	35.5	660	2	G91021	probable transform
572	33	35.5	363	2	AB0721	probable ATP/GTP-b	645	33	35.5	660	2	E64996	hypothetical prote
573	33	35.5	363	2	H64866	probable GTP-bindi	646	33	35.5	661	2	B75084	ferrous iron trans
574	33	35.5	363	2	D90842	probable GTP-bindi	647	33	35.5	662	2	E83201	conserved hypotet
575	33	35.5	363	2	I64150	probable GTP-bindi	648	33	35.5	663	2	S54426	DNA topoisomerase
576	33	35.5	363	2	AD0245	conserved hypotet	649	33	35.5	664	2	S60062	hevin precursor -
577	33	35.5	367	1	I69653	UDPgalactopyranose	650	33	35.5	665	2	B89911	topoisomerase IV a
578	33	35.5	371	2	G76644	hypothetical prote	651	33	35.5	667	2	AD0295	probable formyl tr
579	33	35.5	372	2	F97510	RA483fil.2.1 (cox1	652	33	35.5	672	2	B84782	probable receptor-
580	33	35.5	373	2	F91438	probable periplasm	653	33	35.5	677	2	T19281	hypothetical prote
581	33	35.5	383	1	C53309	pigY protein - Ent	654	33	35.5	681	2	JX0338	rabphilin-3A - mou
582	33	35.5	386	2	A97631	hypothetical 37.4K	655	33	35.5	682	2	T10319	envelope protein E
583	33	35.5	387	2	S77288	carboxymorspermid	656	33	35.5	684	2	I58166	rabphilin-3A - rat
584	33	35.5	391	2	T40029	hypothetical prote	657	33	35.5	686	2	B87624	phospholipase C [i
585	33	35.5	396	2	H40422	hypothetical prote	658	33	35.5	693	2	C84495	hypothetical prote
586	33	35.5	401	2	H84828	hypothetical prote	659	33	35.5	702	2	T01763	threonine-tRNA lig
587	33	35.5	408	2	T01006	hypothetical prote	660	33	35.5	704	2	A48097	rabphilin-3A - bov
588	33	35.5	410	1	IXB310	alpha trans-induci	661	33	35.5	709	2	T51624	threonine-tRNA lig
589	33	35.5	410	2	H9307	bacteriochlorophyl	662	33	35.5	712	1	YSHUT	threonine-tRNA lig
590	33	35.5	413	2	A97173	flagellar switch p	663	33	35.5	734	1	YSBYTC	threonine-tRNA lig
591	33	35.5	417	2	F71238	hypothetical prote	664	33	35.5	745	1	S75354	probable copper-tr
592	33	35.5	418	2	S44646	hypothetical prote	665	33	35.5	746	1	QRECF	ferrienterochelin
593	33	35.5	419	2	S06784	hypothetical prote	666	33	35.5	746	2	G90706	hypothetical prote
594	33	35.5	420	2	A45166	protein-lysine 6-o	667	33	35.5	746	2	B85557	hypothetical prote
595	33	35.5	422	2	S37280	Cyclin A - mouse	668	33	35.5	747	2	T23882	hypothetical prote
596	33	35.5	422	2	S38501	Cyclin A2 - mouse	669	33	35.5	753	2	T19338	hypothetical prote
597	33	35.5	423	2	AC3553	4-aminobutyrate tr	670	33	35.5	765	2	T29582	hypothetical prote
598	33	35.5	426	2	S16416	gene E46 protein -	671	33	35.5	766	1	B43684	probable RNA-direc
599	33	35.5	433	2	T19632	hypothetical prote	672	33	35.5	776	2	T20896	hypothetical prote
600	33	35.5	434	2	D71309	47K integral membr	673	33	35.5	787	2	E82323	organic solvent to
601	33	35.5	436	2	T00908	hypothetical prote	674	33	35.5	790	1	G69071	heavy-metal-transp
602	33	35.5	443	2	A13525	4-aminobutyrate tr	675	33	35.5	790	2	T15709	hypothetical prote
603	33	35.5	445	2	T28988	hypothetical prote	676	33	35.5	802	2	F90060	copper-transportin
604	33	35.5	450	1	DCCHO	ornithine decarbox	677	33	35.5	803	1	E70041	probable copper-tr
605	33	35.5	453	2	JC5607	replication initia	678	33	35.5	812	2	E95029	formate acetyltran
606	33	35.5	455	1	DGHYOC	ornithine decarbox	679	33	35.5	815	2	H97900	formate C-acetyltr
607	33	35.5	455	2	F72326	hemolysin-related	680	33	35.5	815	2	G82861	conjugal transfer
608	33	35.5	455	2	T52155	threonyl-tRNA synt	681	33	35.5	821	2	T24728	hypothetical prote
609	33	35.5	459	2	T04808	hypothetical prote	682	33	35.5	825	2	I46078	endothelin convert
610	33	35.5	465	2	D86166	protein F21B7.12 [683	33	35.5	826	2	G97073	uncharacterized pr
611	33	35.5	466	2	S44878	Zc262.6 protein -	684	33	35.5	863	2	F84504	probable retroelem
612	33	35.5	468	2	T41294	hypothetical prote	685	33	35.5	870	2	T30110	hypothetical prote
613	33	35.5	469	2	C86170	hypothetical prote	686	33	35.5	904	2	T40072	P Type Copper ATPa

687	33	35.5	910	2	G84648	probable disease r	760	32.5	34.9	443	2	AH2415	two-component hybr
688	33	35.5	915	2	B59433	chromosome 5 GAP-1	761	32.5	34.9	491	2	T01856	hypothetical prote
689	33	35.5	921	2	D82513	malt regulatory pr	762	32.5	34.9	499	2	T03213	probable ribosomal
690	33	35.5	944	2	T38130	probable helicase	763	32.5	34.9	532	2	AB1369	conserved hypotet
691	33	35.5	946	2	S48433	inositol-1,4,5-tri	764	32.5	34.9	538	2	T03232	probable ribosomal
692	33	35.5	987	2	A12011	peptide synthetase	765	32.5	34.9	590	2	A96556	unknown protein, 3
693	33	35.5	1011	2	T17430	tol protein - Neur	766	32.5	34.9	635	2	T23465	hypothetical prote
694	33	35.5	1015	2	T31386	hypothetical prote	767	32.5	34.9	681	2	AD3318	DNA primase (EC 2.
695	33	35.5	1040	2	T39936	probable helicase	768	32.5	34.9	695	1	VH1WV	nucleocapsid prote
696	33	35.5	1045	2	S60571	integrin alpha v c	769	32.5	34.9	695	2	S44049	nucleocapsid prote
697	33	35.5	1071	1	PXBVYA	H ₂ -exporting Arpas	770	32.5	34.9	759	2	S62067	Ty1 enhancer activ
698	33	35.5	1081	2	T20698	hypothetical prote	771	32.5	34.9	770	2	B48910	desmocollin lb pre
699	33	35.5	1081	2	S51899	probable protein k	772	32.5	34.9	781	2	T26080	hypothetical prote
700	33	35.5	1083	2	T26844	hypothetical Arpas	773	32.5	34.9	824	2	A48910	desmocollin la pre
701	33	35.5	1088	2	A46080	H ₂ -exporting Arpas	774	32.5	34.9	840	2	I37281	Dadla precursor -
702	33	35.5	1093	2	S86748	hypothetical prote	775	32.5	34.9	893	2	P86476	protein F1504.39 l
703	33	35.5	1093	2	T50652	AP-3 complex beta-3	776	32.5	34.9	894	2	I37282	Decib precursor -
704	33	35.5	1094	2	T50651	AP-3 complex beta-3	777	32.5	34.9	932	2	S65214	probable alpha/gam
705	33	35.5	1099	2	A59311	myosin VIII, ZMW3	778	32.5	34.9	1356	2	JC1402	protein-tyrosine k
706	33	35.5	1099	2	A51065	conserved hypotet	779	32.5	34.9	1367	2	A41328	protein-tyrosine k
707	33	35.5	1116	2	B88612	protein Y76A2A.2 l	780	32.5	34.9	1417	2	T18418	hypothetical prote
708	33	35.5	1135	2	T42723	probable DNA-dirc	781	32.5	34.9	1946	2	AC2141	serine/threonine k
709	33	35.5	1135	2	T42368	DNA-directed RNA p	782	32.5	34.9	3020	2	A43932	mucin 2 precursor,
710	33	35.5	1152	2	T27531	hypothetical prote	783	32.5	34.4	50	2	H82588	hypothetical prote
711	33	35.5	1168	2	T37496	probable pre-mRNA	784	32.5	34.4	73	2	T25926	hypothetical prote
712	33	35.5	1176	2	A22617	paraaporal crystal	785	32.5	34.4	98	2	T26046	hypothetical prote
713	33	35.5	1176	2	JC2219	paraaporal crystal	786	32.5	34.4	104	2	S50936	probable membrane
714	33	35.5	1176	2	JT0241	paraaporal crystal	787	32.5	34.4	109	2	T00234	hypothetical prote
715	33	35.5	1176	2	S02215	paraaporal crystal	788	32.5	34.4	110	2	S41557	hypothetical prote
716	33	35.5	1177	2	A49785	paraaporal crystal	789	32.5	34.4	115	2	A55827	blue copper protei
717	33	35.5	1178	1	UBS8X3	paraaporal crystal	790	32.5	34.4	125	2	T49512	hypothetical prote
718	33	35.5	1189	2	A12493	WP-repeat protein	791	32.5	34.4	136	1	B64956	flagellar protein
719	33	35.5	1191	2	T31091	hypothetical prote	792	32.5	34.4	136	2	H90961	flagellar protein
720	33	35.5	1195	2	S38174	probable purine nu	793	32.5	34.4	136	2	H85809	hypothetical prote
721	33	35.5	1220	2	S17179	Ca2+-transporting	794	32.5	34.4	145	2	H82498	hypothetical prote
722	33	35.5	1238	1	JC5573	copper-transportin	795	32.5	34.4	154	2	E83634	hypothetical prote
723	33	35.5	1287	2	A41685	Slit protein - huma	796	32.5	34.4	158	2	T09295	probable heat choc
724	33	35.5	1320	2	G81017	phosphoribosylform	797	32.5	34.4	159	2	B75151	molybdenum cofacto
725	33	35.5	1332	2	S41552	probable transcrip	798	32.5	34.4	165	2	H71649	hypothetical prote
726	33	35.5	1341	2	S50366	probable membrane	799	32.5	34.4	166	2	NH2568	hypothetical prote
727	33	35.5	1345	1	VCBEH6	major capsid prote	800	32.5	34.4	168	2	E69198	Ni,Fe-Hydrogenase
728	33	35.5	1480	2	T05566	hypothetical prote	801	32.5	34.4	174	2	T50419	conserved hypotet
729	33	35.5	1523	2	T13953	MEGF5 protein - ra	802	32.5	34.4	175	2	AC2876	conserved hypotet
730	33	35.5	1529	2	T16779	hypothetical prote	803	32.5	34.4	177	2	E97652	hypothetical prote
731	33	35.5	1531	2	T42218	slit-1 protein hom	804	32.5	34.4	185	1	A39167	placental protein
732	33	35.5	1549	2	T13940	ankyrin - fruit fl	805	32.5	34.4	185	2	AE0736	probable bacteriop
733	33	35.5	1619	2	S67083	hypothetical prote	806	32.5	34.4	186	2	T39759	hypothetical prote
734	33	35.5	1715	2	T30559	resistance protein	807	32.5	34.4	191	2	S78155	ribosomal protein
735	33	35.5	1744	2	JH0720	tanabin - African	808	32.5	34.4	192	2	D69061	precorrin-8W decar
736	33	35.5	1761	2	T13675	hypothetical prote	809	32.5	34.4	196	2	G89950	conserved hypotet
737	33	35.5	1792	2	T20363	hypothetical prote	810	32.5	34.4	200	2	T25406	hypothetical prote
738	33	35.5	1838	2	H86337	protein F5M15.26 l	811	32.5	34.4	203	2	T48718	mitochondrial ribo
739	33	35.5	2123	2	F86348	hypothetical prote	812	32.5	34.4	204	2	T01447	hypothetical prote
740	33	35.5	2185	1	S60200	acetyl-CoA carboxy	813	32.5	34.4	204	2	T28939	hypothetical prote
741	33	35.5	2324	1	A29924	acetyl-CoA carboxy	814	32.5	34.4	205	2	A71567	probable GMP kinas
742	33	35.5	2364	2	A56577	microtubule-associ	815	32.5	34.4	212	2	F72752	hypothetical prote
743	33	35.5	2427	2	T16613	hypothetical prote	816	32.5	34.4	213	2	D82849	cell division prot
744	33	35.5	2464	1	QKMSD1	microtubule-associ	817	32.5	34.4	213	2	D70211	lipoprotein homolo
745	33	35.5	2717	2	A34203	DNA-binding protei	818	32.5	34.4	215	2	E70350	probable thiamin p
746	33	35.5	2918	2	A54105	fibrillin-2 precur	819	32.5	34.4	219	1	T1BPT2	tail fiber protein
747	33	35.5	4687	1	A39638	plectin - rat	820	32.5	34.4	221	1	T1BPT2	tail fiber protein
748	32.5	34.9	136	2	T45080	hypothetical prote	821	32.5	34.4	226	2	AC0176	probable exported
749	32.5	34.9	207	2	A12505	hypothetical prote	822	32.5	34.4	230	1	T1BPK3	tail fiber protein
750	32.5	34.9	238	2	H82084	aerobic respiratio	823	32.5	34.4	231	2	T45566	hypothetical prote
751	32.5	34.9	241	2	F97202	hypothetical prote	824	32.5	34.4	237	2	E81298	hypothetical prote
752	32.5	34.9	247	2	H86723	transcription regu	825	32.5	34.4	242	2	E89813	hypothetical prote
753	32.5	34.9	332	2	T51269	hypothetical prote	826	32.5	34.4	246	2	T19850	hypothetical prote
754	32.5	34.9	352	2	T05169	hypothetical prote	827	32.5	34.4	247	2	T49991	probable protein p
755	32.5	34.9	371	2	C97355	uncharacterized pr	828	32.5	34.4	254	2	H89772	hypothetical prote
756	32.5	34.9	411	2	T29475	hypothetical prote	829	32.5	34.4	255	2	H83700	transcription acti
757	32.5	34.9	412	2	T09313	immediate-early pr	830	32.5	34.4	255	2	AC3292	glucose-1-phosphat
758	32.5	34.9	413	1	S16426	tyrosine-tRNA liga	831	32.5	34.4	257	2	C81206	frpC operon protei
759	32.5	34.9	441	2	P88930	protein R11G11.12	832	32.5	34.4	259	2	T36172	hypothetical prote

833	32	34.4	259	2	H88969	protein Fl5811.5 [906	32	34.4	403	2	B82982	DNA/pantothenate m
834	32	34.4	261	2	T51243	Scl1 protein [impo	907	32	34.4	403	2	S53477	IMP dehydrogenase
835	32	34.4	264	2	AB2326	hypothetical prote	908	32	34.4	404	2	D86321	hypothetical prote
836	32	34.4	265	2	G37271	metalloproteinase	909	32	34.4	405	2	T37022	probable lycopen
837	32	34.4	268	2	F37271	metalloproteinase	910	32	34.4	410	2	T36610	hypothetical prote
838	32	34.4	268	2	T32775	hypothetical prote	911	32	34.4	412	1	JC4921	hemolysin homolo
839	32	34.4	271	2	S35026	hypothetical prote	912	32	34.4	412	2	JC4921	double C2 protei
840	32	34.4	278	2	C69854	conserved hypotet	913	32	34.4	415	2	T48171	hypothetical prote
841	32	34.4	278	2	AD2345	hypothetical prote	914	32	34.4	416	2	D69251	hypothetical prote
842	32	34.4	278	2	T22640	hypothetical prote	915	32	34.4	421	2	T43534	transcription fact
843	32	34.4	278	2	AD2981	hypothetical prote	916	32	34.4	421	2	T05032	protein kinase hom
844	32	34.4	278	2	H98301	dipeptide transpor	917	32	34.4	424	2	B95201	3-hydroxy-3-methyl
845	32	34.4	281	2	AD10126	conserved hypotet	918	32	34.4	424	2	H98067	hydroxymethylgluta
846	32	34.4	281	2	D82554	tRNA/rRNA methyltr	919	32	34.4	424	2	S27783	hypothetical prote
847	32	34.4	281	2	C82547	hypothetical prote	920	32	34.4	426	2	H87462	enolase [imported]
848	32	34.4	285	2	B82459	hypothetical prote	921	32	34.4	427	2	T46265	hypothetical prote
849	32	34.4	287	2	T40403	hypothetical prote	922	32	34.4	428	2	A81841	phosphorylase hy
850	32	34.4	288	2	D82781	conserved hypotet	923	32	34.4	428	2	D81100	enolase NMB1285 [i
851	32	34.4	289	2	B62907	conserved hypotet	924	32	34.4	431	2	C95023	competence-induced
852	32	34.4	290	2	E37271	metalloproteinase	925	32	34.4	435	2	T24074	hypothetical prote
853	32	34.4	291	2	S48252	serine-rich protei	926	32	34.4	437	2	E71953	hypothetical prote
854	32	34.4	294	2	T20338	hypothetical prote	927	32	34.4	440	2	S37303	sox-4 protein - mo
855	32	34.4	297	2	C96524	Fl1A17.4 [imported	928	32	34.4	443	2	A70438	flagellar export p
856	32	34.4	300	2	AE0762	conserved hypotet	929	32	34.4	444	2	E70201	pantothenate perme
857	32	34.4	304	2	S12975	coat protein - pot	930	32	34.4	447	2	G86940	probable enolase [
858	32	34.4	304	2	AG0926	hypothetical prote	931	32	34.4	451	2	C49898	cellulose phospho
859	32	34.4	304	2	T48281	hypothetical prote	932	32	34.4	453	2	F82702	conserved hypotet
860	32	34.4	306	2	S19997	hypothetical prote	933	32	34.4	455	2	AH0794	o-succinylbenzoate
861	32	34.4	307	2	G69211	conserved hypotet	934	32	34.4	456	2	AE3341	cobQ protein (EC 1
862	32	34.4	308	2	A86246	hypothetical prote	935	32	34.4	460	2	T27770	hypothetical prote
863	32	34.4	308	2	T46234	hypothetical prote	936	32	34.4	461	2	F82700	enolase XF1291 [im
864	32	34.4	308	2	H89839	hypothetical prote	937	32	34.4	461	2	T51458	hypothetical prote
865	32	34.4	310	1	S37695	calcium-binding pr	938	32	34.4	461	2	A46394	suppressor protein
866	32	34.4	311	2	E96714	probable DNA-bind	939	32	34.4	465	2	T26146	hypothetical prote
867	32	34.4	313	2	F71285	hypothetical prote	940	32	34.4	466	2	T44350	hypothetical prote
868	32	34.4	323	2	T28951	hypothetical prote	941	32	34.4	466	2	A11707	transcription regu
869	32	34.4	328	2	AE0301	conserved hypotet	942	32	34.4	468	1	B64896	hypothetical prote
870	32	34.4	330	2	T39698	protein tyrosine p	943	32	34.4	468	2	D85734	hypothetical prote
871	32	34.4	330	2	AG2129	iron(iii) dicitrat	944	32	34.4	468	2	C90884	probable transcrip
872	32	34.4	331	2	AB3678	hypothetical prote	945	32	34.4	469	1	P2WL35	L2 protein - human
873	32	34.4	332	1	DBMSJL	L-lactate dehydrog	946	32	34.4	469	2	S36525	L2 protein - human
874	32	34.4	335	2	T49145	hypothetical prote	947	32	34.4	470	2	B86165	hypothetical prote
875	32	34.4	337	2	T46742	ornithine carbanoy	948	32	34.4	471	1	S62590	peptidyl-prolyl ci
876	32	34.4	340	2	F85724	hypothetical prote	949	32	34.4	472	1	B53236	transcription fact
877	32	34.4	341	2	T47338	hypothetical prote	950	32	34.4	472	2	S36519	L2 protein - human
878	32	34.4	341	2	H90797	probable tellurum	951	32	34.4	474	2	AF0669	probable regulator
879	32	34.4	344	2	B83605	probable acetylpol	952	32	34.4	474	2	I38240	sulfate adenyltr
880	32	34.4	345	2	H90515	lipote-protein li	953	32	34.4	475	1	JN0327	hypothetical prote
881	32	34.4	346	2	T30463	hypothetical prote	954	32	34.4	475	2	E91079	hypothetical prote
882	32	34.4	348	2	AI3626	inositol 2-dehydro	955	32	34.4	475	2	F85924	hypothetical prote
883	32	34.4	354	2	JC4212	nitrilase (EC 3.5.	956	32	34.4	478	1	FOVWVL	hypothetical prote
884	32	34.4	358	2	AC0740	probable integrase	957	32	34.4	481	2	AD1337	transcription regu
885	32	34.4	359	2	JC2134	angiotensin II rec	958	32	34.4	481	2	D83994	xylose kinase xylB
886	32	34.4	361	2	AG0335	chorismate synthas	959	32	34.4	488	2	T09436	gag polyprotein -
887	32	34.4	361	2	D97956	conserved hypotet	960	32	34.4	488	2	FOVWLV	gag polyprotein -
888	32	34.4	363	2	D81037	GTP-binding protei	961	32	34.4	500	1	FOVWLV	gag polyprotein -
889	32	34.4	366	2	AB3061	conserved hypotet	962	32	34.4	500	1	A44001	gag polyprotein -
890	32	34.4	367	2	T10207	oleoyl-lacyl-carri	963	32	34.4	500	2	G71836	anthranilate synth
891	32	34.4	367	2	B56598	endothelial kinase	964	32	34.4	500	2	B64680	anthranilate synth
892	32	34.4	370	2	T40085	gcsS protein - Bac	965	32	34.4	500	2	S33979	gag polyprotein -
893	32	34.4	372	2	T08273	conserved hypotet	966	32	34.4	502	1	FOVWA2	gag polyprotein -
894	32	34.4	373	2	JC7289	G-protein coupled	967	32	34.4	503	2	A54302	zinc transporter 2
895	32	34.4	379	2	C86821	hypothetical prote	968	32	34.4	506	1	A38068	gag polyprotein -
896	32	34.4	383	2	H75139	probable transamin	969	32	34.4	507	2	T11559	gag protein - simi
897	32	34.4	383	2	S53379	probable membrane	970	32	34.4	507	2	S04237	gag polyprotein -
898	32	34.4	385	2	AB5607	hypothetical prote	971	32	34.4	508	1	FOVJJI	gag polyprotein -
899	32	34.4	386	2	E71001	probable transamin	972	32	34.4	511	2	AI3112	hypothetical prote
900	32	34.4	387	2	E71711	probable o-sialogl	973	32	34.4	511	2	D98174	oligopeptide ABC t
901	32	34.4	390	2	G01936	Abl binding protei	974	32	34.4	512	1	FOVWH3	gag polyprotein -
902	32	34.4	391	2	D64366	hypothetical prote	975	32	34.4	512	2	T44982	methylmalonyl-CoA
903	32	34.4	397	2	T35351	hypothetical prote	976	32	34.4	512	2	B71474	probable hsp60 cha
904	32	34.4	401	2	A57226	mel-5332 protein -	977	32	34.4	512	2	H85878	multidrug resistan
905	32	34.4	402	2	S55465	chalcone synthase	978	32	34.4	512	2	F91034	multidrug resistan

979	32	34.4	512	2	D65010	multidrug resistant	1052	32	34.4	721	2	T41530	hypothetical prote
980	32	34.4	515	2	B89648	protein lin-14 [im	1053	32	34.4	726	2	AG0837	TonB-dependent out
981	32	34.4	518	2	G70174	hypothetical prote	1054	32	34.4	729	2	AF0808	probable membrane
982	32	34.4	520	2	C81273	hypothetical prote	1055	32	34.4	736	2	T49652	glycerol-3-phospha
983	32	34.4	521	1	FOLJCA	gag polyprotein -	1056	32	34.4	744	2	H71643	cell division prot
984	32	34.4	521	1	FOLJST	gag polyprotein -	1057	32	34.4	750	2	E84475	probable Athila re
985	32	34.4	521	2	JC5220	protein-tyrosine-p	1058	32	34.4	751	2	I48748	semaphorin E - mou
986	32	34.4	521	2	S53091	gag polyprotein -	1059	32	34.4	751	2	F85043	hypothetical prote
987	32	34.4	521	2	S08435	gag polyprotein -	1060	32	34.4	764	2	I36916	glycoprotein Iib -
988	32	34.4	521	2	S12152	gag polyprotein -	1061	32	34.4	764	2	T07608	chloride channel p
989	32	34.4	522	1	FOLJG2	gag polyprotein -	1062	32	34.4	775	2	T49817	hypothetical prote
990	32	34.4	522	2	B71807	DNA repair protein	1063	32	34.4	776	2	S67053	probable membrane
991	32	34.4	523	1	S48997	IMP dehydrogenase	1064	32	34.4	782	2	S62583	probable transcrip
992	32	34.4	523	1	S59402	IMP dehydrogenase	1065	32	34.4	785	2	AD1893	hydrogenase matura
993	32	34.4	524	2	A64694	DNA repair protein	1066	32	34.4	792	2	C85359	hypothetical prote
994	32	34.4	526	2	F82873	hypothetical prote	1067	32	34.4	793	2	T24270	hypothetical prote
995	32	34.4	527	2	T25131	hypothetical prote	1068	32	34.4	806	2	JC4835	beta-catenin - Hyd
996	32	34.4	529	2	B23595	DNA nucleotidylexo	1069	32	34.4	808	2	T16564	hypothetical prote
997	32	34.4	537	2	T25268	embryonic nuclear	1070	32	34.4	822	2	AD3232	conjugal transfer
998	32	34.4	538	2	H96008	hypothetical prote	1071	32	34.4	822	2	T09221	exocyst complex pr
999	32	34.4	539	2	A40581	embryonic nuclear	1072	32	34.4	826	2	A60385	monocyte surface a
1000	32	34.4	542	2	S58837	hypothetical prote	1073	32	34.4	830	2	S25198	vacuolar membrane
1001	32	34.4	553	2	S22954	finger protein zfp	1074	32	34.4	839	2	S62563	hypothetical prote
1002	32	34.4	554	2	S46346	gag polyprotein -	1075	32	34.4	847	2	G75270	cation-transporin
1003	32	34.4	554	2	T33294	hypothetical prote	1076	32	34.4	850	2	S20462	RNA12 protein - ye
1004	32	34.4	556	2	D88700	protein K0282.4 [i	1077	32	34.4	873	2	F71092	ATP-dependent RNA
1005	32	34.4	559	2	T28693	hypothetical prote	1078	32	34.4	891	2	T19915	hypothetical prote
1006	32	34.4	565	2	H72253	DNA primase - ther	1079	32	34.4	906	2	T45158	pre-mRNA splicing
1007	32	34.4	577	1	VGBEG1	Glycoprotein E - 8	1080	32	34.4	922	2	B82168	insulinase-type zi
1008	32	34.4	579	2	E96496	unknown protein, 5	1081	32	34.4	929	2	A32495	rep-1 protein, for
1009	32	34.4	582	2	H70588	probable proS prot	1082	32	34.4	935	2	S66306	hypothetical prote
1010	32	34.4	583	2	AH1922	hypothetical prote	1083	32	34.4	939	2	AE2275	hypothetical prote
1011	32	34.4	585	2	S38155	hypothetical prote	1084	32	34.4	944	2	T28734	hypothetical prote
1012	32	34.4	587	2	A86203	hypothetical prote	1085	32	34.4	947	2	T00340	hypothetical prote
1013	32	34.4	591	1	S22664	virulence-associat	1086	32	34.4	962	2	I70165	adenosine triphosp
1014	32	34.4	593	2	S15215	virulence-associat	1087	32	34.4	968	2	F70746	probable mmp12 pro
1015	32	34.4	598	2	T40659	probable peroxisom	1088	32	34.4	974	2	T14076	probable villin [i
1016	32	34.4	600	2	T24626	hypothetical prote	1089	32	34.4	982	2	S10340	DNA-directed RNA p
1017	32	34.4	602	2	T50974	related to hxB pro	1090	32	34.4	986	2	T10754	cis-Golgi matrix p
1018	32	34.4	604	2	I36917	glycoprotein Iib -	1091	32	34.4	994	2	A70776	probable glne - My
1019	32	34.4	614	2	T19963	hypothetical prote	1092	32	34.4	1022	2	B84792	probable kinesin h
1020	32	34.4	617	2	AE0394	probable accessory	1093	32	34.4	1029	2	T28956	hypothetical prote
1021	32	34.4	621	2	D70762	probable transfera	1094	32	34.4	1033	2	S72194	hydroxymethylgluta
1022	32	34.4	621	2	A71516	hypothetical prote	1095	32	34.4	1053	2	H64577	type I restriction
1023	32	34.4	622	2	D71078	aldehyde-ferredoxi	1096	32	34.4	1055	2	C75506	hypothetical prote
1024	32	34.4	623	2	T02007	ABC1 protein homol	1097	32	34.4	1070	2	T37876	probable (Xeroderm
1025	32	34.4	623	2	T52128	ABC1 protein homol	1098	32	34.4	1072	2	T24877	hypothetical prote
1026	32	34.4	624	2	S50650	hypothetical prote	1099	32	34.4	1076	2	T24887	hypothetical prote
1027	32	34.4	631	2	D40189	probable biotin-pr	1100	32	34.4	1098	2	T28816	hypothetical prote
1028	32	34.4	633	2	D82597	proteinase IV XP26	1101	32	34.4	1119	2	B70126	surface-located me
1029	32	34.4	635	2	A81656	threonyl-tRNA synt	1102	32	34.4	1124	2	G91055	hypothetical prote
1030	32	34.4	637	2	D97708	cell division prot	1103	32	34.4	1124	2	C85900	hypothetical prote
1031	32	34.4	637	2	C71712	cell division prot	1104	32	34.4	1124	2	D65032	hypothetical prote
1032	32	34.4	638	2	D84453	hypothetical prote	1105	32	34.4	1126	2	JC4019	DNA mismatch repai
1033	32	34.4	640	2	B84478	probable replicati	1106	32	34.4	1129	2	D84022	ATP-dependent nucl
1034	32	34.4	642	2	A82479	threonyl-tRNA synt	1107	32	34.4	1131	2	T19442	hypothetical prote
1035	32	34.4	644	2	A96721	probable peptide t	1108	32	34.4	1131	2	AD2166	two-component aena
1036	32	34.4	650	2	T00081	hypothetical prote	1109	32	34.4	1135	2	JQ2163	hypothetical 126.5
1037	32	34.4	651	2	C75014	hypothetical prote	1110	32	34.4	1145	2	T13810	DNA-directed DNA p
1038	32	34.4	660	2	G71497	threonine-tRNA lig	1111	32	34.4	1145	2	T13808	DNA-directed DNA p
1039	32	34.4	677	2	T40145	probable beta-adap	1112	32	34.4	1146	2	S46837	hypothetical prote
1040	32	34.4	686	2	T15795	hypothetical prote	1113	32	34.4	1162	2	B97852	hypothetical prote
1041	32	34.4	692	2	A36143	phospholipase C (E	1114	32	34.4	1163	2	D82202	vgg protein VC141
1042	32	34.4	692	2	E83230	non-hemolytic phos	1115	32	34.4	1169	2	C71639	hypothetical prote
1043	32	34.4	694	2	F82511	vgg protein VCA00	1116	32	34.4	1176	2	A28065	hypothetical prote
1044	32	34.4	694	2	F90609	exodeoxyribonuclea	1117	32	34.4	1200	2	T48194	protein kinase SK2
1045	32	34.4	700	2	T10566	probable serine/th	1118	32	34.4	1206	2	A34021	Ca2+-transporting
1046	32	34.4	703	2	T39997	Thalp - fission ve	1119	32	34.4	1220	2	A30802	adenosine triphosp
1047	32	34.4	711	2	S68443	double-stranded RN	1120	32	34.4	1220	2	I55491	Ca2+-transporting
1048	32	34.4	711	2	G86536	hypothetical prote	1121	32	34.4	1224	2	S13057	hypothetical prote
1049	32	34.4	711	2	A72098	hypothetical prote	1122	32	34.4	1224	2	H96615	hypothetical prote
1050	32	34.4	715	2	D84549	probable selenium-	1123	32	34.4	1231	2	T18532	serine/threonine pr
1051	32	34.4	718	2	G70978	probable copper-tr	1124	32	34.4	1233	2	T14157	serine/threonine p

1125	32	34.4	1257	2	A88536	protein B0523.5 [i	1198	31.5	33.9	827	2	S75622	hypothetical prote
1126	32	34.4	1263	2	F44466	DNA-directed RNA p	1199	31.5	33.9	840	2	I48968	major fibrous shea
1127	32	34.4	1283	2	T13799	neurexin IV - frui	1200	31.5	33.9	849	2	I49060	major 80,000 Mr fi
1128	32	34.4	1300	2	J73679	probable lipoprote	1201	31.5	33.9	861	2	T41945	primase - human he
1129	32	34.4	1379	2	JC4954	vascular endotheli	1202	31.5	33.9	1024	2	G72041	exodeoxyribonuclea
1130	32	34.4	1384	2	T26656	hypothetical prote	1203	31.5	33.9	1024	2	F86582	exodeoxyribonuclea
1131	32	34.4	1405	2	T04426	hypothetical prote	1204	31.5	33.9	1024	2	D81624	thymotropon-releas
1132	32	34.4	1416	2	E88550	protein ZC84.1 [im	1205	31.5	33.9	1025	2	I59331	probable retroelem
1133	32	34.4	1466	2	G84516	probable retroelem	1206	31.5	33.9	1150	2	H96501	E-selectin ligand-
1134	32	34.4	1499	2	B59431	Rho GTPase activat	1207	31.5	33.9	1175	2	S52417	hypothetical prote
1135	32	34.4	1501	2	T42724	p190-B protein - m	1208	31.5	33.9	1226	2	S69078	capsid protein 25
1136	32	34.4	1509	2	T19486	hypothetical prote	1209	31.5	33.9	1381	2	S55619	breast cancer tumo
1137	32	34.4	1513	1	BNRZ22	DNA-directed RNA p	1210	31.5	33.9	1484	2	T42632	polymorphic membra
1138	32	34.4	1520	2	B82274	conserved hypothet	1211	31.5	33.9	1672	2	C81675	serine/threonine k
1139	32	34.4	1547	2	S69842	tyb protein - yeas	1212	31.5	33.9	1787	2	AC1895	dynein beta heavy
1140	32	34.4	1560	2	T02885	peroxisome prolife	1213	31.5	33.9	1796	2	AC1895	serine/threonine k
1141	32	34.4	1571	2	T14155	zinc finger protei	1214	31.5	33.9	4588	2	T28667	hypothetical prote
1142	32	34.4	1616	2	G64242	cytadherence-acces	1215	31	33.3	66	2	AG1908	hypothetical prote
1143	32	34.4	1727	2	T50073	myosin-like coiled	1216	31	33.3	82	2	AG0714	hypothetical prote
1144	32	34.4	1735	1	S22812	DNA-directed RNA p	1217	31	33.3	98	2	S06671	cinnamomin - Phyto
1145	32	34.4	1759	2	T18868	myoblast city prot	1218	31	33.3	101	2	T21657	hypothetical prote
1146	32	34.4	1825	2	T42725	actin binding prot	1219	31	33.3	103	2	A72713	hypothetical prote
1147	32	34.4	1872	2	JC4976	plexin 3 precursor	1220	31	33.3	110	2	B41323	ribulose-bisphosph
1148	32	34.4	1885	2	T30847	actin binding prot	1221	31	33.3	111	2	B71115	hypothetical prote
1149	32	34.4	1927	2	A59236	embryonic muscle m	1222	31	33.3	111	2	S10222	hypothetical prote
1150	32	34.4	2033	2	T30849	actin binding prot	1223	31	33.3	111	2	S12179	transcription fact
1151	32	34.4	2042	2	T18399	variant-specific s	1224	31	33.3	113	2	S12184	transcription fact
1152	32	34.4	2090	2	S26058	Munc13-3 protein -	1225	31	33.3	114	2	S40340	ig kappa chain V-J
1153	32	34.4	2207	2	T42759	hypothetical prote	1226	31	33.3	114	2	S12185	transcription fact
1154	32	34.4	2287	2	T21312	hypothetical prote	1227	31	33.3	114	2	F90557	hypothetical prote
1155	32	34.4	2297	2	AB2494	hypothetical prote	1228	31	33.3	115	2	S12187	transcription fact
1156	32	34.4	2561	1	I40456	peptide synthetase	1229	31	33.3	118	1	B70021	arsenate reductase
1157	32	34.4	2824	2	T22759	hypothetical prote	1230	31	33.3	118	2	AH0986	phage-like lysozym
1158	32	34.4	2844	2	S28291	hypothetical prote	1231	31	33.3	118	2	S26611	transcription fact
1159	32	34.4	3227	2	T37964	probable ubiquitin	1232	31	33.3	120	2	S16445	transcription fact
1160	32	34.4	3603	1	D69681	peptide synthetase	1233	31	33.3	122	2	JN0441	Shaking-B neural p
1161	32	34.4	3744	2	S46715	hypothetical prote	1234	31	33.3	123	2	S26610	transcription fact
1162	32	34.4	6486	2	T31076	tyrocidine synthet	1235	31	33.3	124	2	S76185	hypothetical prote
1163	31.5	33.9	60	2	S35180	cytochrome P450 (c	1236	31	33.3	127	2	H82181	hypothetical prote
1164	31.5	33.9	91	2	S17637	ig kappa chain V r	1237	31	33.3	135	2	T40281	gtp-binding protei
1165	31.5	33.9	143	2	T36669	probable anti-sigm	1238	31	33.3	136	2	JU0266	envelope polyprote
1166	31.5	33.9	168	2	AE1238	E. coli YbdM prote	1239	31	33.3	136	2	JT0954	envelope polyprote
1167	31.5	33.9	168	2	AE1238	E. coli YbdM prote	1240	31	33.3	139	2	S06550	finger protein (cl
1168	31.5	33.9	200	2	AG2261	transcription regu	1241	31	33.3	142	2	S25093	phospholipase A2 (
1169	31.5	33.9	220	2	T20059	hypothetical prote	1242	31	33.3	142	2	G75109	hypothetical prote
1170	31.5	33.9	274	2	AH2462	biotin acetyl-CoA	1243	31	33.3	145	2	S30247	Hin-1 protein - hu
1171	31.5	33.9	277	2	T20065	hypothetical prote	1244	31	33.3	152	2	T32784	hypothetical prote
1172	31.5	33.9	296	2	S75601	hypothetical prote	1245	31	33.3	153	2	A26092	myosin II regulato
1173	31.5	33.9	302	2	T32234	hypothetical prote	1246	31	33.3	153	2	S77187	hypothetical prote
1174	31.5	33.9	320	2	C83628	probable oxidoredu	1247	31	33.3	154	2	B84973	aspartate carbamoy
1175	31.5	33.9	330	2	T22411	hypothetical prote	1248	31	33.3	154	2	S28181	transcription fact
1176	31.5	33.9	331	2	G02431	geranylgeranyl tra	1249	31	33.3	160	2	C69355	hypothetical prote
1177	31.5	33.9	340	1	C64360	conserved hypothet	1250	31	33.3	165	2	AH3295	acetyltransferase
1178	31.5	33.9	357	2	T46868	protoporphyrin IX	1251	31	33.3	169	2	JC6013	hypothetical k pro
1179	31.5	33.9	357	2	S75252	protoporphyrin IX	1252	31	33.3	171	2	E97074	probable acetyltra
1180	31.5	33.9	370	2	AB3334	daunorubicin resis	1253	31	33.3	171	2	T48393	hypothetical prote
1181	31.5	33.9	374	2	JC2123	major allergen Cry	1254	31	33.3	173	2	S10548	lectin - barnacle
1182	31.5	33.9	380	2	G69893	butyryl-CoA dehydr	1255	31	33.3	178	2	S74564	hypothetical prote
1183	31.5	33.9	380	2	T44811	acyl-CoA dehydroge	1256	31	33.3	184	2	A83316	hypothetical prote
1184	31.5	33.9	380	2	A83458	hypothetical prote	1257	31	33.3	184	2	G85955	hypothetical prote
1185	31.5	33.9	392	2	T35458	hypothetical prote	1258	31	33.3	182	2	D64481	hypothetical prote
1186	31.5	33.9	401	2	A81335	tyrosine-tRNA liga	1259	31	33.3	194	2	A72167	A28L protein - var
1187	31.5	33.9	438	2	D72404	flagellum-specific	1260	31	33.3	199	2	E86081	hypothetical prote
1188	31.5	33.9	559	1	R32M53	ribosomal protein	1261	31	33.3	199	2	S40863	hypothetical 21.8K
1189	31.5	33.9	559	2	T20709	hypothetical prote	1262	31	33.3	199	2	E91234	hypothetical prote
1190	31.5	33.9	591	2	B72121	ATP synthase, chai	1263	31	33.3	203	2	AD1369	hypothetical prote
1191	31.5	33.9	591	2	H86501	ATP synthase subun	1264	31	33.3	207	2	S59142	murB protein - ma
1192	31.5	33.9	595	2	JC8012	G protein-coupled	1265	31	33.3	208	2	C81160	uracil phosphoribo
1193	31.5	33.9	607	2	E84827	hypothetical prote	1266	31	33.3	209	2	F82483	hypothetical prote
1194	31.5	33.9	673	2	T06294	hypothetical prote	1267	31	33.3	212	2	S03070	gag protein - huma
1195	31.5	33.9	673	2	H69828	ABC transporter (A	1268	31	33.3	212	2	D82383	conserved hypothet
1196	31.5	33.9	693	2	T00256	hypothetical prote	1269	31	33.3	213	2	T06333	probable glutathio
1197	31.5	33.9	696	2	JC7361	follitropin recept	1270	31	33.3	217	2	H64956	yedG protein - Esc

1271	31	33.3	218	2	JC7147	trichothecene bios	1344	31	33.3	287	2	T27056	hypothetical prote
1272	31	33.3	219	2	G86620	dethiobiotin synth	1345	31	33.3	290	2	T50434	hypothetical prote
1273	31	33.3	219	2	G72004	hypothetical prote	1346	31	33.3	291	2	AI3092	hypothetical prote
1274	31	33.3	220	2	A81311	probable periplasm	1347	31	33.3	296	2	AB0557	cytochrome o ubiq
1275	31	33.3	221	2	A81311	ubiquitin-protein	1348	31	33.3	296	2	A42226	heme O synthase -
1276	31	33.3	221	2	T43159	endonuclease V [im	1349	31	33.3	296	2	F85539	prothomene IX farne
1277	31	33.3	222	2	F90962	hypothetical prote	1350	31	33.3	296	2	B90689	lipopolysaccharide
1278	31	33.3	222	2	F85810	hypothetical prote	1351	31	33.3	297	2	F64206	antibiotic ABC tra
1279	31	33.3	222	2	A35968	tox regulon transc	1352	31	33.3	297	2	P90287	hypothetical 35.5K
1280	31	33.3	226	2	T37499	probable ubiquitin	1353	31	33.3	303	2	J80379	hypothetical prote
1281	31	33.3	228	2	T15236	hypothetical prote	1354	31	33.3	304	2	A89905	conserved hypochet
1282	31	33.3	230	1	H64098	probable pyridoxam	1355	31	33.3	305	2	A71324	hypothetical prote
1283	31	33.3	230	2	H83325	probable transport	1356	31	33.3	310	2	T31799	hypothetical prote
1284	31	33.3	231	2	B64249	tRNA (Guanine-N1-)	1357	31	33.3	312	2	H97297	probable transcrip
1285	31	33.3	231	2	S73286	phycobilisome rod-	1358	31	33.3	314	2	AG3410	chloroAMPhenicol-se
1286	31	33.3	231	2	S33552	hypothetical prote	1359	31	33.3	314	2	P90569	conserved hypochet
1287	31	33.3	232	1	JH0597	transcription fact	1360	31	33.3	318	2	A99510	hypothetical prote
1288	31	33.3	234	2	A41178	heparin-binding gr	1361	31	33.3	318	2	A85066	hypothetical prote
1289	31	33.3	236	2	E84307	glucose 1-dehydrog	1362	31	33.3	320	1	C71071	hypothetical prote
1290	31	33.3	237	2	S46685	hypothetical prote	1363	31	33.3	323	2	AI2024	hypothetical prote
1291	31	33.3	238	2	S78571	transcription fact	1364	31	33.3	326	1	J17954	alkanal monooxygen
1292	31	33.3	239	2	AF0750	RNA polymerase sig	1365	31	33.3	326	2	GC4196	36K hydrophobic nu
1293	31	33.3	239	2	E90961	RNA polymerase sig	1366	31	33.3	326	2	A96608	hypothetical prote
1294	31	33.3	239	2	JC4346	RNA polymerase sig	1367	31	33.3	327	2	JC4195	36k hydrophobic nu
1295	31	33.3	239	2	E85809	RNA polymerase sig	1368	31	33.3	328	2	F72260	hypothetical prote
1296	31	33.3	239	2	S11895	transcription init	1369	31	33.3	330	2	S49471	transcription init
1297	31	33.3	241	1	QJ1641	phosphoprotein p -	1370	31	33.3	330	2	AG0855	RNA polymerase sig
1298	31	33.3	241	2	T23428	hypothetical prote	1371	31	33.3	330	2	S47534	transcription init
1299	31	33.3	241	2	A87551	glutathione S-tran	1372	31	33.3	331	2	JQ2018	hypothetical 36.5K
1300	31	33.3	241	2	T16802	hypothetical prote	1373	31	33.3	331	2	A86278	hypothetical prote
1301	31	33.3	242	2	A96794	unknown protein F1	1374	31	33.3	331	2	A99179	conserved hypochet
1302	31	33.3	245	2	S10658	hypothetical prote	1375	31	33.3	332	1	DEHULM	L-lactate dehydrog
1303	31	33.3	245	2	H86151	hypothetical prote	1376	31	33.3	332	2	T00847	probable membrane
1304	31	33.3	246	2	C64054	tRNA (Guanine-N1-)	1377	31	33.3	334	2	F89008	protein W08A12.4 [
1305	31	33.3	247	2	C82307	tRNA (Guanine-N1-)	1378	31	33.3	335	2	A40467	interleukin-5 rece
1306	31	33.3	249	2	C81180	tRNA (Guanine-N1-)	1379	31	33.3	336	2	G95051	ketol-acid reducto
1307	31	33.3	249	2	A81924	probable tRNA (gua	1380	31	33.3	336	2	AD1566	hypothetical prote
1308	31	33.3	251	2	T23566	hypothetical prote	1381	31	33.3	337	2	AI2723	naphthalene 1,2-di
1309	31	33.3	251	2	H82864	conserved hypochet	1382	31	33.3	337	2	B97505	phenol hydroxylase
1310	31	33.3	252	2	C83178	tRNA (Guanine-N1-)	1383	31	33.3	337	2	D70132	hypothetical prote
1311	31	33.3	252	2	F65084	hypothetical prote	1384	31	33.3	338	2	A82890	hypothetical prote
1312	31	33.3	252	2	S30292	mating-type switch	1385	31	33.3	340	2	B86778	ketol-acid reducto
1313	31	33.3	255	2	T24406	hypothetical prote	1386	31	33.3	340	2	C97922	ketol-acid reducto
1314	31	33.3	256	2	AI1119	transcription regu	1387	31	33.3	343	2	G71499	probable D-Ala-D-A
1315	31	33.3	256	2	AD1480	transcription regu	1388	31	33.3	343	2	T19082	hypothetical prote
1316	31	33.3	257	2	C97109	specialized DNA-de	1389	31	33.3	343	2	T22053	probable ketol-aci
1317	31	33.3	257	2	T40621	probable transcrip	1390	31	33.3	344	1	S35140	hypothetical prote
1318	31	33.3	257	2	T40880	hypothetical prote	1391	31	33.3	347	2	T40599	channel protein vi
1319	31	33.3	258	2	T34432	hypothetical prote	1392	31	33.3	347	2	AD3513	transcription fact
1320	31	33.3	261	2	T41508	hypothetical prote	1393	31	33.3	348	1	B46216	glycerol-3-phospha
1321	31	33.3	261	2	D90582	hypothetical prote	1394	31	33.3	349	2	A25952	conserved hypochet
1322	31	33.3	262	2	H83136	probable transcrip	1395	31	33.3	349	2	D69856	orf U81053 - infec
1323	31	33.3	263	2	G81272	hypothetical prote	1396	31	33.3	351	2	D48552	hypothetical prote
1324	31	33.3	263	4	L67792	probable glucosylc	1397	31	33.3	351	2	S52708	G protein-coupled
1325	31	33.3	266	1	WQECWP	phosphotransferase	1398	31	33.3	354	2	B55733	lipopolysaccharide
1326	31	33.3	266	2	H90944	mannose-specific p	1399	31	33.3	354	2	AG3315	G protein-coupled
1327	31	33.3	266	2	C85793	PTS enzyme IIC, ma	1400	31	33.3	355	2	G88216	protein B0495.1 [i
1328	31	33.3	268	2	AB1087	PTS system mannose	1401	31	33.3	355	2	F96540	beta-mannanase [im
1329	31	33.3	268	2	AB1450	PTS system mannose	1402	31	33.3	357	2	S63142	hypothetical prote
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1331	31	33.3	272	2	T33515	hypothetical prote	1404	31	33.3	358	2	S45911	hypothetical prote
1332	31	33.3	272	2	F70979	hypothetical prote	1405	31	33.3	359	2	T02608	hypothetical prote
1333	31	33.3	273	2	T50938	Ditr protein [impo	1406	31	33.3	360	2	AE0172	probable outer mem
1334	31	33.3	274	2	T76777	O9 mannan biosynth	1407	31	33.3	361	2	A53860	chondroadherin pre
1335	31	33.3	276	2	T38825	hypothetical prote	1408	31	33.3	363	2	G70145	glycerol-3-phospha
1336	31	33.3	278	2	A56570	homeobox protein D	1409	31	33.3	363	2	C70462	DNA polymerase III
1337	31	33.3	280	2	I55577	Fc gamma (IgG) rec	1410	31	33.3	363	2	S66114	creatine kinase ho
1338	31	33.3	281	1	T15613	probable phosphoes	1411	31	33.3	364	1	JT0741	GTP-binding protei
1339	31	33.3	281	2	T50351	probable methyltra	1412	31	33.3	364	2	A55014	GTP-binding protei
1340	31	33.3	282	2	B84984	Geranyltransf	1413	31	33.3	366	2	AH2237	septum site-determ
1341	31	33.3	283	2	S42634	homeoprotein, IDX-	1414	31	33.3	368	1	S64487	GTP-binding protei
1342	31	33.3	284	2	D81075	conserved hypochet	1415	31	33.3	370	2	A27098	larvicidal toxin 4
1343	31	33.3	284	2	S39581	IPP1 protein - mou	1416	31	33.3	370	2	S07712	larvicidal toxin 4

1417 31 33.3 370 2 D28211 larvicidal toxin 4
1418 31 33.3 370 2 G90122 hypothetical prote
1419 31 33.3 370 2 T52141 hypothetical prote
1420 31 33.3 372 2 T06745 hypothetical prote
1421 31 33.3 374 1 LQBR4 RNA ligase (ATP) (
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1426 31 33.3 381 2 T10707 adenosylmethionine
1427 31 33.3 381 2 T49544 hypothetical prote
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1429 31 33.3 383 2 JC2472 brain and reproduc
1430 31 33.3 384 2 S58446 sigma S - Salmonel
1431 31 33.3 384 2 A86324 protein Fl4D16.19
1432 31 33.3 385 2 S66292 actin-crosslinking
1433 31 33.3 386 2 D59237 probable citrate s
1434 31 33.3 387 2 S55550 5-HT4S receptor -
1435 31 33.3 387 2 G64489 hypothetical prote
1436 31 33.3 388 2 T31306 hypothetical prote
1437 31 33.3 390 2 B84727 molybdopterin synt
1438 31 33.3 390 2 T41199 dom34 protein homo
1439 31 33.3 391 2 H97491 alanine racemase (
1440 31 33.3 391 2 AG2709 alanine racemase (
1441 31 33.3 392 2 T01617 probable protein k
1442 31 33.3 393 2 A80216 phosphoribosylglyc
1443 31 33.3 396 2 H72224 hypothetical prote
1444 31 33.3 397 2 JE0082 GPI-linked recepto
1445 31 33.3 397 2 AC2006 hypothetical prote
1446 31 33.3 398 2 S56699 naringenin-chalcon
1447 31 33.3 399 2 AD2917 conserved hypothet
1448 31 33.3 399 2 G97691 hypothetical prote
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1450 31 33.3 402 2 D75592 hypothetical prote
1451 31 33.3 403 1 S35541 transcription fact
1452 31 33.3 404 2 T21251 hypothetical prote
1453 31 33.3 406 2 S55549 serotonin 4 recept
1454 31 33.3 410 2 S68515 probable arginine
1455 31 33.3 410 2 A41465 arginine deiminase
1456 31 33.3 411 1 OXMSL protein-lysine 6-o
1457 31 33.3 412 2 T41552 hypothetical prote
1458 31 33.3 412 2 B81356 ankyrin repeat-con
1459 31 33.3 413 2 E86400 protein T17H3.4 [1
1460 31 33.3 413 2 AC3614 dtdp-4-dehydroxam
1461 31 33.3 414 2 T38742 hypothetical prote
1462 31 33.3 417 1 OXHUL protein-lysine 6-o
1463 31 33.3 417 2 A96610 probable pectinase
1464 31 33.3 418 2 E86395 hypothetical prote
1465 31 33.3 420 2 S21052 interleukin-5 rece
1466 31 33.3 421 2 C82253 folylpolyglutamate
1467 31 33.3 423 2 E72004 adenosylmethionine
1468 31 33.3 423 2 F86620 hypothetical prote
1469 31 33.3 423 2 T09338 DnaJ-like protein
1470 31 33.3 424 2 F82503 proton/glutamate s
1471 31 33.3 425 2 T64250 hypothetical prote
1472 31 33.3 425 2 F83990 lactose transport
1473 31 33.3 426 2 T41682 hypothetical prote
1474 31 33.3 429 2 B90576 hemolysin c [impor
1475 31 33.3 429 2 T45040 hypothetical prote
1476 31 33.3 430 1 A46216 transcription fact
1477 31 33.3 431 1 JC2002 transcription fact
1478 31 33.3 432 2 T34154 hypothetical prote
1479 31 33.3 434 2 A12379 hypothetical prote
1480 31 33.3 435 2 T23364 hypothetical prote
1481 31 33.3 435 2 S72701 adenosylmethionine
1482 31 33.3 437 2 E70540 probable adenosylm
1483 31 33.3 438 2 T45602 glucosyltransferas
1484 31 33.3 438 2 T38946 melanoma ubiqutou
1485 31 33.3 438 2 F81659 D-alanyl-D-alanine
1486 31 33.3 440 2 T32151 hypothetical prote
1487 31 33.3 440 2 S69728 hypothetical prote
1488 31 33.3 441 2 T48960 vacuolar H(+)-ATPase
1489 31 33.3 443 2 H84414 hypothetical prote

ALIGNMENTS

RESULT 1

F86909
probable DNA gyrase subunit A [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: F86909
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Holt,
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: F86909
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1249 <STO>
A;Cross-references: UNIPARC:UPI0000165F27; GB:AL450380; NID:g13092418; PIDN:CAC29514.1;
C;Genetics:
A;Gene: gyrA

Query Match 47.3%; Score 44; DB 2; Length 1249;
Best Local Similarity 46.7%; Pred. No. 39;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 VEEDQFSQNPFISCFE 18

Db 469 VEEDSFNQHNVDVCVQ 483

RESULT 2

T10006
DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) A - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10006
R;Cole, S.T.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z16916
A;Accession: T10006
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1273 <COL>
A;Cross-references: UNIPROT:Q57532; UNIPARC:UPI000016FAEB; EMBL:Z70722; NID:e1059634; PFI
C;Genetics:
C;Keywords: isomerase

Query Match 47.3%; Score 44; DB 2; Length 1273;
Best Local Similarity 46.7%; Pred. No. 40;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 VEEDQFSQNPFISCFE 18

Db 469 VEEDSFNQHNVDVCVQ 483

RESULT 3

T29509
 hypothetical protein W05H7.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
 C:Accession: T29509
 R:Wohldmann, P.; Le, T.T.
 submitted to the EMBL Data Library, April 1997
 A:Description: The sequence of C. elegans cosmid W05H7.
 A:Reference number: Z20630
 A:Accession: T29509
 A>Status: preliminary; translated from GS/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-221 <W0H>
 A:Cross-references: UNIPARC:UPI000017935A; EMBL:U97552; PIDN:AAB52865.1; GSPDB:GN000028;
 A:Experimental source: strain Bristol N2; clone W05H7
 C:Genetics:
 A:Gene: CESP:W05H7.5
 A:Map position: X
 A:Introns: 30/1; 61/1; 172/3; 183/1
 C:Superfamily: Caenorhabditis elegans hypothetical protein W05H7.5

Query Match 46.2%; Score 43; DB 2; Length 221;
 Best Local Similarity 53.3%; Pred. No. 8.4;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 SLVEEDQFSQNPISC 16

Db 152 SIVNPHFSDSPISC 166
 ||:| ||:| ||:| ||:|

RESULT 4

E84536
 hypothetical protein Atg16090 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C:Accession: E84536
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, J.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: E84536
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-518 <STO>
 A:Cross-references: UNIPROT:Q9XII0; UNIPARC:UPI000009CCB6; GB:AE002093; NID:G4678205; PI
 C:Genetics:
 A:Gene: Atg16090
 A:Map position: 2

Query Match 46.2%; Score 43; DB 2; Length 518;
 Best Local Similarity 53.8%; Pred. No. 22;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 VEEDQFSQNPISC 16

Db 216 VEDELSHSPCSC 228
 ||:| ||:| ||:| ||:|

RESULT 5

S38171
 peptide transport protein PTR2 - yeast (Saccharomyces cerevisiae)
 N:Alternate names: peptide permease PTR2; protein YKR093W; protein YKR413
 C:Species: Saccharomyces cerevisiae
 C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
 C:Accession: S38171; S40646; S37700
 R:Baladron, V.; Ballesta, J.P.G.; Bou, G.; del Rey, P.; Esteban, P.F.; Garcia-Cantalejo,
 submitted to the Protein Sequence Database, March 1994
 A:Reference number: S38158
 A:Accession: S38171
 A:Molecule type: DNA

A:Residues: 1-601 <BAL>
 A:Cross-references: UNIPROT:P32901; UNIPARC:UPI00001329B5; EMBL:Z28318; NID:G486582; PID
 A:Experimental source: strain S288C
 R:Bou, G.; Esteban, P.F.; Baladron, V.; Gonzalez, G.A.; Cantalejo, J.G.; Remacha, M.; Jin
 Yeast 9, 1349-1354, 1993
 A:Title: The complete sequence of a 15 820 bp segment of Saccharomyces cerevisiae chromo
 A:Reference number: S40644; MUID:94205265; PMID:8154186
 A:Accession: S40646
 A:Molecule type: DNA
 A:Residues: 1-601 <BOU>
 A:Cross-references: UNIPARC:UPI00001329B5; EMBL:X73541; NID:G450550; PIDN:CAA51947.1; PI
 A:Experimental source: strain S288C
 A:Note: the authors did not translate the codon for residue 200
 R:Becker, J.M.; Perry, J.R.; Basrai, M.A.; Naider, F.R.
 submitted to the EMBL Data Library, March 1993
 A:Description: Isolation and characterization of a Saccharomyces cerevisiae peptide tran
 A:Reference number: S37700
 A:Accession: S37700
 A:Molecule type: DNA
 A:Residues: 1-38, 'T', 40-466, 'LLANTRICLDFFRDLCLYHWG', 470, 'RLFQS', 471, 'SPHEIVY', 473-474, '
 A:Cross-references: UNIPARC:UPI000017B2F9; EMBL:L11994
 C:Genetics:
 A:Gene: SGD:PTR2
 A:Cross-references: SGD:S0001801; MIPS:YKR093W
 A:Map position: 11R
 C:Keywords: membrane protein

Query Match 46.2%; Score 43; DB 2; Length 601;
 Best Local Similarity 72.7%; Pred. No. 26;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 EEDQFSQNPIS 15

Db 569 EEDFDLNPIS 579
 ||:| ||:| ||:| ||:|

RESULT 6

I38754
 transcription factor REST (version 1) - human (fragment)
 N:Alternate names: neural-restrictive silencer factor; R1-silencing transcription factor
 C:Species: Homo sapiens (man)
 C>Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
 C:Accession: I38754
 R:Schoenherr, C.J.; Anderson, D.J.
 Science 267, 1360-1363, 1995
 A:Title: The neuron-restrictive silencer factor (NRSF): a coordinate repressor of multip
 A:Reference number: I38754; MUID:95176234; PMID:7871435
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-316 <RES>
 A:Cross-references: UNIPROT:Q12956; UNIPARC:UPI0000070017; EMBL:U13877; NID:G606943; PID
 C:Genetics:
 A:Gene: GDB:REST; NRSF
 A:Cross-references: GDB:702138
 A:Map position: 4q12-4q12
 C:Keywords: transcription regulation

Query Match 45.2%; Score 42; DB 2; Length 316;
 Best Local Similarity 53.3%; Pred. No. 19;
 Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 SLVEEDQFSQNPISC 16

Db 207 STAEEDFSKGPINC 221
 ||:| ||:| ||:| ||:|

RESULT 7

T45592
 hypothetical protein F1A12.70 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 31-Dec-2004
 C:Accession: T45592

R;Foldes, R.L.; Adams, S.L.; Fantaste, R.P.; Kamboj, R.K.
Biochim. Biophys. Acta 1223, 155-159, 1994
A;Title: Human N-methyl-D-aspartate receptor modulatory subunit hNR2A: cloning and sequence
A;Reference number: S47555; MUID:94339179; PMID:8061049
A;Accession: S47555
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1464 <POL>
A;Cross-references: UNIPROT:Q12879; UNIPARC:UPI000000D7AB; GB:U09002; NID:G558748; PID:N
F;428-854/Domain: glutamate receptor homology <GRH>

Query Match 45.2%; Score 42; DB 2; Length 1464;
Best Local Similarity 46.7%; Pred. No. 1.le+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VSLVEEDQFSONPIS 15
| : : : : :
Db 1018 VDSIRQDSLQNPFVS 1032

RESULT 13
S37138
protoporphyrin IX magnesium chelatase (EC 4.99.1.-) - *Cryptomonas* sp.
C;Species: *Cryptomonas* sp.
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S37138
R;Douglas, S.E.; Reith, M.
submitted to the EMBL Data Library, March 1993
A;Description: A bchl homolog, encoding a subunit of Mg chelatase, is located on the pl
A;Reference number: S37138
A;Accession: S37138
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-353 <DOU>
A;Cross-references: UNIPROT:Q39516; UNIPARC:UPI0000127871; EMBL:Z21976; NID:G398949; PID
C;Genetics:
A;Start codon: GTG
C;Superfamily: magnesium chelatase, subunit Chl1
C;Keywords: lyase

Query Match 44.6%; Score 41.5; DB 2; Length 353;
Best Local Similarity 42.1%; Pred. No. 26;
Matches 8; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

Qy 1 VSLVEE-DQFSQNPISCFE 18
| : : : : :
Db 225 VKVIEQRSEFDKNPSACLE 243

RESULT 14
A89858
hypothetical protein SA0781 [imported] - *Staphylococcus aureus* (strain N315)
C;Species: *Staphylococcus aureus*
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: A89858
R;Auroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: A89858
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-355 <KUR>
A;Cross-references: UNIPROT:Q99VF6; UNIPARC:UPI000000C7F68; GB:BA000018; PID:gl3700723; F
C;Genetics:
A;Experimental source: strain N315
A;Gene: SA0781

Query Match 44.6%; Score 41.5; DB 2; Length 355;
Best Local Similarity 34.6%; Pred. No. 26;

Matches 9; Conservative 3; Mismatches 5; Indels 9; Gaps 1;

Qy 1 VSLVEEDQF-----SQNPISCF 17
| : : : : :
Db 106 VKIIEEQQFKCHIDTIKKQVPVCCF 131

RESULT 15
T16128
hypothetical protein F21H12.5 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16128
R;Favell, T.
submitted to the EMBL Data Library, July 1995
A;Description: The sequence of *C. elegans* cosmid F21H12.
A;Reference number: Z18464
A;Accession: T16128
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-632 <FAV>
A;Cross-references: UNIPROT:Q09312; UNIPARC:UPI000012A562; EMBL:U23176; NID:G726404; PID
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: C8SP:F21H12.5
A;Introns: 14/3; 92/3; 151/2; 235/3; 440/2; 483/2; 551/2

Query Match 44.6%; Score 41.5; DB 2; Length 632;
Best Local Similarity 56.2%; Pred. No. 50;
Matches 9; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Qy 2 SLVEEDQFSONPISCF 17
| : : : : :
Db 115 SRLSDDFSON-VRCP 129

Search completed: December 22, 2005, 03:05:58
Job time : 47.8163 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 22, 2005, 02:42:57 ; Search time 54 Seconds
(without alignments)
235.176 Million cell updates/sec

Title: US-10-063-553-48_COPY_32_49
Perfect score: 93
Sequence: 1 VSLVBDQFSQNFISCFE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Uniprot_05_80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	93	100.0	229	2 QH5X9 HUMAN	Qh5x9 homo sapien
2	93	100.0	229	2 Q53R12 HUMAN	Q53r12 homo sapien
3	93	100.0	229	2 Q6UW61 HUMAN	Q6uw61 homo sapien
4	93	100.0	229	2 Q5U609 HUMAN	Q5u609 homo sapien
5	70	75.3	226	2 Q5CQV8 MOUSE	Q5cq8 m mus muscu
6	70	75.3	226	2 Q9D3R0 MOUSE	Q9d3r0 mus musculus
7	70	75.3	226	2 Q9D3Q0 MOUSE	Q9d3q0 mus musculus
8	47	50.5	126	2 Q9C252 NEUCR	Q9c252 neurospora
9	46	49.5	601	2 Q7V7K2 PROMM	Q7v7k2 prochloroco
10	45	48.4	143	2 Q4N5J1 THEPA	Q4n5j1 theileria p
11	45	48.4	238	2 Q7T301 BRARE	Q7t301 brachydanio
12	45	48.4	410	2 Q9VDK6 DROME	Q9vdk6 drosophila
13	45	48.4	575	2 Q61CF7 CAEBR	Q61cf7 caenorhabdi
14	45	48.4	805	2 Q55DX2 DICDI	Q55dx2 dictyosteli
15	44	47.3	1273	1 GYRA MYCLE	Qy7532 mycobacteri
16	44	47.3	1710	2 Q4RM05 TETNG	Q4rm05 tetraodon n
17	43.5	46.8	1144	2 Q612X4 CAEBR	Q612x4 caenorhabdi
18	43	46.2	124	2 Q61LX4 PLAF7	Q61lx4 plasmodium
19	43	46.2	216	2 Q58AT8 CAEBL	Q58at8 caenorhabdi
20	43	46.2	435	2 Q54F45 DICDI	Q54f45 dictyosteli
21	43	46.2	491	2 Q90D04 9HIV1	Q90d04 human immun
22	43	46.2	518	2 Q9X110 ARATH	Q9x110 arabidopsis
23	43	46.2	601	1 PFR2 YEAST	P32901 saccharomyc
24	43	46.2	890	2 Q87GP6 VIBPA	Q87gp6 vibrio para
25	43	46.2	1112	2 Q4N6M1 THEPA	Q4n6m1 theileria p
26	43	46.2	1418	2 Q86HT4 DICDI	Q86ht4 dictyosteli
27	43	46.2	1466	2 Q554X7 DICDI	Q554x7 dictyosteli
28	43	46.2	1679	2 Q7PHR1 ANOGA	Q7phr1 anopheles g
29	43	46.2	1749	2 Q7RGH9 PLAYO	Q7rg9 plasmodium
30	43	46.2	3005	2 Q50LG3 ALTAL	Q50lg3 alternaria
31	42.5	45.7	209	2 Q8W1X7 ALLCE	Q8w1x7 allium cepa

32	42	45.2	87	2	Q57L77 SALCH	Q57l77 salmonella
33	42	45.2	182	2	Q582P7 TRYXP	Q582p7 trypanosoma
34	42	45.2	226	2	Q5M469 STRT2	Q5m469 streptococc
35	42	45.2	226	2	Q5L2L6 STRT1	Q5l2l6 streptococc
36	42	45.2	316	2	Q12956 HUMAN	Q12956 homo sapien
37	42	45.2	388	2	Q8KLJ8 STRTO	Q8klj8 streptomyc
38	42	45.2	420	2	Q9SNC3 ARATH	Q9snc3 arabidopsis
39	42	45.2	454	2	Q8IWI3 HUMAN	Q8iwi3 homo sapien
40	42	45.2	472	2	Q5OVT4 ENTHI	Q5ovt4 entamoeba h
41	42	45.2	522	2	Q6O694 MOUSE	Q6o694 mus musculu
42	42	45.2	525	2	Q4VAD6 MOUSE	Q4vad6 mus musculu
43	42	45.2	549	2	Q8JTM8 LSDV	Q8jtm8 lumpy skin
44	42	45.2	550	2	Q91ML3 LSDV	Q91ml3 lumpy skin
45	42	45.2	551	2	Q8JTY6 LSDV	Q8jty6 lumpy skin
46	42	45.2	681	2	Q12957 HUMAN	Q12957 homo sapien
47	42	45.2	762	2	Q9AMC0 DESPS	Q9amc0 desulfotale
48	42	45.2	852	2	Q9CW43 MOUSE	Q9cw43 mus musculu
49	42	45.2	900	2	Q6EQM5 ORYSA	Q6eqm5 oryza sativ
50	42	45.2	948	2	Q8S7M6 ORYSA	Q8s7m6 oryza sativ
51	42	45.2	982	2	Q7XBZ3 ORYSA	Q7xbz3 oryza sativ
52	42	45.2	1065	2	Q21992 CAEBL	Q21992 caenorhabdi
53	42	45.2	1082	2	Q8VIG1 MOUSE	Q8vig1 mus musculu
54	42	45.2	1097	2	Q13127 HUMAN	Q13127 homo sapien
55	42	45.2	1126	2	Q59ER1 HUMAN	Q59er1 homo sapien
56	42	45.2	1464	1	NMDE1 HUMAN	Q12879 homo sapien
57	42	45.2	1464	1	NMDE1 PANTR	Q5is45 pan troglod
58	42	45.2	1464	2	Q547U9 HUMAN	Q547u9 homo sapien
59	42	45.2	1491	2	Q59EW6 HUMAN	Q59ew6 homo sapien
60	42	45.2	1587	2	Q53P23 ORYSA	Q53p23 oryza sativ
61	42	45.2	2418	2	Q8I1R9 PLAF7	Q8i1r9 plasmodium
62	42	45.2	4337	2	Q54B24 DICDI	Q54b24 dictyosteli
63	41.5	44.6	333	1	CHLI GUITH	Q39516 guillardia
64	41.5	44.6	355	2	Q99VF6 STAAN	Q99vf6 staphylococ
65	41.5	44.6	355	2	Q931V4 STAAM	Q931v4 staphylococ
66	41.5	44.6	632	1	FBF2 CAEBL	Q09312 caenorhabdi
67	41	44.1	160	2	Q4XX10 PLACH	Q4xx10 plasmodium
68	41	44.1	187	2	Q5TF17 HUMAN	Q5tf17 homo sapien
69	41	44.1	239	1	GRPE PROMP	Q7v3q4 prochloroco
70	41	44.1	254	2	Q76930 9HIV2	Q76930 human immun
71	41	44.1	260	2	Q8LFC3 ARATH	Q8lfc3 arabidopsis
72	41	44.1	302	2	Q54964 RAT	Q54964 rattus norv
73	41	44.1	316	2	Q6PNE0 HUMAN	Q6pne0 homo sapien
74	41	44.1	319	1	SPV1 HUMAN	Q43609 homo sapien
75	41	44.1	326	1	239A HUMAN	Q15442 homo sapien
76	41	44.1	326	1	239A MOUSE	Q01292 mus musculu
77	41	44.1	334	2	Q5OSV9 ENTHI	Q5osv9 entamoeba h
78	41	44.1	339	2	Q6FEN2 ACIAD	Q6fen2 acinetobact
79	41	44.1	362	2	Q54EV8 DICDI	Q54ev8 dictyosteli
80	41	44.1	388	2	Q4SXK3 TETNG	Q4sxk3 tetraodon n
81	41	44.1	400	2	Q5RGZ5 BRARE	Q5rgz5 brachydanio
82	41	44.1	402	2	Q9SRU1 ARATH	Q9srui arabidopsis
83	41	44.1	421	2	Q5E9M2 BOVIN	Q5e9m2 bos taurus
84	41	44.1	421	2	Q5E9P4 BOVIN	Q5e9p4 bos taurus
85	41	44.1	421	2	Q5EAB8 BOVIN	Q5eab8 bos taurus
86	41	44.1	449	2	Q22822 ARATH	Q22822 arabidopsis
87	41	44.1	496	1	CBLC MOUSE	Q80x11 mus musculu
88	41	44.1	510	2	Q4RUC1 TETNG	Q4ruc1 tetraodon n
89	41	44.1	512	2	Q93ZR8 ARATH	Q93zr8 arabidopsis
90	41	44.1	526	2	Q4S388 TETNG	Q4s388 tetraodon n
91	41	44.1	545	2	Q9HEK1 NEUCR	Q9hek1 neurospora
92	41	44.1	559	2	Q53PG5 ORYSA	Q53pg5 oryza sativ
93	41	44.1	564	2	Q7RVW0 NEUCR	Q7rvw0 neurospora
94	41	44.1	606	2	Q6Y9B1 BORHE	Q6y9b1 borrelia he
95	41	44.1	606	2	Q8BI29 MOUSE	Q8bi29 mus musculu
96	41	44.1	609	2	Q7R0R9 GIALA	Q7r0r9 giardia lam
97	41	44.1	739	2	Q4T141 TETNG	Q4t141 tetraodon n
98	41	44.1	766	1	PRTP_EHVI	P68351 equine herp
99	41	44.1	766	1	PRTP_EHVI1	Q6dlh9 equine herp
100	41	44.1	793	1	LHR2A MOUSE	Q66n9 equine herp
101	41	44.1	822	1	LHR2A RAT	Q99kc8 mus musculu
102	41	44.1	822	2	Q4S8A9 TETNG	Q75we7 rattus norv
103	41	44.1	837	1	SYFB_PROMA	Q4s8a9 tetraodon n
104	41	44.1	837	1	SYFB_PROMA	Q7vbx6 prochloroco

105 41 44.1 925 1 YE9G SCHPO
 106 41 44.1 929 2 Q4RW90 TETNG
 107 41 44.1 1069 2 Q54963 RAT
 108 41 44.1 1117 2 Q54963 RAT
 109 41 44.1 1203 2 Q51Y30 MAGR
 110 41 44.1 1337 2 Q4WHR7 ASPFU
 111 41 44.1 1447 2 Q5CFG8 CRYHO
 112 41 44.1 2270 2 Q6BGF9 PARTE
 113 41 44.1 11696 2 Q5CV09 CRYPV
 114 40.5 43.5 496 2 Q4UEB8 THEAN
 115 40.5 43.5 792 1 SYFB CHLPN
 116 40.5 43.5 801 2 Q95L13 BOVIN
 117 40.5 43.5 894 2 Q9BJD6 STRPU
 118 40.5 43.5 2274 2 Q54W13 DICDI
 119 40 43.0 95 1 SCR23 ARATH
 120 40 43.0 235 1 Y559 MYCPN
 121 40 43.0 242 2 Q4KL96 XENLA
 122 40 43.0 267 2 Q9D9F7 MOUSE
 123 40 43.0 276 2 Q50TC5 ENTHI
 124 40 43.0 277 1 LGT BACSK
 125 40 43.0 312 2 Q93RA5 TETH
 126 40 43.0 317 1 PHEG AGLNE
 127 40 43.0 332 2 Q8QFN6 ELAQU
 128 40 43.0 332 2 Q8QFN7 ELAQU
 129 40 43.0 348 2 Q6IEL0 ORYSA
 130 40 43.0 348 2 Q6QHD1 ORYSA
 131 40 43.0 356 2 Q96ZC9 PODCA
 132 40 43.0 369 2 Q8JV08 CSV
 133 40 43.0 370 2 Q5F3Z4 CHICK
 134 40 43.0 373 2 Q8BQUL MOUSE
 135 40 43.0 390 2 Q6LS58 STROH
 136 40 43.0 392 2 Q4LS74 STAHJ
 137 40 43.0 398 2 Q78YC4 BRARE
 138 40 43.0 405 2 Q5AVS5 EWENI
 139 40 43.0 421 2 Q9NXT9 HUMAN
 140 40 43.0 430 2 Q93KW3 STRVR
 141 40 43.0 445 2 Q86YG4 HUMAN
 142 40 43.0 446 2 Q5AD28 CANAL
 143 40 43.0 456 2 Q4RR95 TETNG
 144 40 43.0 457 2 Q99KJ4 MOUSE
 145 40 43.0 484 2 Q78J30 MOUSE
 146 40 43.0 510 2 Q6L1S7 CAEBR
 147 40 43.0 510 2 Q8JAI1 SIVCZ
 148 40 43.0 512 2 Q8JAH2 SIVCZ
 149 40 43.0 527 2 Q9NIV0 DICDI
 150 40 43.0 534 2 Q6NRT8 XENLA
 151 40 43.0 578 2 Q57VA6 9TRYP
 152 40 43.0 596 2 Q5FUU2 GLUOX
 153 40 43.0 600 2 Q6TFP4 HUMAN
 154 40 43.0 600 2 Q812D9 RAT
 155 40 43.0 600 2 Q8BRG6 MOUSE
 156 40 43.0 600 2 Q56A24 RAT
 157 40 43.0 615 2 Q8O4Q2 GADMO
 158 40 43.0 616 2 Q5AR94 EWENI
 159 40 43.0 618 2 Q92200 EMICEL
 160 40 43.0 619 2 Q4RV91 TETNG
 161 40 43.0 620 2 Q9N9D4 9DIPT
 162 40 43.0 624 2 Q9D5K3 MOUSE
 163 40 43.0 627 2 Q4GZ34 9TRYP
 164 40 43.0 695 1 SVTC RAT
 165 40 43.0 722 1 SVTC MOUSE
 166 40 43.0 735 2 Q7X1F3 9LACT
 167 40 43.0 855 2 Q80TH0 MOUSE
 168 40 43.0 888 2 Q6LJF0 PHOPR
 169 40 43.0 934 2 Q7SDR7 NEUCR
 170 40 43.0 943 2 Q7QE10 ANOGA
 171 40 43.0 971 2 Q5ISN1 MACPA
 172 40 43.0 1052 2 Q5TUB0 ANOGA
 173 40 43.0 1056 2 Q4PI36 USTMA
 174 40 43.0 1215 2 Q54AY2 DICDI
 175 40 43.0 1215 2 Q513V5 ENTHI
 176 40 43.0 1476 1 ATP7A CRIGR
 177 40 43.0 1482 2 Q4F8H5 BRARE

178 40 43.0 1491 1 ATP7A MOUSE
 179 40 43.0 1492 1 ATP7A RAT
 180 40 43.0 1500 2 ATP7A_HUMAN
 181 40 43.0 1500 2 Q5JQN4 HUMAN
 182 40 43.0 1590 2 Q6BCK2 MOUSE
 183 40 43.0 1591 2 Q6BCK2 MOUSE
 184 40 43.0 1591 1 UN13B HUMAN
 185 40 43.0 1591 1 UN13B HUMAN
 186 40 43.0 1591 2 Q5VM8 HUMAN
 187 40 43.0 1591 2 Q5RAK9 PONPY
 188 40 43.0 1620 2 Q4LE73 HUMAN
 189 40 43.0 1622 1 UN13B RAT
 190 40 43.0 1622 2 Q5VM9 HUMAN
 191 40 43.0 1622 2 Q5VM9 HUMAN
 192 40 43.0 1622 2 Q5VM9 HUMAN
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 250 40 43.0 1622 2 Q5VM9 HUMAN

Q64430 mus musculus
 P70705 rattus norv
 Q40466 homo sapien
 Q5JQN4 homo sapien
 Q6BCK2 mus musculus
 Q41795 homo sapien
 Q9Z1N9 mus musculus
 Q5VM8 mus musculus
 Q5RAK9 pongo pygma
 Q4LE73 homo sapien
 Q62769 rattus norv
 Q5VM9 mus sapien
 Q4TBR0 tetraodon n
 Q7RZX2 neucra
 Q4772 leishmania
 Q48259 tetraodon n
 Q7R1E2 giardia lam
 Q81288 plasmodium
 Q10331 schizosacch
 Q82196 arabidopsis
 Q84585 paramem
 Q44779 caenorhabdi
 Q61XE2 caenorhabdi
 Q9F1P2 burkholderi
 Q50ZT6 entamoeba h
 Q4T3X8 tetraodon n
 Q4JAS5 aulofolobus
 Q9GV20 ciona savig
 Q4W43 plasmodium
 Q4L205 burkholderi
 Q8SXQ3 drosophila
 Q96067 drosophila
 Q4UE00 theileria a
 Q97SM3 streptococ
 Q56AQ2 bacillus th
 Q65J18 bacillus th
 Q8D746 streptococ
 Q4VXJ0 homo sapien
 Q7PRG6 anopheles g
 Q81135 plasmodium
 Q5L2Y1 geobacillus
 Q9PKG5 chlamydia m
 Q5QT25 oryza sativ
 Q63K88 burkholderi
 Q62CU2 burkholderi
 P45593 escherichia
 Q731F9 bacillus ce
 Q6XR96 uncultured
 Q8BW5 encephalito
 Q6M1G1 bdellovibri
 P83592 corallina o
 Q7XZS8 corallina o
 Q49872 mycobacteri
 Q50XN8 entamoeba h
 Q9V4H8 drosophila
 Q3EX5 sus scrofa
 Q32233 egkistrodon
 Q7NQ22 chromobacte
 Q8WRU3 trypanosoma
 Q505M0 xenopus lae
 Q7PKD4 anopheles g
 Q5LH60 bacteroides
 Q64Y19 bacteroides
 Q57729 brucella ab
 Q8FW63 brucella su
 Q8YC63 brucella me
 Q4XPC4 plasmodium
 Q9NP56 homo sapien
 Q5WVY9 homo sapien
 Q6LFW8 PHOPR
 Q515E5 ENTHI
 Q4IML0 gibberella

251	39	41.9	475	2	Q8S7F0_ORYSA	Q8e7f0 oryza sativ	324	38	40.9	75	2	Q9NZG9_HUMAN	Q9nzs9 homo sapien
252	39	41.9	493	2	Q9G2B6_PLAY7	Q9g2b6 plasmodium	325	38	40.9	76	2	Q5TF80_ANOGA	Q5tfs0 anopheles g
253	39	41.9	503	2	Q9LFV2_ARATH	Q9lfv2 arabidopsis	326	38	40.9	81	2	Q4NCAB_5MICC	Q4ncab athrobacte
254	39	41.9	508	2	Q5VNG4_ORYSA	Q5vng4 oryza sativ	327	38	40.9	96	2	Q6YJW1_ORYSA	Q6ywj1 oryza sativ
255	39	41.9	508	2	Q4V398_ARATH	Q4v398 arabidopsis	328	38	40.9	100	2	Q9ZME4_HELPF	Q9zme4 helicobacte
256	39	41.9	509	2	Q6VG50_SIVC2	Q6vg50 chimpanzee	329	38	40.9	101	2	Q5TVP9_BRARE	Q5tvp9 brachydanio
257	39	41.9	516	2	Q8M385_ORYSA	Q8m385 oryza sativ	330	38	40.9	104	1	D1RCL1_HUMAN	Q969k9 homo sapien
258	39	41.9	526	2	Q8QL72_NPMC	Q8ql72 mamestra co	331	38	40.9	122	1	Q4WVQ2_ASPFU	Q4wvq2 aspergillus
259	39	41.9	538	2	Q6N0K3_RHOPA	Q6n0k3 rhodopseudo	332	38	40.9	122	2	Q515Y4_ENTHI	Q515y4 entameoba h
260	39	41.9	576	1	FTI_BUCBP	Q89b04 buchnera ap	333	38	40.9	140	2	Q6ZUV6_HUMAN	Q6zuv6 homo sapien
261	39	41.9	585	2	Q9U2Y8_CAEEL	Q9u2y8 caenorhabdi	334	38	40.9	144	2	Q5V686_HALMA	Q5v686 halosarcula
262	39	41.9	586	2	Q4LEB1_HUMAN	Q4leb1 homo sapien	335	38	40.9	165	2	Q86U80_HUMAN	Q86u80 homo sapien
263	39	41.9	607	2	Q5SW05_CRYNE	Q5sw05 cryptococcu	336	38	40.9	166	2	Q6LHC9_PHOPR	Q6lhc9 photobacter
264	39	41.9	607	2	Q5KJ31_CRYNE	Q5kjj1 cryptococcu	337	38	40.9	176	2	Q6CD85_YARLI	Q6cd85 yarrowia li
265	39	41.9	607	2	Q7IA50_SNUCL	Q7ia50 mamestra co	338	38	40.9	181	2	Q4X980_PLACH	Q4x980 plasmodium
266	39	41.9	637	2	Q5WAV1_BACSK	Q5wavi bacillus cl	339	38	40.9	183	2	Q9D2S7_MOUSE	Q9d2s7 mus musculu
267	39	41.9	659	2	Q6FRU1_CANGA	Q6frul candida gla	340	38	40.9	186	2	Q5ZSE7_LEGPH	Q5zse7 legionella
268	39	41.9	659	2	Q8DR86_STRR6	Q8dr86 streptococc	341	38	40.9	195	2	Q4WY06_ASPFU	Q4wy06 aspergillus
269	39	41.9	662	2	Q5FRJ9_HUMAN	Q5frj9 homo sapien	342	38	40.9	201	2	Q8CS12_MOUSE	Q8cs12 mus musculu
270	39	41.9	669	2	Q5V4P7_HALMA	Q5v4p7 haloarcula	343	38	40.9	202	2	Q8LXK9_ORYSA	Q8lmx9 oryza sativ
271	39	41.9	699	2	Q4YX57_PLABE	Q4yx57 plasmodium	344	38	40.9	205	2	Q4XC15_PLACH	Q4xc15 plasmodium
272	39	41.9	710	2	Q54J66_DICDI	Q54j66 dictyosteli	345	38	40.9	214	2	Q7S2G9_NEUCR	Q7s2g9 neurospora
273	39	41.9	714	2	Q86K58_DICDI	Q86k58 dictyosteli	346	38	40.9	215	2	Q54730_SYNP7	Q54730 synecococc
274	39	41.9	774	2	Q7RR25_PLAYO	Q7rr25 plasmodium	347	38	40.9	216	2	Q5N261_SYNP6	Q5n261 synecococc
275	39	41.9	784	2	Q4IN01_GIBZE	Q4in01 gibberella	348	38	40.9	217	2	Q9LIJ7_ARATH	Q9lij7 arabidopsis
276	39	41.9	809	2	Q9R9U6_PSEPU	Q9r9u6 pseudomonas	349	38	40.9	219	2	Q8Q0G6_METWA	Q8q0g6 methanosarc
277	39	41.9	814	2	Q4RFH4_TETNG	Q4rfh4 tetraodon n	350	38	40.9	219	2	Q8PSS8_METWA	Q8pss8 methanosarc
278	39	41.9	926	2	Q655X4_ORYSA	Q655x4 oryza sativ	351	38	40.9	224	2	Q5W400_9HIV1	Q5w400 human immun
279	39	41.9	929	2	Q32491_BACNO	Q32491 bacteroides	352	38	40.9	225	2	Q7VPV1_CHLPN	Q7vpv1 chlamydia p
280	39	41.9	999	2	Q94111_BRANA	Q94111 brassica na	353	38	40.9	225	2	Q9Z7X2_CHLPN	Q9z7x2 chlamydia p
281	39	41.9	1001	1	AHM5_ARATH	Q9e7j8 arabidopsis	354	38	40.9	226	2	Q57V30_9TRYP	Q57v30 trypanosoma
282	39	41.9	1001	2	Q4KD06_ARATH	Q4kd06 arabidopsis	355	38	40.9	226	2	Q92N72_RHIME	Q92n72 rhizobium m
283	39	41.9	1012	2	Q6H621_ORYSA	Q6h621 oryza sativ	356	38	40.9	277	2	Q8FFC6_ECOL6	Q8ffc6 escherichia
284	39	41.9	1038	2	Q7SE85_ASHGO	Q7se85 ashbya goss	357	38	40.9	287	2	Q97XZ6_SULSO	Q97xz6 sulfolobus
285	39	41.9	1064	2	Q8XLD9_CLOPE	Q8xld9 clostridium	358	38	40.9	288	2	Q5HU35_CAMJ5	Q5hu35 campylobact
286	39	41.9	1077	2	Q7RDA2_PLAYO	Q7rda2 plasmodium	359	38	40.9	288	2	Q9PNM5_CAMJ5	Q9pnm5 campylobact
287	39	41.9	1124	2	Q9R0T2_RAT	Q9r0t2 rattus norv	360	38	40.9	297	2	Q5NGL9_FRATT	Q5ngl9 francisella
288	39	41.9	1161	2	Q5DT60_MOUSE	Q5dt60 mus musculu	361	38	40.9	303	2	Q9PVG2_XENLA	Q9pvg2 xenopus lae
289	39	41.9	1177	2	Q55JP8_CRYNE	Q55jp8 cryptococcu	362	38	40.9	309	2	Q7ZAV1_9HIV1	Q7zav1 human immun
290	39	41.9	1177	2	Q5K9V4_CRYNE	Q5k9v4 cryptococcu	363	38	40.9	319	2	Q5Y172_XENTR	Q5y172 xenopus tro
291	39	41.9	1185	2	Q4QBVA_LEIMA	Q4qbva leishmania	364	38	40.9	324	2	Q4R6T4_MACFA	Q4r6t4 macaca fasc
292	39	41.9	1299	2	Q57VF2_9TRYP	Q57vf2 trypanosoma	365	38	40.9	331	1	LDHC_VIII_VU	Q29563 vulpes vulp
293	39	41.9	1334	2	Q5FFB0_EHRHG	Q5ffb0 ehrlichia r	366	38	40.9	337	2	Q5ULS2_9CAUD	Q5uls2 lactobacill
294	39	41.9	1354	2	Q4U3V3_HUMAN	Q4u3v3 homo sapien	367	38	40.9	339	1	RAD51_CRIGR	P70099 cricetulus
295	39	41.9	1368	2	Q99ZW2_STRPY	Q99zw2 streptococc	368	38	40.9	339	1	RAD51_MOUSE	Q06299 homo sapien
296	39	41.9	1413	2	Q4UJ10_THEAN	Q4uj10 theileria a	369	38	40.9	339	1	RAD51_MOUSE	Q08297 mus musculu
297	39	41.9	1432	2	Q4U3G5_CANPA	Q4u3g5 canis famil	370	38	40.9	339	2	Q5U0A5_HUMAN	Q5u0a5 homo sapien
298	39	41.9	1451	1	ATP7B_RAT	Q4u3g5 canis famil	371	38	40.9	339	2	Q6FHX9_HUMAN	Q6fhx9 homo sapien
299	39	41.9	1452	2	Q9QU84_RAT	Q9qu84 rattus norv	372	38	40.9	339	2	Q8MK18_CANPA	Q8mk18 canis famil
300	39	41.9	1462	1	ATP7B_MOUSE	Q64446 mus musculu	373	38	40.9	340	2	Q6ZNA8_HUMAN	Q6zna8 homo sapien
301	39	41.9	1465	1	ATP7B_HUMAN	P35670 homo sapien	374	38	40.9	345	1	YGN8_YEAST	P53122 saccharomyc
302	39	41.9	1465	2	ATP7X7_HUMAN	Q5t7x7 homo sapien	375	38	40.9	351	2	Q5AF67_CANAL	Q5af67 candida alb
303	39	41.9	1505	1	ATP7B_SHEEP	Q9xt50 ovis aries	376	38	40.9	354	2	Q4WM90_ASPFU	Q4wm90 aspergillus
304	39	41.9	1626	2	Q4S7J8_TETNG	Q4s7j8 tetraodon n	377	38	40.9	361	2	Q97BN5_STRPN	Q97bn5 streptococc
305	39	41.9	1743	2	Q9XW45_CAEEL	Q9xw45 caenorhabdi	378	38	40.9	364	2	Q5DEP0_SCHUA	Q5dep0 schistosoma
306	39	41.9	1868	2	Q4RWX5_TETNG	Q4rwx5 tetraodon n	379	38	40.9	369	2	Q74NA2_NANEO	Q74na2 nanoarchaeu
307	39	41.9	2202	2	Q4QEP5_LEIMA	Q4qep5 leishmania	380	38	40.9	385	2	Q93787_CAEEL	Q93787 caenorhabdi
308	39	41.9	2291	2	Q9W1A9_DROME	Q9w1a9 drosophila	381	38	40.9	392	2	Q7ZVV4_BRARE	Q7zvv4 brachydanio
309	39	41.9	2943	2	Q8IK94_PLAY7	Q8ik94 plasmodium	382	38	40.9	393	2	Q5XG38_XENTR	Q5xg38 xenopus tro
310	39	41.9	5095	2	Q4Q3Q7_LEIMA	Q4q3q7 leishmania	383	38	40.9	395	1	TP2H2_HUMAN	Q13888 homo sapien
311	38.5	41.4	169	2	Q6C1V7_YARLI	Q6c1v7 yarrowia li	384	38	40.9	395	2	Q6PIK8_HUMAN	Q6pi88 homo sapien
312	38.5	41.4	300	2	Q76EH3_GYMSI	Q76eh3 gymnodinium	385	38	40.9	395	2	Q6GR42_XENLA	Q6gr42 xenopus lae
313	38.5	41.4	300	2	Q76E15_9DINO	Q76e15 symbiodiniu	386	38	40.9	395	2	Q4T3D5_TETNG	Q4t3d5 tetraodon n
314	38.5	41.4	355	2	Q8NXG7_STAAR	Q8nxg7 staphylococ	387	38	40.9	396	1	TP2H2_MOUSE	Q7jib4 mus musculu
315	38.5	41.4	355	2	Q6GIG7_STAAR	Q6gig7 staphylococ	388	38	40.9	396	2	Q7TPV0_MOUSE	Q7tpv0 mus musculu
316	38.5	41.4	355	2	Q6GB05_STAAS	Q6gb05 staphylococ	389	38	40.9	398	2	Q91YN8_MOUSE	Q91yn8 mus musculu
317	38.5	41.4	355	2	Q5HHG4_STAAC	Q5hhg4 staphylococ	390	38	40.9	407	2	Q6BHM6_DEBHA	Q6bhm6 debaryomyce
318	38.5	41.4	438	2	Q9VNP8_DROME	Q9vnp8 drosophila	391	38	40.9	414	1	PP2C3_SCHPO	Q09173 schizosacch
319	38.5	41.4	514	2	Q6BZG1_DEBHA	Q6bzg1 debaryomyce	392	38	40.9	421	2	Q6GMC6_XENLA	Q6gmc6 xenopus lae
320	38.5	41.4	583	2	Q8ENC6_OCEIH	Q8enc6 oceanobacil	393	38	40.9	424	2	Q96T72_HUMAN	Q96t72 homo sapien
321	38.5	41.4	690	2	Q8IM21_PLAY7	Q8im21 plasmodium	394	38	40.9	425	2	Q4V7N9_XENLA	Q4v7n9 xenopus lae
322	38.5	41.4	873	2	Q6OMQ0_CAEER	Q6omq0 caenorhabdi	395	38	40.9	426	1	PDB7A_RAT	Q08593 rattus norv
323	38.5	41.4	2823	2	Q7RGM8_PLAYO	Q7rgm8 plasmodium	396	38	40.9	428	2	Q53W10_ORYSA	Q53w10 oryza sativ

397	38	40.9	429	2	Q5QMR2_ORYSA	Q5qmr2 oryza sativ	470	38	40.9	776	2	Q5APV3_CANAL	Q5afv3 candida alb
398	38	40.9	429	2	Q8GAH1_ARTNI	Q8gah1 arthrobacte	471	38	40.9	790	2	Q8CHT2_MOUSE	Q8cht2 mus musculus
399	38	40.9	430	2	Q13226_ARTNI	Q13226 arthrobacte	472	38	40.9	790	2	Q8BLV2_MOUSE	Q8blv2 mus musculus
400	38	40.9	432	2	Q6LZB4_METNP	Q6lzb4 methanococc	473	38	40.9	797	2	Q5AQJ4_EMENI	Q5aqj4 aspergillus
401	38	40.9	436	2	Q42954_SCHPO	Q42954 schizosacch	474	38	40.9	807	2	Q8K3R3_MOUSE	Q8k3r3 mus musculus
402	38	40.9	441	2	Q4Y727_PLACH	Q4y727 plasmodium	475	38	40.9	811	2	Q9FH14_ARATH	Q9fh14 arabidopsis
403	38	40.9	446	2	Q9C729_ARATH	Q9c729 arabidopsis	476	38	40.9	831	2	Q8CDM4_MOUSE	Q8cdm4 mus musculus
404	38	40.9	448	1	YAP1_CHICK	Yap1 chick galli	477	38	40.9	841	2	Q6MDJ4_PARUM	Q6mdj4 parachlamyd
405	38	40.9	451	2	Q4VAZ3_DROME	Q4vaz3 drosophila	478	38	40.9	844	2	O14147_SCHPO	O14147 schizosacch
406	38	40.9	455	2	Q4PDU6_USTWA	Q4pdu6 ustilago ma	479	38	40.9	845	2	O68PV3_ORYSA	O68pv3 oryza sativ
407	38	40.9	455	2	Q7XUV8_ORYSA	Q7xuv8 oryza sativ	480	38	40.9	855	2	Q5OSE9_ENTHI	Q5ose9 entamoeba h
408	38	40.9	456	1	PDE7A_MOUSE	P70453 mus musculus	481	38	40.9	882	2	Q9VZQ9_DROME	Q9vzq9 drosophila
409	38	40.9	456	2	Q5RSB5_PONPY	Q5rsb5 pongo pygma	482	38	40.9	891	2	O8IIR1_PLAF7	O8iir1 plasmodium
410	38	40.9	472	2	Q7R601_GIALA	Q7r601 giardia lam	483	38	40.9	913	2	P90742_CABEL	P90742 caenorhabdi
411	38	40.9	472	2	Q92PH9_RHIME	Q92ph9 rhizobium m	484	38	40.9	926	2	P7XVB0_ORYSA	P7xvb0 oryza sativ
412	38	40.9	482	1	PDE7A_HUMAN	Q13946 homo sapien	485	38	40.9	927	2	O8IRD5_DROME	O8ird5 drosophila
413	38	40.9	482	2	Q6P5G2_MOUSE	Q6p5g2 mus musculus	486	38	40.9	946	2	O4XOP4_ASFPU	O4xop4 aspergillus
414	38	40.9	489	2	Q8QNN7_PHYSC	Q8qnn7 ectocarpus	487	38	40.9	950	2	Q8K4M9_RAT	Q8k4m9 rattus norv
415	38	40.9	503	2	O23215_ARATH	O23215 arabidopsis	488	38	40.9	969	2	Q7RMK2_PLAYO	Q7rmk2 plasmodium
416	38	40.9	504	2	Q7MXT9_PORGI	Q7mxt9 porphyromon	489	38	40.9	976	2	Q54H51_DICDI	Q54h51 dictyosteli
417	38	40.9	510	2	O5DCH4_SCHJA	O5dch4 schistosoma	490	38	40.9	984	2	O55HV7_CRYNE	O55hv7 cryptococcu
418	38	40.9	512	2	Q4VAV2_DROME	Q4vav2 drosophila	491	38	40.9	986	2	O5K7E1_CRYNE	O5k7e1 cryptococcu
419	38	40.9	529	2	Q9PVG3_XENLA	Q9pvg3 xenopus lae	492	38	40.9	992	2	Q7XNJ9_ORYSA	Q7xnj9 oryza sativ
420	38	40.9	532	2	Q69VQ6_ORYSA	Q69vq6 oryza sativ	493	38	40.9	995	2	Q4P9K4_USTWA	Q4p9k4 ustilago ma
421	38	40.9	535	2	Q54EK8_DICDI	Q54ek8 dictyosteli	494	38	40.9	997	1	CEBP2_MOUSE	P53569 mus musculu
422	38	40.9	535	2	Q7RH26_PLAYO	Q7rh26 plasmodium	495	38	40.9	998	1	CEBP2_HUMAN	O03701 homo sapien
423	38	40.9	538	2	O8IQS7_DROME	O8iqs7 drosophila	496	38	40.9	998	2	O6NEA7_XENLA	O6nea7 xenopus lae
424	38	40.9	542	2	Q4T2I3_TETNG	Q4t2i3 tetraodon n	497	38	40.9	1054	2	O8NE75_HUMAN	O8ne75 homo sapien
425	38	40.9	551	2	Q9SVE6_ARATH	Q9sve6 arabidopsis	498	38	40.9	1068	1	PK3CA_BOVIN	P32871 bos taurus
426	38	40.9	551	2	Q83DR2_COXBU	Q83dr2 coxiella bu	499	38	40.9	1068	1	PK3CA_HUMAN	P42336 homo sapien
427	38	40.9	558	2	Q9M084_ARATH	Q9m084 arabidopsis	500	38	40.9	1069	2	Q4LE51_HUMAN	Q4le51 homo sapien
428	38	40.9	560	1	TATR_NFVCF	P41716 choristoneu	501	38	40.9	1073	2	Q4QOM9_LEIMA	Q4qom9 leishmania
429	38	40.9	560	2	Q77DF7_NPVCF	Q77df7 choristoneu	502	38	40.9	1082	2	Q4PEH9_USTWA	Q4peh9 ustilago ma
430	38	40.9	562	2	Q50XK3_ENTHI	Q50xk3 entamoeba h	503	38	40.9	1110	2	Q4IAB3_GIBZE	Q4iab3 gibberella
431	38	40.9	562	2	Q848R2_ORYSA	Q848r2 oryza sativ	504	38	40.9	1120	2	Q5SQV1_CRYNE	Q5sqv1 cryptococcu
432	38	40.9	572	2	Q4R9C1_MACPA	Q4r9c1 macaca fasc	505	38	40.9	1126	2	Q5KFB5_CRYNE	Q5kfb5 cryptococcu
433	38	40.9	574	1	MBRL_MOUSE	Q8ci2 mus musculus	506	38	40.9	1136	2	Q6I5B8_ORYSA	Q6i5b8 oryza sativ
434	38	40.9	595	2	Q55BH0_DICDI	Q55bh0 dictyosteli	507	38	40.9	1176	2	Q9RC30_BACTK	Q9rc30 bacillus th
435	38	40.9	605	2	Q6IN82_XENLA	Q6in82 xenopus lae	508	38	40.9	1276	2	Q03016_YEAST	Q03016 saccharomyc
436	38	40.9	607	1	PANX2_MOUSE	Q6in2 mus musculus	509	38	40.9	1291	2	Q94I49_ORYSA	Q94i49 oryza sativ
437	38	40.9	620	1	MBRL_HUMAN	Q6imp4 mus musculus	510	38	40.9	1292	2	Q8SSQ8_ORYSA	Q8ssq8 oryza sativ
438	38	40.9	620	2	Q8TLE0_METAC	Q8tle0 methanosarc	511	38	40.9	1364	2	O59757_SCHPO	O59757 schizosacch
439	38	40.9	623	2	Q6T448_LEIMA	Q6t448 leishmania	512	38	40.9	1388	2	O5I890_9PRIM	O5i890 saimiri bol
440	38	40.9	626	2	Q6L542_ORYSA	Q6l542 oryza sativ	513	38	40.9	1411	2	Q6FSJ5_CANGA	Q6fsj5 candida gla
441	38	40.9	631	2	Q66J88_XENLA	Q66j88 xenopus lae	514	38	40.9	1579	2	Q9ARZ4_ORYSA	Q9ar24 oryza sativ
442	38	40.9	633	1	PANX2_HUMAN	Q36rd6 homo sapien	515	38	40.9	1607	2	Q9XS00_ORYSA	Q9xs00 oryza sativ
443	38	40.9	641	2	Q8MJD4_RABIT	Q8mjd4 oryctolagus	516	38	40.9	1727	2	Q4SDE7_TETNG	Q4sde7 tetraodon n
444	38	40.9	645	2	Q4I3R8_GIBZE	Q4i3r8 gibberella	517	38	40.9	1752	2	Q4Z6E8_PLABE	Q4z6e8 plasmodium
445	38	40.9	650	2	Q8H724_ORYSA	Q8h724 oryza sativ	518	38	40.9	1781	2	O6BK91_DEBHA	O6bk91 debaryomyce
446	38	40.9	653	1	KNCA4_HUMAN	P22459 homo sapien	519	38	40.9	1847	2	Q8CZT9_YERPE	Q8cz29 versinia pe
447	38	40.9	653	2	O5REB6_PONPY	Q5reb6 pongo pygma	520	38	40.9	2134	2	Q8ZHV3_YERPE	Q8zhv3 versinia pe
448	38	40.9	654	1	KNCA4_MOUSE	Q6l423 mus musculus	521	38	40.9	2201	1	POLL_RVCV	Q6w8w4 r knal poly
449	38	40.9	654	1	KNCA4_MUSPF	Q28527 mustela put	522	38	40.9	2367	1	Q4QFY9_LEIMA	Q4qfy9 leishmania
450	38	40.9	654	2	Q8CBF8_MOUSE	Q8cbf8 mus musculus	523	38	40.9	3213	2	Q4HZN3_GIBZE	Q4hzn3 gibberella
451	38	40.9	655	1	KNCA4_RAT	P15385 rattus norv	524	38	40.9	3311	2	Q74QP0_YERPE	Q74qp0 versinia pe
452	38	40.9	660	1	KNCA4_BOVIN	Q05037 bos taurus	525	38	40.9	3577	2	Q7YV66_9TRYP	Q7yv66 trypanosoma
453	38	40.9	661	2	Q9GLF1_BOVIN	Q9glf1 bos taurus	526	38	40.9	3886	2	Q666G1_YERPS	Q666g1 versinia ps
454	38	40.9	662	2	Q5ADT2_CANAL	Q5adt2 candida alb	527	38	40.9	4684	2	Q4QFY9_LEIMA	Q4qfy9 leishmania
455	38	40.9	664	1	PANX2_RAT	P60571 rattus norv	528	37.5	40.3	219	2	Q6BF14_PARTE	Q6bf14 paramecium
456	38	40.9	667	2	Q4JGM2_MOUSE	Q4jgm2 mus musculus	529	37.5	40.3	344	2	Q7RL10_PLAYO	Q7rl10 plasmodium
457	38	40.9	684	2	Q4WOY0_ASFPU	Q4woy0 aspergillus	530	37.5	40.3	372	2	Q9HQQ1_HALSA	Q9hq1 halobacteri
458	38	40.9	684	2	Q7QX17_GIALA	Q7qx17 giardia lam	531	37.5	40.3	392	1	PANX3_HUMAN	Q96q0 homo sapien
459	38	40.9	690	2	Q5RG85_BRARE	Q5rg85 brachydanio	532	37.5	40.3	392	1	PANX3_MOUSE	Q8ceq0 mus musculu
460	38	40.9	710	2	Q9IFQ5_IRV6	Q9ifq5 chilo iride	533	37.5	40.3	392	1	PANX3_RAT	P60572 rattus norv
461	38	40.9	715	2	O6CGA7_YARLI	Q6cga7 yarrowia li	534	37.5	40.3	392	2	Q6IMP0_MOUSE	Q6imp0 mus musculu
462	38	40.9	723	2	Q5ZLC2_CHICK	Q5zlc2 gallus galli	535	37.5	40.3	804	2	Q7NAD0_PHOLL	Q7nad0 photorhabdu
463	38	40.9	726	2	O6CEG1_YARLI	Q6ceg1 yarrowia li	536	37.5	40.3	838	2	Q9C815_ARATH	Q9c815 arabidopsis
464	38	40.9	730	2	O5LEV6_ENTHI	Q5lev6 entamoeba h	537	37.5	40.3	900	2	Q7RMZ9_PLAYO	Q7rmz9 plasmodium
465	38	40.9	748	1	TREB_EMENI	Q42777 emeritella	538	37.5	40.3	1021	2	O8IDW2_PLAF7	O8idw2 plasmodium
466	38	40.9	748	2	Q5B1E5_EMENI	Q5b1e5 aspergillus	539	37.5	40.3	1195	2	O6BK97_DEBHA	O6bk97 debaryomyce
467	38	40.9	757	1	DNM1_YEAST	P54861 saccharomyc	540	37.5	40.3	3317	2	Q7QJK9_ANOGA	Q7qjk9 anopheles g
468	38	40.9	772	1	RAD15_SCHPO	P26659 schizosacch	541	37	39.8	49	2	Q7RBP3_PLASMOD	Q7rbp3 plasmodium
469	38	40.9	775	2	Q6NZF7_MOUSE	Q6nzf7 mus musculu	542	37	39.8	58	2	Q85WY7_PINKO	Q85wy7 pinus korai

543	37	39.8	84	2	Q9AYP3_ORYSA	Q9AYD3_oryza sativ	616	37	39.8	331	2	Q9NDG0_TRIVA	Q9NDG0_trichomonas
544	37	39.8	95	2	Q655C6_ORYSA	Q655C6_oryza sativ	617	37	39.8	332	2	Q7QAA2_ANOGA	Q7QAA2_anopheles g
545	37	39.8	101	2	Q4MEF2_THEFA	Q4MEF2_thellieria p	618	37	39.8	332	2	Q9BIH7_ANOGA	Q9BIH7_anopheles g
546	37	39.8	115	2	Q5PR01_RAT	Q5PR01_rattus norv	619	37	39.8	333	2	Q8IHT3_PLAF7	Q8IHT3_plasmodium
547	37	39.8	117	2	Q51VK2_MAGGR	Q51VK2_magnaporthe	620	37	39.8	334	2	Q81CY1_BACCR	Q81CY1_bacillus ce
548	37	39.8	124	2	Q52117_BRUAB	Q52117_bruceella ab	621	37	39.8	336	2	Q8A2D9_BACTN	Q8A2D9_bacteroides
549	37	39.8	131	2	Q61OC1_CAEBR	Q61OC1_caenorhabdi	622	37	39.8	339	1	RAD51_FABIT	Q77507_oryctolagus
550	37	39.8	132	2	Q974W6_SULTO	Q974W6_sulfolobus	623	37	39.8	341	1	APHA_MYCRA	Q48935_mycoplana r
551	37	39.8	145	2	Q4IBB8_GIBZE	Q4IBB8_gibberella	624	37	39.8	343	2	Q5LIA5_BACFN	Q5LIA5_bacteroides
552	37	39.8	146	2	Q59855_CANAL	Q59855_candida alb	625	37	39.8	343	2	Q64ZB8_BACFR	Q64ZB8_bacteroides
553	37	39.8	151	2	Q8J4W6_9HIV1	Q8J4W6_human immu	626	37	39.8	347	2	Q8ESK7_OCEIH	Q8ESK7_oceanobacil
554	37	39.8	155	2	Q6RTW8_9HIV1	Q6RTW8_human immu	627	37	39.8	353	2	Q7Z783_HUMAN	Q7Z783_homo sapien
555	37	39.8	172	2	Q95VY8_DROME	Q95VY8_drosophila	628	37	39.8	362	2	Q96893_HUMAN	Q96893_homo sapien
556	37	39.8	175	2	Q94JH8_ORYSA	Q94JH8_oryza sativ	629	37	39.8	364	2	Q4YOG6_PLACH	Q4YOG6_plasmodium
557	37	39.8	176	2	Q61722_DROME	Q61722_drosophila	630	37	39.8	365	1	SERC_LAGLA	Q9CH55_lactococcus
558	37	39.8	180	2	Q95XK9_SUNMU	Q95XK9_suncus muri	631	37	39.8	369	2	Q57EJ0_BRUAB	Q57EJ0_bruceella ab
559	37	39.8	189	2	Q80S24_BFV	Q80S24_barmah fore	632	37	39.8	369	2	Q8G211_BRUSU	Q8G211_brucella su
560	37	39.8	193	1	UGP15_ARATH	Q9C7F7_arabidopsis	633	37	39.8	373	2	Q7Q190_ANOGA	Q7Q190_anopheles g
561	37	39.8	194	2	Q8L9Q7_ARATH	Q8L9Q7_arabidopsis	634	37	39.8	377	2	Q8YFW9_BRUME	Q8YFW9_bruceella me
562	37	39.8	194	2	Q9KT22_VIBCH	Q9KT22_vibrio chol	635	37	39.8	378	2	Q7Q9L8_ANOGA	Q7Q9L8_anopheles g
563	37	39.8	197	2	Q8PKZ6_METWA	Q8PKZ6_methanosarc	636	37	39.8	381	2	Q6QH99_9BACE	Q6QH99_bacteroides
564	37	39.8	198	2	Q4XQJ4_PLACH	Q4XQJ4_plasmodium	637	37	39.8	381	2	Q4KGV6_PSEF5	Q4KGV6_pseudomonas
565	37	39.8	199	2	Q7RC35_PLAYO	Q7RC35_plasmodium	638	37	39.8	382	2	Q6FUL7_CANGA	Q6FUL7_candida gla
566	37	39.8	203	2	Q8TK31_METAC	Q8TK31_methanosarc	639	37	39.8	385	2	Q5LRT4_SILFO	Q5LRT4_silicibacte
567	37	39.8	205	2	Q6M114_METWP	Q6M114_methanococc	640	37	39.8	386	2	Q17559_CAEBL	Q17559_caenorhabdi
568	37	39.8	206	2	Q67YC9_ARATH	Q67YC9_arabidopsis	641	37	39.8	390	2	Q6L5Q8_STRMT	Q6L5Q8_streptococc
569	37	39.8	206	2	Q8LB66_ARATH	Q8LB66_arabidopsis	642	37	39.8	393	2	Q96SK0_HUMAN	Q96SK0_homo sapien
570	37	39.8	212	2	Q5TEN0_HUMAN	Q5TEN0_homo sapien	643	37	39.8	393	2	Q9BWS9_HUMAN	Q9BWS9_homo sapien
571	37	39.8	223	2	Q9D9V5_MOUSE	Q9D9V5_mus musculu	644	37	39.8	393	2	Q9BY52_HUMAN	Q9BY52_homo sapien
572	37	39.8	227	2	Q5A1E6_CANAL	Q5A1E6_candida alb	645	37	39.8	393	2	Q5RFF6_PONPY	Q5RFF6_pongo pygma
573	37	39.8	229	2	Q9LK42_ARATH	Q9LK42_arabidopsis	646	37	39.8	393	2	Q4K2S4_STRPN	Q4K2S4_streptococc
574	37	39.8	238	2	Q688X6_ORYSA	Q688X6_oryza sativ	647	37	39.8	403	2	Q7P8S5_ANOGA	Q7P8S5_anopheles g
575	37	39.8	241	2	SCPA_LACJO	Q7QYV5_giardia lam	648	37	39.8	409	2	Q6ORL3_CAEBR	Q6ORL3_caenorhabdi
576	37	39.8	247	1	Q97FS0_CLOAB	Q97FS0_lactobacill	649	37	39.8	409	2	Q4YWE9_PLABE	Q4YWE9_plasmodium
577	37	39.8	249	2	Q5TW44_ANOGA	Q5TW44_anopheles g	650	37	39.8	412	2	Q8MXG8_CAEBL	Q8MXG8_caenorhabdi
578	37	39.8	255	2	Q9TXO8_CAEBL	Q9TXO8_caenorhabdi	651	37	39.8	413	2	Q53CX2_9GAMA	Q53CX2_macaca fusc
579	37	39.8	259	2	Q85953_SPHAR	Q85953_sphingomona	652	37	39.8	414	2	Q9GNU8_PLAFA	Q9GNU8_plasmodium
580	37	39.8	265	2	Q8BPC4_MOUSE	Q8BPC4_mus musculu	653	37	39.8	414	2	Q8IEF6_PLAF7	Q8IEF6_plasmodium
581	37	39.8	267	2	Q9UYN6_PYRAB	Q9UYN6_pyrococcus	654	37	39.8	415	2	Q5ROW1_IDILIO	Q5ROW1_idiomarina
582	37	39.8	271	2	Q62T44_BACLD	Q62T44_bacillus li	655	37	39.8	420	1	YAGA_SCHPO	Q09873_schizosacch
583	37	39.8	273	2	Q73Q97_TREDE	Q73Q97_treponema d	656	37	39.8	428	2	Q7QNP7_GIALA	Q7QNP7_giardia lam
584	37	39.8	276	2	Q4PDY1_USTWA	Q4PDY1_ustilago ma	657	37	39.8	429	2	Q88HM5_PSEPK	Q88HM5_pseudomonas
585	37	39.8	279	2	Q9FH59_ARATH	Q9FH59_arabidopsis	658	37	39.8	433	2	Q96LW3_HUMAN	Q96LW3_homo sapien
586	37	39.8	282	2	Q5L517_CHLAY	Q5L517_chlamydomphi	659	37	39.8	434	2	Q7MTM5_WOLSU	Q7MTM5_wolinella s
587	37	39.8	286	2	Q7RG83_PLAYO	Q7RG83_plasmodium	660	37	39.8	436	2	Q8MXG9_CAEBL	Q8MXG9_caenorhabdi
588	37	39.8	293	2	Q5WHZ2_BACSK	Q5WHZ2_bacillus cl	661	37	39.8	439	2	Q54YJ2_DICDI	Q54YJ2_dictyosteli
589	37	39.8	296	2	Q9CT68_MOUSE	Q9CT68_m mus muscu	662	37	39.8	441	2	Q8C1B9_MOUSE	Q8C1B9_homo sapien
590	37	39.8	302	2	Q5CT68_MOUSE	Q5CT68_m mus muscu	663	37	39.8	441	2	Q9KAM7_BACHD	Q9KAM7_bacillus ha
591	37	39.8	303	1	FBM13_BRARE	Q6NYD4_brachydanio	664	37	39.8	445	2	MP1E3_MOUSE	P48957_mus musculu
592	37	39.8	303	2	Q65HP1_BACLD	Q65HP1_bacillus li	665	37	39.8	447	1	Q8NFL8_HUMAN	Q8NFL8_homo sapien
593	37	39.8	307	2	Q90ZT5_XENLA	Q90ZT5_xenopus lae	666	37	39.8	452	2	Q4H3A9_CIOIN	Q4H3A9_ciona intes
594	37	39.8	307	2	Q6GNB0_XENLA	Q6GNB0_xenopus lae	667	37	39.8	455	2	Q821P8_CHLCV	Q821P8_chlamydomphi
595	37	39.8	311	2	Q5TSR8_ANOGA	Q5TSR8_anopheles g	668	37	39.8	457	2	Q5L4Z6_CHLAB	Q5L4Z6_chlamydomphi
596	37	39.8	312	2	Q54BF6_DICDI	Q54BF6_dictyosteli	669	37	39.8	458	2	Q8M495_ARATH	Q8M495_arabidopsis
597	37	39.8	313	1	SPY2_CHICK	Q9PT12_gallus gall	670	37	39.8	460	2	GSA_CHERE	Q39566_chlamydomon
598	37	39.8	314	2	Q5HZ42_RAT	Q5HZ42_rattus norv	671	37	39.8	463	1	Q6C9M8_YARLI	Q6C9M8_yarrowia li
599	37	39.8	314	2	Q90ZT6_XENLA	Q90ZT6_xenopus lae	672	37	39.8	463	2	Q81046_ARATH	Q81046_arabidopsis
600	37	39.8	314	2	Q5Y173_XENTR	Q5Y173_xenopus tro	673	37	39.8	465	2	Q6IS76_HUMAN	Q6IS76_homo sapien
601	37	39.8	314	2	Q5PRF7_XENTR	Q5PRF7_xenopus tro	674	37	39.8	466	2	Q8S7V6_ORYSA	Q8S7V6_oryza sativ
602	37	39.8	315	1	SPY2_HUMAN	Q43597_homo sapien	675	37	39.8	466	2	Q9AUI5_MEDTR	Q9AUI5_medicago tr
603	37	39.8	315	1	SPY2_MOUSE	Q9QXV8_mus musculu	676	37	39.8	466	2	Q84UE1_MEDTR	Q84UE1_medicago tr
604	37	39.8	315	2	Q5T6Z7_HUMAN	Q5T6Z7_homo sapien	677	37	39.8	467	2	Q5EFD8_TRIVA	Q5EFD8_trichomonas
605	37	39.8	315	2	Q5R959_PONPY	Q5R959_pongo pygma	678	37	39.8	472	2	Q8C150_MOUSE	Q8C150_mus musculu
606	37	39.8	315	2	Q866R9_CERAE	Q866R9_cercopithe	679	37	39.8	474	2	Q7QDV1_ANOGA	Q7QDV1_anopheles g
607	37	39.8	315	2	Q8KAC7_CHLTE	Q8KAC7_chlorobitum	680	37	39.8	476	2	Q6Z799_ARATH	Q6Z799_arabidopsis
608	37	39.8	316	2	Q8T221_METKA	Q8T221_methanopyru	681	37	39.8	481	2	Q64WS1_ARATH	Q64WS1_arabidopsis
609	37	39.8	316	2	Q6Z0A5_ORYSA	Q6Z0A5_oryza sativ	682	37	39.8	481	2	Q8R203_MOUSE	Q8R203_mus musculu
610	37	39.8	324	2	Q831C4_ENTFA	Q831C4_enterococcu	683	37	39.8	483	2	Q7RDX2_PLAYO	Q7RDX2_plasmodium
611	37	39.8	330	2	Q4Y677_PLACH	Q4Y677_plasmodium	684	37	39.8	487	2	Q8H7L9_ORYSA	Q8H7L9_oryza sativ
612	37	39.8	331	2	Q9NDF9_TRIVA	Q9NDF9_trichomonas	685	37	39.8	498	2	Q6NQ51_ARATH	Q6NQ51_arabidopsis
613	37	39.8	331	2	Q9NDF8_TRIVA	Q9NDF8_trichomonas	686	37	39.8	499	2	Q6XH61_9ASTR	Q6XH61_matricaria
614	37	39.8	331	2	Q9NDF6_TRIVA	Q9NDF6_trichomonas	687	37	39.8	501	2	Q59785_SCHPO	Q59785_schizosacch
615	37	39.8	331	2	Q9NDF7_TRIVA	Q9NDF7_trichomonas	688	37	39.8	505	2		

689	37	39.8	506	2	Q6MM6_BDEBA	Q6mm6 bdellovibri	762	37	39.8	936	2	Q5CNV6_CRYHO	Q5cnv6 cryptospori
690	37	39.8	507	2	Q9LMF6_ARATH	Q9lmf6 arabidopsis	763	37	39.8	948	2	Q61XA1_CABER	Q61xa1 caenorhabdi
691	37	39.8	508	2	Q6E278_ARATH	Q6e278 arabidopsis	764	37	39.8	989	1	FRQ_NEUCR	P19970 neurospora
692	37	39.8	509	2	Q9X185_ARATH	Q9x185 arabidopsis	765	37	39.8	993	2	Q81IG5_BACCR	Q81ig5 bacillus ce
693	37	39.8	510	1	GAG_S1WVS	F31634 simian immu	766	37	39.8	998	2	Q5A8A5_CANAL	Q5a8a5 candida alb
694	37	39.8	510	2	Q6Z341_ORYSA	Q6z341 oryza sativ	767	37	39.8	1016	2	Q67U26_ORYSA	Q67u26 oryza sativ
695	37	39.8	513	2	Q6ZM76_BRARE	Q6zm76 brachydanio	768	37	39.8	1032	2	Q7RR11_PLAYO	Q7rr11 plasmodium
696	37	39.8	514	2	Q7WUM2_ACTWI	Q7wm2 actinoplanes	769	37	39.8	1047	2	Q23269_ARATH	Q23269 arabidopsis
697	37	39.8	514	2	Q62M76_BRARE	Q62m76 brachydanio	770	37	39.8	1058	2	Q8RGV8_SALTI	Q8rgv8 salmonella
698	37	39.8	526	2	Q02190_CIOIN	Q02190 ciona intes	771	37	39.8	1062	2	Q8RV24_ARATH	Q8rv24 arabidopsis
699	37	39.8	526	2	Q4H359_CIOIN	Q4h359 ciona intes	772	37	39.8	1064	2	Q9MAU0_ARATH	Q9mau0 arabidopsis
700	37	39.8	528	2	Q4YTZ2_PLABE	Q4ytz2 plasmodium	773	37	39.8	1067	2	Q4L744_STAHH	Q4l744 staphylococ
701	37	39.8	529	1	NMT_AJECA	F34763 ajellomyces	774	37	39.8	1070	2	Q6BVK2_DBBHA	Q6bvk2 debaryomyce
702	37	39.8	532	2	Q8GV16_ORYSA	Q8gv16 oryza sativ	775	37	39.8	1071	2	Q62CH9_BURMA	Q62ch9 burkholderi
703	37	39.8	540	2	Q8K2A4_MOUSE	Q8k2a4 mus musculu	776	37	39.8	1105	2	Q7MFH6_VIBVY	Q7mfh6 vibrio vuln
704	37	39.8	540	2	Q8J1B9_MOUSE	Q8j1b9 mus musculu	777	37	39.8	1114	2	Q5K7U0_CRYNE	Q5k7u0 cryptococcu
705	37	39.8	546	2	Q8E443_MYCPE	Q8e443 mycoplasma	778	37	39.8	1114	2	Q5S1A4_CRYNE	Q5s1a4 cryptococcu
706	37	39.8	546	2	Q5XKG7_HUMAN	Q5xkg7 homo sapien	779	37	39.8	1118	2	Q4P7X3_USTMA	Q4p7x3 ustiliago ma
707	37	39.8	546	2	Q726H6_DESVH	Q726h6 desulfovibr	780	37	39.8	1125	2	Q63KK6_BURPS	Q63kk6 burkholderi
708	37	39.8	553	2	Q5X117_RAT	Q5x117 rattus norv	781	37	39.8	1126	2	Q5TMW2_ANOGA	Q5tmw2 anopheles g
709	37	39.8	553	2	Q86CZ6_CABEL	Q86cz6 caenorhabdi	782	37	39.8	1145	2	Q7PZ65_ANOGA	Q7pze5 anopheles g
710	37	39.8	574	2	Q5AJA6_CANAL	Q5aja6 candida alb	783	37	39.8	1164	2	Q4S6H5_TETNG	Q4s6h5 tetraodon n
711	37	39.8	583	2	Q81WH5_HUMAN	Q81wh5 homo sapien	784	37	39.8	1170	1	ITAZ_BOVIN	P53710 bos taurus
712	37	39.8	587	2	Q8NFL4_HUMAN	Q8nfl4 homo sapien	785	37	39.8	1214	2	Q4N5A7_THBPA	Q4n5a7 theileria p
713	37	39.8	592	2	Q6MF24_PARUM	Q6mf24 parachlamyd	786	37	39.8	1230	2	Q7R656_GIALA	Q7r656 giardia lam
714	37	39.8	592	2	Q02191_CIOIN	Q02191 ciona intes	787	37	39.8	1256	2	Q4S276_TETNG	Q4s276 tetraodon n
715	37	39.8	592	2	Q7UV94_RHOBA	Q7uv94 rhodopirell	788	37	39.8	1265	2	Q7G647_ORYSA	Q7g647 oryza sativ
716	37	39.8	593	2	Q73D18_BACCL	Q73d18 bacillus ce	789	37	39.8	1265	2	Q8W5E1_ORYSA	Q8w5e1 oryza sativ
717	37	39.8	593	2	Q81V45_BACAN	Q81v45 bacillus an	790	37	39.8	1323	2	Q7XXG9_ORYSA	Q7xxg9 oryza sativ
718	37	39.8	593	2	Q63FZ0_BACCC	Q63fz0 bacillus ce	791	37	39.8	1390	2	Q51UE4_MAGGR	Q51ue4 magnaporth
719	37	39.8	600	2	Q605T7_METCA	Q605t7 methylococc	792	37	39.8	1421	2	Q4WID6_ASFPF	Q4wid6 aspergillus
720	37	39.8	605	2	Q8BDR3_PAPVR	Q8bdr3 reindeer pa	793	37	39.8	1473	2	Q54TV0_DICDI	Q54tv0 dictyosteli
721	37	39.8	606	1	ALBU1_YENLA	P08759 xenopus lae	794	37	39.8	1478	2	Q6CUQ0_KLJULA	Q6cuq0 kluyveromyc
722	37	39.8	641	2	Q68E90_AERPU	Q68e90 aeromonas p	795	37	39.8	1482	2	Q4SJX4_TETNG	Q4sjx4 tetraodon n
723	37	39.8	647	1	KBPI_YEAST	P40489 saccharomyc	796	37	39.8	1526	2	Q6CAZ5_YARLI	Q6caz5 yarrowia li
724	37	39.8	651	2	Q9W7F8_BRARE	Q9w7f8 brachydanio	797	37	39.8	1562	2	Q54L85_DICDI	Q54l85 dictyosteli
725	37	39.8	651	2	Q5TVS1_BRARE	Q5tvsl brachydanio	798	37	39.8	1568	2	Q7Z8R6_9SACH	Q7z8r6 pichia inos
726	37	39.8	652	2	Q21306_CABEL	Q21306 caenorhabdi	799	37	39.8	1592	2	Q4PGM7_USTMA	Q4pgm7 ustiliago ma
727	37	39.8	658	2	Q5G45_DICDI	Q5g45 dictyosteli	800	37	39.8	1596	2	Q57XS0_9TRYP	Q57xs0 trypanosoma
728	37	39.8	663	2	Q8D403_VIBVU	Q8d403 vibrio vuln	801	37	39.8	1605	2	Q7XNT6_ORYSA	Q7xnt6 oryza sativ
729	37	39.8	678	2	Q7QUM5_GIALA	Q7qum5 giardia lam	802	37	39.8	1649	2	Q60K37_CABER	Q60k37 caenorhabdi
730	37	39.8	694	2	Q4R6C7_MACFA	Q4r6c7 macaca fasc	803	37	39.8	1649	2	Q4S0X4_TETNG	Q4s0x4 tetraodon n
731	37	39.8	694	2	Q5P9E1_ANANM	Q5p9e1 anaplasm m	804	37	39.8	1703	1	UN13A_HUMAN	Q9upw8 homo sapien
732	37	39.8	695	2	Q8R428_CAVPO	Q8r428 cavia porce	805	37	39.8	1709	2	Q4SDC9_TETNG	Q4sdc9 tetraodon n
733	37	39.8	701	2	Q51OK9_MAGGR	Q51ok9 magnaporth	806	37	39.8	1712	2	Q4KUS2_MOUSE	Q4kus2 mus musculu
734	37	39.8	707	2	Q96MP4_HUMAN	Q96mp4 homo sapien	807	37	39.8	1714	2	Q4UJ04_THEAN	Q4uj04 theileria a
735	37	39.8	718	2	Q6C6P5_YARLI	Q6c6p5 yarrowia li	808	37	39.8	1722	2	Q8S636_ORYSA	Q8s636 oryza sativ
736	37	39.8	731	2	Q4TI49_TETNG	Q4ti49 tetraodon n	809	37	39.8	1735	1	UN13A_RAT	Q62768 rattus norv
737	37	39.8	733	2	Q8NC68_HUMAN	Q8nc68 homo sapien	810	37	39.8	1736	2	Q95PH7_DICDI	Q95ph7 dictyosteli
738	37	39.8	733	2	Q9BZ01_HUMAN	Q9bz01 pongo pygma	811	37	39.8	1736	2	Q86AT9_DICDI	Q86at9 dictyosteli
739	37	39.8	733	2	Q5R570_PONPY	Q5r570 pongo pygma	812	37	39.8	1864	2	Q6LFE6_PLAF7	Q6lfe6 plasmodium
740	37	39.8	759	2	Q6FZ15_BARQU	Q6fz15 bartonella	813	37	39.8	1902	2	Q4RV37_TETNG	Q4rv37 tetraodon n
741	37	39.8	759	2	Q4P4W5_USTMA	Q4p4w5 ustiliago ma	819	37	39.8	2002	2	Q5CW10_CRYPV	Q5cw10 cryptospori
742	37	39.8	760	2	Q4MV80_BACCE	Q4mv80 bacillus ce	820	37	39.8	2060	2	Q9P980_PICAN	Q9p980 pichia angu
743	37	39.8	767	2	Q6MTA3_ASFPF	Q6mta3 aspergillus	821	37	39.8	2254	2	Q80N16_9PICO	Q80n16 ljungan vir
744	37	39.8	770	2	Q4W859_ASFPF	Q4w859 aspergillus	822	37	39.8	2380	2	Q86C65_DICDI	Q86c65 dictyosteli
745	37	39.8	774	2	Q7RTG3_PLAYO	Q7rtg3 plasmodium	823	37	39.8	2750	2	Q54V59_DICDI	Q54v59 dictyosteli
746	37	39.8	783	2	Q967G0_CRYPV	Q967g0 cryptospori	824	37	39.8	3374	2	Q8JJZ3_9FLAV	Q8jjz3 montana myo
747	37	39.8	796	2	Q8G9U8_DICDI	Q8g9u8 dictyosteli	825	37	39.8	4837	2	Q54MQ5_DICDI	Q54mq5 dictyosteli
748	37	39.8	799	2	Q9V964_DROME	Q9v964 drosophila	826	37	39.8	10061	2	Q81321_PLAF7	Q81321 plasmodium
749	37	39.8	811	2	Q55112_DICDI	Q55112 dictyosteli	827	37	39.8	12268	2	Q8MQ08_CABEL	Q8mq08 caenorhabdi
750	37	39.8	814	2	Q4HND2_CAMUP	Q4hnd2 campylobact	828	37	39.8	13100	2	Q8MQ08_CABEL	Q8mq08 caenorhabdi
751	37	39.8	816	2	Q5GTP5_WOLTR	Q5gtp5 wolbachia s	829	37	39.8	78	2	Q92A11_RICCN	Q92a11 rickettsia
752	37	39.8	818	2	Q73G34_WOLPM	Q73g34 wolbachia p	830	37	39.8	238	2	Q8PTP0_METMA	Q8ptp0 methanosarc
753	37	39.8	826	2	Q622U6_CABER	Q622u6 caenorhabdi	831	37	39.8	274	2	Q18773_CABER	Q18773 caenorhabdi
754	37	39.8	866	2	Q6FY30_CANGA	Q6fy30 candida gla	832	37	39.8	296	2	Q6CZS8_ERMCT	Q6czs8 erwinia car
755	37	39.8	870	2	Q6UANO_TETNG	Q6uano tetraodon n	833	37	39.8	307	2	Q4R7D4_MACFA	Q4r7d4 macaca fasc
756	37	39.8	876	2	Q6NEQ4_CORDI	Q6neq4 corynebacte	834	37	39.8	308	2	Q9VNL8_DROME	Q9vnl8 drosophila
757	37	39.8	898	2	Q8H902_ORYSA	Q8h902 oryza sativ							
758	37	39.8	898	2	Q6NZG4_MOUSE	Q6nzg4 mus musculu							
759	37	39.8	930	2	Q6CHP7_YARLI	Q6chp7 yarrowia li							
760	37	39.8	931	2	Q5I9W1_CABEL	Q5i9w1 caenorhabdi							
761	37	39.8	936	2	Q5CVN3_CRYPV	Q5cvn3 cryptospori							

835	36.5	39.2	377	2	Q64172_HUMAN	Q64172_homo sapien	908	36	38.7	213	2	Q57MX7_SALCH	Q57mx7 salmonella
836	36.5	39.2	433	2	Q4UBN5_THEAN	Q4ubn5 theileria a	909	36	38.7	218	1	Y363_RICPR	Q92dg6 rickettsia
837	36.5	39.2	499	2	Q6TUH4_RAT	Q6tuh4 rattus norv	910	36	38.7	218	2	Q8NJA4_9HYPO	Q8nja4 fusarium au
838	36.5	39.2	608	2	Q86AG5_DICTDI	Q86ag5 dictyosteli	911	36	38.7	218	2	Q8NIF1_9HYPO	Q8nif1 fusarium me
839	36.5	39.2	655	2	Q55IA2_DICTDI	Q55ia2 dictyosteli	912	36	38.7	218	2	Q7LJG9_9HYPO	Q7ljg9 fusarium me
840	36.5	39.2	657	1	THOCL_HUMAN	Q96f9 homo sapien	913	36	38.7	218	2	Q4XK65_PLACH	Q4xk65 plasmodium
841	36.5	39.2	657	1	THOCL_MOUSE	Q8r3n mus musculu	914	36	38.7	219	2	Q4XJSA_TETNG	Q4xjsa tetraodon n
842	36.5	39.2	729	2	Q4R966_MACPA	Q4r966 macaca fasc	915	36	38.7	221	2	Q7RAV7_GIALA	Q7rav7 giardia lam
843	36.5	39.2	803	1	GYRB_SALTY	P0a214 salmonella	916	36	38.7	222	2	Q4Q912_LEIMA	Q4q912 leishmania
844	36.5	39.2	803	1	GYRB_SALTY	P0a213 salmonella	917	36	38.7	224	2	Q5T4P8_HUMAN	Q5t4p8 homo sapien
845	36.5	39.2	804	2	Q57103_SALCH	Q57103 salmonella	918	36	38.7	226	2	Q5T4P9_HUMAN	Q5t4p9 homo sapien
846	36.5	39.2	804	2	Q5PKU9_SALPA	Q5pk9 salmonella	919	36	38.7	227	2	Q80561_ARATH	Q80561 arabidopsis
847	36.5	39.2	805	2	Q6CYR7_ERWCT	Q6cyr7 erwinia car	920	36	38.7	227	2	Q8ESP1_OCEBH	Q8esp1 oceanobacil
848	36.5	39.2	813	2	Q9JHD1_MOUSE	Q9jhd1 mus musculu	921	36	38.7	229	2	Q4RR14_TETNG	Q4rr14 tetraodon n
849	36.5	39.2	813	2	Q4OM9_MOUSE	Q4om9 mus musculu	922	36	38.7	230	2	Q4SW99_TETNG	Q4sw99 tetraodon n
850	36.5	39.2	832	1	PCAF_HUMAN	Q92831 homo sapien	923	36	38.7	232	2	Q7Z2T5_HUMAN	Q7z2t5 homo sapien
851	36.5	39.2	832	1	PCAF_HUMAN	Q51708 bacteroides	924	36	38.7	233	2	Q8XMB3_CLOPE	Q8xmb3 clostridium
852	36.5	39.2	1056	2	Q5L7U8_BACFN	Q5l7u8 bacteroides	925	36	38.7	234	2	Q6HZG7_BACAN	Q6hzg7 bacillus an
853	36.5	39.2	1056	2	Q64N19_BACFR	Q64n19 bacteroides	926	36	38.7	235	2	Q4Q9H9_LEIMA	Q4q9h9 leishmania
854	36.5	39.2	1526	2	Q8IK87_PLAF7	Q8ik87 plasmodium	927	36	38.7	235	2	Q8KYS9_BACAN	Q8kys9 bacillus an
855	36.5	39.2	1756	1	YCPI_PINTH	P41647 pinus thub	928	36	38.7	235	2	Q4MP09_BACCE	Q4mp09 bacillus ce
856	36.5	39.2	2269	2	Q54NC6_DICTDI	Q54nc6 dictyosteli	929	36	38.7	236	2	Q6F006_BACAN	Q6f006 bacillus an
857	36.5	39.2	3085	2	Q4SYV0_TETNG	Q4syv0 tetraodon n	930	36	38.7	236	2	Q9M4D3_MAIZE	Q9m4d3 zea mays (m
858	36	38.7	4196	1	DYHC_SCHPO	P42559 manduca sex	931	36	38.7	237	2	Q9UL48_HUMAN	Q9ul48 homo sapien
859	36	38.7	47	2	Q5V6T6_HALMA	Q5v6t6 halocaula	932	36	38.7	239	2	Q7U978_SYNPX	Q7u978 synchococc
860	36	38.7	49	2	Q86Y25_HUMAN	Q86y25 homo sapien	933	36	38.7	245	1	DERL1_DROME	Q9vq57 drosophila
861	36	38.7	53	2	Q6RQ00_SPOFR	Q6keq0 spodoptera	934	36	38.7	245	1	Y9K1_ENCCU	Q8stc1 encephalito
862	36	38.7	61	2	Q9SP88_MESMA	Q9sp88 mesobuthus	935	36	38.7	246	2	Q71XK4_LISMF	Q71xk4 listeria mo
863	36	38.7	61	2	Q967L8_MESMA	Q967l8 mesobuthus	936	36	38.7	246	2	Q8Y5A6_LISMO	Q8y5a6 listeria mo
864	36	38.7	63	2	Q6JSD9_HUMAN	Q6jed9 homo sapien	937	36	38.7	248	2	Q81R91_BACAN	Q81r91 bacillus an
865	36	38.7	68	2	Q9JW83_NEIMA	Q9jw83 neisseria m	938	36	38.7	253	2	Q4MRT9_BACCE	Q4mrt9 bacillus ce
866	36	38.7	70	2	P79261_MACMU	Q92w61 macaca mula	939	36	38.7	255	2	Q8EKB4_SHEON	Q8ekb4 shewanella
867	36	38.7	72	2	Q8TP30_METAC	Q8tp30 methanosarc	940	36	38.7	258	1	Y706_ENCCU	Q8sv55 encephalito
868	36	38.7	94	2	Q56WL3_ARATH	Q56wl3 arabidopsis	941	36	38.7	258	2	Q64EC4_9ARCH	Q64ec4 uncultured
869	36	38.7	103	2	Q8VWY0_CUCSA	Q8vwy0 cucumis sat	942	36	38.7	262	2	Q6WZA5_STRVI	Q6wza5 streptomyce
870	36	38.7	105	2	Q5WVY0_ORYSA	Q5wvy0 oryza sativ	943	36	38.7	267	2	Q63C13_BACCC	Q63c13 bacillus ce
871	36	38.7	108	1	Y3403_METUJ	Q60302 methanococc	944	36	38.7	268	2	Q9Y7L2_SCHPO	Q9y7l2 schizosacch
872	36	38.7	111	2	Q8ZUX1_PYRAE	Q8zux1 pyrobaculum	945	36	38.7	271	1	CBIO_SALTY	Q8z5n5 salmonella
873	36	38.7	121	2	Q95NV8_DROME	Q95nv8 drosophila	946	36	38.7	271	1	CBIO_SALTY	Q05596 salmonella
874	36	38.7	122	2	Q9VKK5_DROME	Q9vkk5 drosophila	947	36	38.7	271	2	Q5PDU4_SALPA	Q5pd4 salmonella
875	36	38.7	122	2	Q8QZ24_MOUSE	Q8qz24 mus musculu	948	36	38.7	272	2	Q8EJU1_SHEON	Q8eju1 shewanella
876	36	38.7	123	2	Q4Z715_PLABE	Q4z715 plasmodium	949	36	38.7	273	1	GAH6_HUMAN	Q8n84 homo sapien
877	36	38.7	124	2	Q4PL10_SAMCR	Q4pl10 samia cynth	950	36	38.7	281	2	Q61BA9_HUMAN	Q61ba9 homo sapien
878	36	38.7	125	1	ALLS_SPOFR	Q86f8 spodoptera	951	36	38.7	281	2	Q61BA9_HUMAN	Q61ba9 streptococc
879	36	38.7	125	2	Q26115_PSEUI	Q26115 pseudaletia	952	36	38.7	282	1	LRPR_STRBQ	Q54087 streptococc
880	36	38.7	150	2	Q8Q5A8_SIVCZ	Q8q5a8 chimpanzee	953	36	38.7	282	2	Q7N8Q7_PHOLL	Q7n8q7 photorhabdu
881	36	38.7	151	2	Q6ZSE1_HUMAN	Q6zes1 homo sapien	954	36	38.7	282	2	Q8NZA7_STRP8	Q8nza7 streptococc
882	36	38.7	156	2	Q8EP94_OCEBH	Q8ep94 oceanobacil	955	36	38.7	282	2	Q8K5R9_STRP3	Q8k5r9 streptococc
883	36	38.7	157	2	Q4X110_PLACH	Q4x110 plasmodium	956	36	38.7	289	2	Q4VSR6_PIG	Q4v86 sus scrofa
884	36	38.7	162	2	Q8RDM2_FUSNN	Q8rdm2 fusobacteri	957	36	38.7	289	2	F77507_ECOLI	F77507 escherichia
885	36	38.7	166	2	Q9X2X7_BACAN	Q9x2x7 bacillus an	958	36	38.7	296	2	Q877Z1_STRP3	Q877z1 streptococc
886	36	38.7	167	2	P89672_9CALI	P89672 san miguel	959	36	38.7	296	2	Q5X9T7_STRP6	Q5x9t7 streptococc
887	36	38.7	168	2	Q8YSE6_ANASP	Q8yse6 anabaena sp	960	36	38.7	297	1	YACD_BACSU	P37566 bacillus su
888	36	38.7	171	2	Q5PR44_BRARE	Q5pr44 brachydanio	961	36	38.7	298	2	Q9M4G3_MAIZE	Q9m4g3 zea mays (m
889	36	38.7	174	2	Q8L865_ARATH	Q8l865 arabidopsis	962	36	38.7	300	2	Q5U675_HUMAN	Q5u675 homo sapien
890	36	38.7	176	2	Q9L214_ARATH	Q9l214 arabidopsis	963	36	38.7	300	2	Q5FL97_LACAC	Q5fl97 lactobacill
891	36	38.7	181	2	Q68236_BORBU	Q68236 borrelia bu	964	36	38.7	302	1	ICOSL_HUMAN	Q75144 homo sapien
892	36	38.7	183	2	Q8SVT1_ENCCU	Q8svt1 encephalito	965	36	38.7	304	2	Q8KW55_9RHO	Q8kw55 ruegeria sp
893	36	38.7	185	2	Q6M181_METWP	Q6m181 methanococc	966	36	38.7	309	2	Q899L3_CLOTE	Q899l3 clostridium
894	36	38.7	186	2	Q8QMP4_9PHYC	Q8qmp4 ectocarpus	967	36	38.7	309	2	Q7WP36_VIBVY	Q7wp36 vibrio vuln
895	36	38.7	187	2	Q69144_CLOPA	Q69144 clostridium	968	36	38.7	314	2	Q9BRF8_HUMAN	Q9brf8 homo sapien
896	36	38.7	189	2	Q8TP31_METAC	Q8tp31 methanosarc	969	36	38.7	314	2	Q9H9M9_HUMAN	Q9h9m9 homo sapien
897	36	38.7	194	2	Q5VTP5_BRARE	Q5vtp5 brachydanio	970	36	38.7	314	2	Q9NUT6_HUMAN	Q9nut6 homo sapien
898	36	38.7	195	2	Q79EJ3_ECOLI	Q79ej3 escherichia	971	36	38.7	314	2	Q5RCR9_PONPY	Q5rcr9 pongo pygma
899	36	38.7	196	1	ENGB_STARR	Q6gg32 staphylococ	972	36	38.7	314	2	Q6LXG6_PONPY	Q6lxc6 photobacter
900	36	38.7	203	1	CTF2_PANTR	Q6r2r2 pan troglod	973	36	38.7	315	2	Q5R6B0_PONPY	Q5r6b0 pongo pygma
901	36	38.7	204	2	Q5RGNS_BRARE	Q5rgns brachydanio	974	36	38.7	317	1	RPOA_MESFL	Q6flw7 mesoplasma
902	36	38.7	207	2	Q4HF63_CAMCO	Q4hf63 campylobact	975	36	38.7	319	2	Q5TU72_ANOGA	Q5tu72 anopheles g
903	36	38.7	208	2	Q6LYC5_METWP	Q6lyc5 methanococc	976	36	38.7	321	2	Q70KC5_EUCUG	Q70kc5 eucalyptus
904	36	38.7	212	2	Q5WX12_LEGPL	Q5wx12 legionella	977	36	38.7	327	2	Q5F966_NEIG1	Q5f966 neisseria g
905	36	38.7	212	2	Q5X558_LEGPA	Q5x558 legionella	978	36	38.7	327	2	Q4P2F0_NEIGO	Q4p2f0 neisseria g
906	36	38.7	212	2	Q5ZWH4_LEGPH	Q5zwh4 legionella	979	36	38.7	327	2	Q9JU60_NEIMA	Q9ju60 neisseria m
907	36	38.7	212	2	Q6MEJ5_PAROW	Q6mej5 parachlamyd	980	36	38.7	327	2	Q9JZ63_NEIMB	Q9jz63 neisseria m

981	36	38.7	331	2	Q68X12_RICTY	Q68x12 rickettsia	1054	36	38.7	470	2	Q68EK2_BRARE	Q68ek2 brachydanio
982	36	38.7	332	1	LDHA_RAT	P04642 rattus norv	1055	36	38.7	478	2	Q6ESE0_RAT	Q6ese0 rattus norv
983	36	38.7	332	1	Q7QPE7_GIALA	P04642 rattus norv	1056	36	38.7	483	1	UXAB_YERPE	Q8zic5 yersinia pe
984	36	38.7	334	2	Q6BHW7_DEBHA	Q6bhw7 debaryomyce	1057	36	38.7	483	2	Q66S9N_YERPS	Q66sn9 yersinia ps
985	36	38.7	335	2	Q8BPK6_OCEIH	Q8bpk6 oceanobacil	1058	36	38.7	486	2	Q6BRY8_DEBHA	Q6bry8 debaryomyce
986	36	38.7	338	2	Q9PSY4_NEUCR	Q9psy4 neurospora	1059	36	38.7	493	2	Q6CGB7_YARLI	Q6cgb7 yarrowia li
987	36	38.7	338	2	Q5R918_PONYA	Q5r918 pongo pygma	1060	36	38.7	500	2	Q52V15_9VIRU	Q52v15 mint virus
988	36	38.7	343	2	Q6BQF7_DEBHA	Q6bqf7 debaryomyce	1061	36	38.7	501	2	Q8I516_PLAF7	Q8i516 plasmodium
989	36	38.7	349	2	Q8IAG2_CAEEL	Q8iag2 caenorhabdi	1062	36	38.7	506	1	GAG_SIYMI	F05894 simian immu
990	36	38.7	353	2	Q7VLV5_HAEPU	Q7vlv5 haemophilus	1063	36	38.7	506	2	Q8H0D7_9GENT	Q8h0d7 ophiorthiza
991	36	38.7	354	2	Q8CAZ8_MOUSE	Q8caz8 mus musculu	1064	36	38.7	509	2	Q8T3H5_DROME	Q8t3h5 drosophila
992	36	38.7	356	2	Q4UM00_RICPE	Q4um00 rickettsia	1065	36	38.7	509	2	Q9VVQ9_DROME	Q9vvq9 drosophila
993	36	38.7	356	2	Q6GSK5_BAHE	Q6gsk5 bartonella	1066	36	38.7	510	2	Q5EB91_RAT	Q5eb91 rattus norv
994	36	38.7	358	2	Q4QOM2_LEIMA	Q4qom2 leishmania	1067	36	38.7	514	2	Q5WQ06_NEUCR	Q5wq06 buchnera ap
995	36	38.7	359	1	PEX12_CRILLO	Q9et67 cricetulus	1068	36	38.7	521	2	Q7RZ86_NEUCR	Q7rz86 neurospora
996	36	38.7	359	1	PEX12_HUMAN	Q00623 homo sapien	1069	36	38.7	531	2	Q4Q076_LEIMA	Q4q076 leishmania
997	36	38.7	359	1	PEX12_MOUSE	Q8vc48 mus musculu	1070	36	38.7	537	2	Q8H0D7_9GENT	Q8h0d7 ophiorthiza
998	36	38.7	359	1	Q5SWQ8_MOUSE	Q5swq8 mus musculu	1071	36	38.7	541	2	Q661T7_BORGA	Q661t7 borrelia ga
999	36	38.7	361	2	Q7RU38_NEUCR	Q7ru38 neurospora	1072	36	38.7	542	2	Q5ISA5_9PRIM	Q5isa5 saimiri bol
1000	36	38.7	361	2	Q54RJ5_DICDI	Q54rj5 dictyosteli	1073	36	38.7	543	1	YDE3_SCHPO	Q10437 schizosacch
1001	36	38.7	363	2	Q93778_CAEEL	Q93778 caenorhabdi	1074	36	38.7	544	2	Q6ZNA6_HUMAN	Q6zna6 homo sapien
1002	36	38.7	366	2	Q7PMX2_ANOGA	Q7pmx2 anopheles g	1075	36	38.7	545	2	Q5ZOV3_NOCFA	Q5zov3 nocardia fa
1003	36	38.7	368	2	Q60MW8_CAEER	Q60mw8 caenorhabdi	1076	36	38.7	550	2	Q8NXX0_YARLI	Q8nxx0 yarrowia li
1004	36	38.7	370	2	Q6NGX8_CORDI	Q6ngx8 corynebacte	1077	36	38.7	550	2	Q9VAJ7_DROME	Q9vaj7 drosophila
1005	36	38.7	373	2	Q4R318_MACPA	Q4r318 macaca fasc	1078	36	38.7	552	2	Q5IH50_ENTHI	Q5ih50 entamoeba h
1006	36	38.7	383	2	Q7MPQ7_VIBVY	Q7mpq7 vibrio vuln	1079	36	38.7	555	2	Q8IIC9_PLAF7	Q8iic9 plasmodium
1007	36	38.7	384	2	Q7RGG2_PLAYO	Q7rgg2 plasmodium	1080	36	38.7	555	2	Q6SZP8_PHYIN	Q6szp8 phytophchor
1008	36	38.7	387	1	TOM40_YEAST	P23644 saccharomyc	1081	36	38.7	556	2	Q9IGC6_NPVEP	Q9igc6 epiphyas po
1009	36	38.7	387	2	Q6BIQ9_YEAST	Q6biq9 saccharomyc	1082	36	38.7	558	1	GLTUL_MOUSE	Q9jjj1 m putative
1010	36	38.7	388	1	SHT4R_CAVPO	Q70528 cavia porce	1083	36	38.7	558	1	SYQ_BRAJA	Q89kr6 bradyrhizob
1011	36	38.7	389	2	Q4ZOF6_MOUSE	Q4zof6 mus musculu	1084	36	38.7	558	2	Q6GT0_MOUSE	Q6gt0 mus musculu
1012	36	38.7	390	2	Q4K2Q5_STRPN	Q4k2q5 streptococc	1085	36	38.7	560	2	Q6NSR6_RHOPA	Q6nsr6 rhodopseudo
1013	36	38.7	390	2	Q5LHH7_BACFN	Q5lhh7 bacteroides	1086	36	38.7	562	1	SYQ_NEIMA	P57000 neisseria m
1014	36	38.7	390	2	Q5LHH7_BACFN	Q5lhh7 bacteroides	1087	36	38.7	562	1	SYQ_NEIMA	P57000 neisseria m
1015	36	38.7	391	1	Q64IF1_BACFR	Q64if1 bacteroides	1088	36	38.7	564	2	Q5E0C5_VIBF1	Q5e0c5 vibrio fisc
1016	36	38.7	391	1	Q60FT2_PORGI	Q60ft2 porphyromon	1089	36	38.7	564	2	Q7TPI4_RAT	Q7tpi4 rattus norv
1017	36	38.7	393	2	Q5CB12_9THEM	Q5cb12 porphyromon	1090	36	38.7	570	2	Q5CP21_CRYPV	Q5cp21 cryptospori
1018	36	38.7	399	2	Q6BRL7_DEBHA	Q6brl7 debaryomyce	1091	36	38.7	570	2	Q5CL15_CRYHO	Q5cl15 cryptospori
1019	36	38.7	401	2	Q93408_XENLA	Q93408 xenopus lae	1092	36	38.7	573	2	Q5P7G0_NEIG1	Q5p7g0 neisseria g
1020	36	38.7	401	2	Q9YHW3_XENLA	Q9yhw3 xenopus lae	1093	36	38.7	579	1	Y751_OGEIH	Q8es91 oceanobacil
1021	36	38.7	403	1	YD87_SCHPO	Q10412 schizosacch	1094	36	38.7	579	2	Q4XVH9_PLACH	Q4xvh9 halobacteri
1022	36	38.7	408	2	Q5BJM5_RAT	Q5bjm5 rattus norv	1095	36	38.7	581	2	Q74485_SCHPO	Q74485 schizosacch
1023	36	38.7	408	2	Q9JIV0_MOUSE	Q9jiv0 mus musculu	1096	36	38.7	584	2	Q583W8_9TRYP	Q583w8 trypanosoma
1024	36	38.7	408	2	Q9CXH2_MOUSE	Q9cxh2 mus musculu	1097	36	38.7	584	2	Q8ELJ0_OCEIH	Q8elj0 oceanobacil
1025	36	38.7	408	2	Q53GL0_HUMAN	Q53gl0 homo sapien	1098	36	38.7	586	2	Q4SDQ7_TETNG	Q4sdq7 tetraodon n
1026	36	38.7	409	2	Q9NRV3_HUMAN	Q9nr3 homo sapien	1099	36	38.7	586	2	DCEI_FELCA	P14748 felis silve
1027	36	38.7	409	2	Q6Q2D6_BOMMO	Q6q2d6 bombyx mori	1100	36	38.7	594	1	DCEI_HUMAN	Q92259 homo sapien
1028	36	38.7	410	2	Q6FJY4_CANGA	Q6fjy4 candida gla	1101	36	38.7	594	1	DCEI_PANTR	Q51868 pan troglod
1029	36	38.7	411	2	Q8SV00_DROME	Q8sv00 drosophila	1102	36	38.7	594	1	DCEI_PIG	P48319 sus scrofa
1030	36	38.7	416	2	Q4V8D6_RAT	Q4v8d6 rattus norv	1103	36	38.7	594	1	DCEI_PIG	Q53tq7 homo sapien
1031	36	38.7	416	2	Q5V694_HALMA	Q5v694 haloarcula	1104	36	38.7	594	2	Q8IYV8_HUMAN	Q8iyv8 homo sapien
1032	36	38.7	419	2	Q9H2Y3_HUMAN	Q9h2y3 homo sapien	1105	36	38.7	594	2	O16382_CAEEL	Q81v88 caenorhabdi
1033	36	38.7	419	2	Q9HAW0_HUMAN	Q9haw0 homo sapien	1106	36	38.7	597	2	O16382_CAEEL	Q81v88 caenorhabdi
1034	36	38.7	419	2	Q9NUY6_HUMAN	Q9nu6 homo sapien	1107	36	38.7	597	2	O6D919_XENTR	Q6d9y9 xenopus tro
1035	36	38.7	419	2	Q9CZF0_MOUSE	Q9czf0 m mus muscu	1108	36	38.7	598	2	O6DCZ1_XENLA	Q6dcz1 xenopus lae
1036	36	38.7	420	2	Q9CZF0_MOUSE	Q9czf0 m mus muscu	1109	36	38.7	602	2	O6CLX0_KLULA	Q6clx0 kluyveromyc
1037	36	38.7	425	2	Q4Q016_LEIMA	Q4q016 leishmania	1110	36	38.7	602	2	Q9N403_CAEEL	Q9n403 caenorhabdi
1038	36	38.7	431	2	Q5LID0_ARATH	Q5lido arabidopsis	1111	36	38.7	605	2	O5B888_EMENI	O5b888 aspergillus
1039	36	38.7	431	2	Q5LID0_ARATH	Q5lido arabidopsis	1112	36	38.7	614	1	FBFI_CAEEL	Q9n5m6 caenorhabdi
1040	36	38.7	431	2	Q8FPT3_VIBPA	Q8fpt3 vibrio para	1113	36	38.7	622	1	MUTL_CLOAB	Q97120 clostridium
1041	36	38.7	431	2	Q8FPT3_VIBPA	Q8fpt3 vibrio para	1114	36	38.7	624	1	GLSA2_BRAJA	Q89kv2 bradyrhizob
1042	36	38.7	435	2	Q8I251_HUMAN	Q8i251 homo sapien	1115	36	38.7	630	2	O6BK57_DEBHA	Q6bk57 debaryomyce
1043	36	38.7	440	1	HIPA_ECOLI	P23874 escherichia	1116	36	38.7	630	2	O6KIK0_MYCMO	Q6kik0 mycoplasma
1044	36	38.7	447	2	Q4HII9_CAMCO	Q4hi9 campylobact	1117	36	38.7	633	1	GIDA2_FUSNN	Q8ri88 fusobacteri
1045	36	38.7	448	2	O5XGMO_XENLA	Q5xgm0 xenopus lae	1118	36	38.7	633	2	Q5E0B6_VIBF1	Q5e0b6 vibrio fisc
1046	36	38.7	449	2	O22820_ARATH	O22820 arabidopsis	1119	36	38.7	640	2	Q7RW79_NEUCR	Q7rw79 neurospora
1047	36	38.7	452	2	Q4JLP9_LACRE	Q4jlp9 lactobacill	1120	36	38.7	640	2	Q8SRH2_ENCCU	Q8srh2 encephalito
1048	36	38.7	455	2	Q7T3E7_BRARE	Q7t3e7 brachydanio	1121	36	38.7	643	2	Q8CTZ1_STAEP	Q8ctz1 staphylococ
1049	36	38.7	458	2	Q4Z5A0_PLABE	Q4z5a0 plasmodium	1122	36	38.7	643	2	Q9ERV6_MOUSE	Q9erv6 mus musculu
1050	36	38.7	461	2	Q86K22_DICDI	Q86k22 dictyosteli	1123	36	38.7	644	2	Q9CGW3_LACIA	Q9cgw3 lactococcus
1051	36	38.7	463	2	Q4UER5_THEAN	Q4uer5 theileria a	1124	36	38.7	646	1	SRP72_YEAST	P28688 saccharomyc
1052	36	38.7	466	2	Q84UE2_MEDTR	Q84ue2 medicago tr	1125	36	38.7	649	2	Q4HA25_9DEIO	Q4ha25 deinococcus
1053	36	38.7	470	2	Q9LUI1_ARATH	Q9lui1 arabidopsis	1126	36	38.7	652	2	Q6A146_HUMAN	Q6a146 homo sapien

1273	36	38.7	2222	2	Q4PAX7_USTWA	Q4pax7_ustlago ma	1346	35	37.6	130	2	Q9YEK2_ABRPE	Q9yek2_aeropyrum p
1274	36	38.7	2254	2	Q6ZM94_BRARE	Q6zm94_brachydanio	1347	35	37.6	131	2	Q4H5G0_9DBIO	Q4h5g0_deinococcus
1275	36	38.7	2301	2	Q6BG00_PARTE	Q6bg00_parametricum	1348	35	37.6	132	2	Q54I88_DICDI	Q54i88_dictyosteli
1276	36	38.7	2470	2	Q4RV69_TETNG	Q4rv69_tetraodon n	1349	35	37.6	136	2	Q62492_MOUSE	Q62492_mus musculus
1277	36	38.7	2497	2	Q7RJm2_PLATO	Q7rjm2_plasmodium	1350	35	37.6	139	2	Q9WBL1_9HIV1	Q9wbl1_human immun
1278	36	38.7	2578	2	Q5W0B2_MOUSE	Q5w0b2_homo sapien	1351	35	37.6	147	2	Q9ZBB8_AZOVI	Q9zbb8_azotobacter
1279	36	38.7	2789	2	Q9BXT5_HUMAN	Q9bxt5_homo sapien	1352	35	37.6	147	2	Q4IU11_AZOVI	Q4iu11_azotobacter
1280	36	38.7	3417	2	Q4SXF9_TETNG	Q4sxf9_tetraodon n	1353	35	37.6	147	2	Q8R2K8_MOUSE	Q8r2k8_mus musculus
1281	36	38.7	3834	2	Q600K9_MYCHV	Q600k9_mycoplasma	1354	35	37.6	148	2	Q8K3T8_MOUSE	Q8k3t8_mus musculus
1282	36	38.7	3855	2	Q8IDL5_PLAF7	Q8idl5_plasmodium	1355	35	37.6	154	2	Q7NHS4_GLOVI	Q7nhs4_gloeobacter
1283	36	38.7	4727	2	Q8GR92_MYCWO	Q8gr92_mycoplasma	1356	35	37.6	155	2	Q8SQX9_ENCCU	Q8sqx9_encephalito
1284	36	38.7	4753	1	LRP_CABEL	Q04833_caenorhabdi	1357	35	37.6	155	2	Q4I6Z0_GIBZE	Q4i6z0_gibberella
1285	36	38.7	7191	2	Q6XA09_9PLEO	Q6xa09_alternaria	1358	35	37.6	156	2	Q93D85_STRMU	Q93d85_streptococc
1286	35.5	38.2	99	2	O55556_NPVLS	O55556_leucania se	1359	35	37.6	157	1	GYRI_ECOLI	GYRI_ESCHERICHIA
1287	35.5	38.2	110	2	O5XV44_ARATH	O5xv44_arabidopsis	1360	35	37.6	157	2	Q8FG58_ECOL6	Q8fg58_escherichia
1288	35.5	38.2	134	2	Q7P9W5_RICSI	Q7p9w5_rickettsia	1361	35	37.6	157	2	Q8X8U1_ECO57	Q8x8u1_escherichia
1289	35.5	38.2	161	2	Q7LIAB7_9NUCL	Q7liab7_mamestra co	1362	35	37.6	160	2	Q44535_AZOVI	Q44535_azotobacter
1290	35.5	38.2	161	2	Q8JM58_9NUCL	Q8jms8_mamestra co	1363	35	37.6	160	2	Q4IZU5_AZOVI	Q4izus_azotobacter
1291	35.5	38.2	161	2	Q8QLD9_NPVMC	Q8qld9_mamestra co	1364	35	37.6	161	2	Q20424_CABEL	Q20424_caenorhabdi
1292	35.5	38.2	181	2	O5XV45_ARATH	O5xv45_arabidopsis	1365	35	37.6	161	2	O92453_NPVBM	O92453_bombyx mori
1293	35.5	38.2	181	2	Q9N088_HUMAN	Q9n088_homo sapien	1366	35	37.6	167	2	O5C6R2_SCHA	O5c6r2_schistosoma
1294	35.5	38.2	270	2	Q9KKS3_VIBCH	Q9kks3_vibrio chol	1367	35	37.6	170	2	O5WKN0_BACSK	O5wkn0_bacillus cl
1295	35.5	38.2	278	2	Q5CNL7_VRYHO	Q5cnl7_cryptospori	1368	35	37.6	172	2	Q4Q869_LEIMA	Q4q869_leishmania
1296	35.5	38.2	319	2	Q8DAC1_VIBVU	Q8dac1_vibrio vuln	1369	35	37.6	172	2	Q9CRU8_MOUSE	Q9crus_mus musculus
1297	35.5	38.2	319	2	Q7MJV0_VIBVU	Q7mjv0_vibrio vuln	1370	35	37.6	172	2	Q9PMQ3_CHICK	Q9pmq3_gallus gall
1298	35.5	38.2	349	2	O64469_ARATH	O64469_arabidopsis	1371	35	37.6	173	2	Q973Y0_SULTO	Q973y0_sulfolobus
1299	35.5	38.2	353	2	O6DFK1_XENLA	O6dfk1_xenopus lae	1372	35	37.6	175	2	Q4UGR5_THEAN	Q4ugr5_theileria a
1300	35.5	38.2	356	1	CHLI_PORPU	P51394_porphyra pu	1373	35	37.6	176	2	O567L5_BRARE	O567l5_brachydanio
1301	35.5	38.2	367	2	Q8DIS0_SYNEL	Q8dis0_synecococc	1374	35	37.6	176	2	Q9PMQ2_CHICK	Q9pmq2_gallus gall
1302	35.5	38.2	380	2	Q6ETT0_ORYSA	Q6ett0_oryza sativ	1375	35	37.6	182	2	O57U02_9TRYP	O57u02_trypanosoma
1303	35.5	38.2	387	2	Q6ETT3_ORYSA	Q6ett3_oryza sativ	1376	35	37.6	185	1	BMF_RAT	BMF_rattus norv
1304	35.5	38.2	388	2	Q4IST0_GIBZE	Q4ist0_gibberella	1377	35	37.6	189	2	Q4IJF9_GIBZE	Q4ijf9_gibberella
1305	35.5	38.2	401	2	Q9CQ08_LACLA	Q9cq08_lactococcus	1378	35	37.6	201	2	O67XT3_ARATH	O67xt3_arabidopsis
1306	35.5	38.2	413	2	Q9AZT7_9CAUD	Q9azt7_bacterioph	1379	35	37.6	202	2	O5Q0A6_ARATH	O5q0a6_arabidopsis
1307	35.5	38.2	453	2	Q8BUQ6_MOUSE	Q8buq6_mus musculus	1380	35	37.6	203	2	Q5E0A3_VIBF1	Q5e0a3_vibrio fisc
1308	35.5	38.2	537	2	O60XU0_CAEER	Q60xu0_caenorhabdi	1381	35	37.6	204	2	Q7MVA4_PORGI	Q7mva4_porphyromon
1309	35.5	38.2	589	1	SYD2_STRMU	Q8dr9_streptococc	1382	35	37.6	204	2	P89134_SHEV	P89134_simian hemo
1310	35.5	38.2	591	1	VATA_CHLTR	Q9pk85_chlamydia t	1383	35	37.6	206	2	Q4YMC7_PLABE	Q4ymc7_plasmodium
1311	35.5	38.2	591	1	VATA_CHLTR	O84310_chlamydia t	1384	35	37.6	218	2	Q4YUQ3_9ADEN	Q4yuq3_turkey aden
1312	35.5	38.2	657	2	Q7QZY1_ANOGA	Q7qzy1_anopheles g	1385	35	37.6	219	1	ATPD_CHLRE	ATPD_chlamydomon
1313	35.5	38.2	742	1	CDCH_HALSA	Q9hpf0_halobacteri	1386	35	37.6	219	2	Q9SBM2_VOLCA	Q9sbm2_volvox cart
1314	35.5	38.2	781	2	Q6CAB4_YARLT	Q6cab4_yarrowia li	1387	35	37.6	220	2	Q4G133_HUMAN	Q4g133_homo sapien
1315	35.5	38.2	920	2	O5B413_EMENI	Q5b413_aspergillus	1388	35	37.6	223	2	Q63211_RAT	Q63211_rattus norv
1316	35.5	38.2	1256	2	O8NEN5_HUMAN	Q8nen5_homo sapien	1389	35	37.6	224	2	Q6DRS0_BORGA	Q6drs0_borrelia ga
1317	35.5	38.2	1258	2	Q9SSP0_ARATH	Q9ssp0_arabidopsis	1390	35	37.6	224	2	O5WLB8_BACSK	O5wlb8_bacillus cl
1318	35.5	38.2	1633	2	Q61SD4_CAEER	Q61sd4_caenorhabdi	1391	35	37.6	224	2	O662K6_BORGA	O662k6_borrelia ga
1319	35.5	38.2	1779	2	Q6TYB9_CAEER	Q6tyb9_caenorhabdi	1392	35	37.6	226	2	Q8C617_MOUSE	Q8c617_mus musculus
1320	35.5	38.2	1901	2	Q9DHH8_YLDV	Q9dhh8_yaba-like d	1393	35	37.6	227	2	O5QPL2_HUMAN	O5qpl2_homo sapien
1321	35	37.6	35	2	Q65VP2_MANSM	Q65vp2_mannheimia	1394	35	37.6	228	2	Q898N4_CLOTE	Q898n4_clostridium
1322	35	37.6	58	2	O5T9D9_HUMAN	Q5t9d9_homo sapien	1395	35	37.6	231	2	Q71B79_9HIV1	Q71b79_human immun
1323	35	37.6	69	2	Q4LAN9_STAHI	Q4lan9_staphylococ	1396	35	37.6	233	2	Q4TDI6_TETNG	Q4tdi6_tetraodon n
1324	35	37.6	70	2	O58LS6_9CAUD	Q58ls6_cyanophaga	1397	35	37.6	234	2	Q9MZ06_BOVIN	Q9mz06_bos taurus
1325	35	37.6	74	2	Q4RBD2_TETNG	Q4rbd2_tetraodon n	1398	35	37.6	235	2	Q60ZX7_CAEER	Q60zx7_caenorhabdi
1326	35	37.6	76	2	O5Z8Z9_ORYSA	Q5z8z9_oryza sativ	1399	35	37.6	236	2	Q7P8A1_FUSNV	Q7p8a1_fusobacteri
1327	35	37.6	80	2	O54B26_DICDI	O54b26_dictyosteli	1400	35	37.6	237	2	Q4ZXV7_XENLA	Q4zxv7_xenopus lae
1328	35	37.6	84	2	O8PVH8_METWA	Q8pvh8_methanosarc	1401	35	37.6	240	2	Q4ZVB7_PSESY	Q4zvb7_pseudomonas
1329	35	37.6	84	2	Q8TIW2_METAC	Q8tiw2_methanosarc	1402	35	37.6	241	2	Q73Q19_TREDE	Q73q19_treponema d
1330	35	37.6	89	1	SEMI_YEAST	Q94742_saccharomyc	1403	35	37.6	241	2	Q9YWR4_9HIV1	Q9ywr4_human immun
1331	35	37.6	93	2	Q6AM53_COTJA	Q6aw53_coturnix co	1404	35	37.6	244	2	Q8TI96_DICDI	Q8ti96_dictyosteli
1332	35	37.6	93	2	Q6AM54_COTJA	Q6aw54_coturnix co	1405	35	37.6	245	1	NUK_WHEAT	NUK_wheat
1333	35	37.6	93	2	Q6AM55_COTJA	Q6aw55_coturnix co	1406	35	37.6	245	2	O55BY1_DICDI	O55by1_dictyosteli
1334	35	37.6	101	2	Q8ZWY2_PYRAE	Q8zw2_pyrobaculum	1407	35	37.6	245	2	Q8S034_ORYSA	Q8s034_oryza sativ
1335	35	37.6	104	2	Q6XW3_MOUSE	Q6xw3_mus musculus	1408	35	37.6	245	2	Q85XC3_HORVU	Q85xc3_hordeum vul
1336	35	37.6	105	2	Q5FTU2_GLUOX	Q5ftu2_gluconobact	1409	35	37.6	247	2	Q4XT75_PLACH	Q4xt75_plasmodium
1337	35	37.6	107	2	O5CA12_SCHA	Q5ca12_schistosoma	1410	35	37.6	250	2	Q4S562_TETNG	Q4s562_tetradodon n
1338	35	37.6	107	2	Q4VS17_BOVIN	Q4vs17_bos taurus	1411	35	37.6	251	2	Q8GF12_EDWTA	Q8gf12_edwardsell
1339	35	37.6	107	2	O6Z617_ORYSA	Q6z617_oryza sativ	1412	35	37.6	252	2	Q95RQ2_DRONE	Q95rq2_drosophila
1340	35	37.6	111	2	O5BPN5_EMENI	O5bfn5_aspergillus	1413	35	37.6	254	1	CYSH_MYCBO	CYSH_mycobacteri
1341	35	37.6	118	2	Q60M15_CAEER	Q60m15_caenorhabdi	1414	35	37.6	254	1	CYSH_MYCTU	CYSH_mycobacteri
1342	35	37.6	119	2	Q9QHS9_PALPH	Q9qhs9_gallid herp	1415	35	37.6	255	2	Q9VYH8_DRONE	Q9vyh8_drosophila
1343	35	37.6	125	2	Q8TR09_METAC	Q8tr09_methanosarc	1416	35	37.6	258	1	PSBI_CABEL	PSbi_caenorhabdi
1344	35	37.6	126	2	O5HVU4_CAMJR	Q5hvu4_campylobact	1417	35	37.6	258	2	Q60IX4_CAEER	Q60ix4_caenorhabdi
1345	35	37.6	126	2	Q99MH4_CRIGR	Q99mh4_cricetulus	1418	35	37.6	259	2	Q76LJ3_COTJA	Q76lj3_coturnix co

1419 35 37.6 260 2 Q7YTU3 CAEEL
1420 35 37.6 262 2 Q5CE28 CRYHO
1421 35 37.6 262 2 Q5CGP2 CRYHO
1422 35 37.6 263 2 Q5CRF7 CRYHO
1423 35 37.6 263 2 Q4RP96 TETNG
1424 35 37.6 265 2 Q8IR80 DROME
1425 35 37.6 265 2 Q91916 XENLA
1426 35 37.6 266 1 Y309 CHLTR
1427 35 37.6 267 1 XPA XENLA
1428 35 37.6 267 2 Q7PV22 ANOGA
1429 35 37.6 268 2 Q7ULD3 RHOB
1430 35 37.6 268 2 Q76LJ2 COTJA
1431 35 37.6 275 2 Q6FBG6 ACIAD
1432 35 37.6 275 2 Q6MQX1 BDEBA
1433 35 37.6 275 2 Q87RI6 VIBPA
1434 35 37.6 278 1 PARB CAMJE
1435 35 37.6 278 2 Q5TUT7 ANOGA
1436 35 37.6 278 2 Q5HX65 CAMJR
1437 35 37.6 278 2 Q7NZJ1 CHRVO
1438 35 37.6 279 2 Q4MY8 BACCE
1439 35 37.6 279 2 Q6HE24 BACHK
1440 35 37.6 279 2 Q818V7 BACCR
1441 35 37.6 279 2 Q81M92 BACAN
1442 35 37.6 279 2 Q635B6 BACCZ
1443 35 37.6 281 1 HS32 DICDI
1444 35 37.6 281 2 Q559F2 DICDI
1445 35 37.6 281 2 Q5CG22 CRYHO
1446 35 37.6 282 2 Q5BMS4 HYPO
1447 35 37.6 282 2 Q73595 CHICK
1448 35 37.6 284 2 Q4KSV8 VIBCH
1449 35 37.6 284 2 Q9L976 STAHI
1450 35 37.6 292 2 Q50WQ3 ENTHI
1451 35 37.6 292 2 Q99M29 MOUSE
1452 35 37.6 296 2 Q7A3C3 STAAH
1453 35 37.6 296 2 Q99R56 STAAH
1454 35 37.6 297 2 Q17229 CAEEL
1455 35 37.6 299 2 Q87LN8 VIBPA
1456 35 37.6 301 2 Q54G79 DICDI
1457 35 37.6 303 2 Q51E73 ENTHI
1458 35 37.6 303 2 Q5R5D6 PONFY
1459 35 37.6 304 2 Q8EBD3 SHEON
1460 35 37.6 305 2 Q6CJ66 KLULA
1461 35 37.6 307 2 Q6VW3 METVO
1462 35 37.6 308 2 Q9CX77 MUSCUL
1463 35 37.6 309 2 Q94601 SCHPO
1464 35 37.6 309 2 Q9VV01 DROME
1465 35 37.6 310 2 Q8C7C5 MOUSE
1466 35 37.6 313 2 Q8L282 ARATH
1467 35 37.6 315 2 Q7PP0 ANOGA
1468 35 37.6 316 2 Q7YTD4 SACKO
1469 35 37.6 316 2 Q4FVU3 LEIMA
1470 35 37.6 324 2 Q6BRM8 DEBHA
1471 35 37.6 324 2 Q65678 ARATH
1472 35 37.6 327 2 Q8DTA5 STRMU
1473 35 37.6 331 1 LDHA MOUSE
1474 35 37.6 331 2 Q54M88 DICDI
1475 35 37.6 332 2 Q4R859 MACFA
1476 35 37.6 332 2 Q564E2 MOUSE
1477 35 37.6 333 2 Q4ML92 BACCE
1478 35 37.6 333 2 Q6H193 BACHK
1479 35 37.6 334 2 Q8AP1 BACTN
1480 35 37.6 334 2 Q81Q14 BACAN
1481 35 37.6 334 2 Q63AV7 BACCZ
1482 35 37.6 335 2 Q4XN72 PLACH
1483 35 37.6 335 2 Q8GV61 ARATH
1484 35 37.6 335 2 Q8L851 ARATH
1485 35 37.6 335 2 Q8S3D9 ARATH
1486 35 37.6 340 2 Q61J06 DROME
1487 35 37.6 340 2 Q8A1T1 BACTN
1488 35 37.6 340 2 Q8EM4 OCEIH
1489 35 37.6 341 2 Q72XJ2 BACC1
1490 35 37.6 342 2 Q6FKL0 CANGA
1491 35 37.6 343 2 Q50SP5 ENTHI

Q7YTU3 caenorhabdi
Q5CE28 cryptospori
Q5CGP2 cryptospori
Q5CRF7 cryptospori
Q4RP96 tetraodon n
Q8IR80 drosophila
Q91916 xenopus lae
Q84311 chlamydia t
P27088 xenopus lae
Q7PV22 anopheles g
Q7ULD3 rhodopirell
Q76LJ2 coturnix co
Q6FBG6 acinetobact
Q6MQX1 bdellovibri
Q87RI6 vibrio para
Q5TUT7 campylobact
Q5HX65 campylobact
Q7NZJ1 chromobacte
Q4MY8 bacillus ce
Q6HE24 bacillus th
Q818V7 bacillus ce
Q81M92 bacillus an
Q635B6 bacillus ce
P54658 dictyosteli
Q559F2 dictyosteli
Q5CG22 cryptospori
Q5BMS4 gibberella
Q73595 gallus gall
Q9KSV8 vibrio chol
Q9L976 staphylococ
Q50WQ3 entamoeba h
Q99M29 mus musculu
Q7A3C3 staphylococ
Q99R56 staphylococ
Q17229 caenorhabdi
Q87LN8 vibrio para
Q54G79 dictyosteli
Q51E73 entamoeba h
Q5R5D6 pongo pygma
Q8EBD3 shewanella
Q6CJ66 kluyveromyc
Q6VW3 methanococc
Q9CX77 mus musculu
Q94601 schizosacch
Q9VV01 drosophila
Q8C7C5 mus musculu
Q8L282 arabidopsis
Q7YTD4 saccoglossu
Q4FVU3 leishmania
Q6BRM8 debaryomyce
Q65678 arath
Q8DTA5 streptococ
Q6151 mus musculu
Q54M88 dictyosteli
Q4R859 macaca fasc
Q564E2 mus musculu
Q4ML92 bacillus ce
Q6H193 bacillus th
Q8AP1 bacteroides
Q81Q14 bacillus an
Q63AV7 bacillus ce
Q4XN72 plasmodium
Q8GV61 arabidopsis
Q8L851 arabidopsis
Q8S3D9 arabidopsis
Q61J06 drosophila
Q8A1T1 bacteroides
Q8EM4 oceanobacil
Q72XJ2 bacillus ce
Q6FKL0 candida gla
Q50SP5 entamoeba h

1492 35 37.6 344 1 Y182 ARCFU
1493 35 37.6 344 2 Q9JPB3 RHOGF
1494 35 37.6 344 2 Q50905 BORBU
1495 35 37.6 346 2 Q77363 PLAF7
1496 35 37.6 348 2 Q6TKV4 ECOLI
1497 35 37.6 349 1 SAPD HAEIN
1498 35 37.6 349 2 Q4G306 HORVD
1499 35 37.6 349 2 Q4QL76 HAEI8
1500 35 37.6 350 2 Q6HY82 BACAN

Q30055 archaeoglob
Q9JPB3 rhodocyclu
Q50905 borrelia bu
Q77363 plasmodium
Q6TKV4 escherichia
P45288 haemophilus
Q4G306 hordeum vul
Q4QL76 haemophilus
Q6HY82 bacillus an

ALIGNMENTS

RESULT 1

Q9H5X9 HUMAN PRELIMINARY; PRT; 229 AA.
AC Q9H5X9;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DE 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ22800.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]

NUCLEOTIDE SEQUENCE.
RC TISSUE=ileal mucosa;
RA Kawakami T., Nocchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
RA Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
RA Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y.,
RA Ohayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,
RA Isogai T., Sugano S.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK026453; BAB15488.1; -; mRNA.
DR Ensembl: ENSG00000168955; Homo sapiens.
DR GO: GO:0016021; C:integral to membrane, IEA.
DR InterPro: IPR008661; L6_membrane.
DR Pfam: PF05805; L6_membrane; 1.
SQ SEQUENCE 229 AA; 25103 MW; B7505D2798B34CDF CRC64;

Query Match 100.0%; Score 93; DB 2; Length 229;

Best Local Similarity 100.0%; Pred. No. 8.1e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSLVEDQPSQNPISCFE 18

|||||

Db 32 VSLVEDQPSQNPISCFE 49

RESULT 2

Q53R12 HUMAN PRELIMINARY; PRT; 229 AA.
AC Q53R12;
DT 13-SEP-2005 (T-EMBLrel. 31, Created)
DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
DE Hypothetical protein FLJ22800.
GN Names=PLJ22800;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]

NUCLEOTIDE SEQUENCE.

RA Nguyen C., Harris A., Meyer R.;

RT "The sequence of Homo sapiens BAC clone RP11-563C6.";

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

RN [2]

NUCLEOTIDE SEQUENCE.

RA Waterston R.H.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Waterston R.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Wilson R.K.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC097662; AAY24253.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 229 AA; 1718R0594997A1A1 CRC64;

Query Match 100.0%; Score 93; DB 2; Length 229;
 Best Local Similarity 100.0%; Pred. No. 8.1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSLVEEDQFSQNPISCFE 18
 |||||
 Db 32 VSLVEEDQFSQNPISCFE 49

RESULT 3

Q6UWS1 HUMAN
 ID Q6UWS1_HUMAN PRELIMINARY; PRT; 229 AA.
 AC Q6UWS1; 2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE TCCE518.
 GN ORFNames=UNC0518;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Batton D., Foster J.S., Grimaldi C., Gu Q., Hays P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Wagts A.,
 RA Vandlen R.L., Watanabe C., Wleand D., Woods K., Xie M.-H.,
 RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
 RA Wood W.I., Godowski P.J., Gray A.M.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment."
 RL Genome Res. 13:2265-2270(2003).
 DR EMBL; AY358671; AAQ89034.1; -; mRNA.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR InterPro; IPR008661; L6_membrane.
 DR Pfam; PF05805; L6_membrane; 1.
 SQ SEQUENCE 229 AA; 25109 MW; 1718ED342C58C903 CRC64;

Query Match 100.0%; Score 93; DB 2; Length 229;
 Best Local Similarity 100.0%; Pred. No. 8.1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSLVEEDQFSQNPISCFE 18
 |||||
 Db 32 VSLVEEDQFSQNPISCFE 49

RESULT 4

Q5U609 HUMAN
 ID Q5U609_HUMAN PRELIMINARY; PRT; 229 AA.
 AC Q5U609;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)

DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Transmembrane 4 L six family member 20.
 GN Name=TM4SF20;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heifetz F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Scheetz T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.H.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Harte S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smillius D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Colon;
 RG NIH MGC Project;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC035754; AAH35754.1; -; mRNA.
 DR Ensembl; ENSG00000168955; Homo sapiens.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR InterPro; IPR008661; L6_membrane.
 DR Pfam; PF05805; L6_membrane; 1.
 KW Transmembrane.
 SQ SEQUENCE 229 AA; 25137 MW; B750504AFD7C247D CRC64;

Query Match 100.0%; Score 93; DB 2; Length 229;
 Best Local Similarity 100.0%; Pred. No. 8.1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSLVEEDQFSQNPISCFE 18
 |||||
 Db 32 VSLVEEDQFSQNPISCFE 49

RESULT 5

Q9CQY8 MOUSE
 ID Q9CQY8_MOUSE PRELIMINARY; PRT; 226 AA.
 AC Q9CQY8;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Mus musculus 11 days pregnant adult female ovary and uterus cDNA,
 DE RIKEN full-length enriched library, clone:5033426G15 product:similar
 DE to CDNA: FLJ22800 FIS, CLONE KAI2630 (Mus musculus 10 day old male
 DE pancreas cDNA, RIKEN full-length enriched library, clone:1810018L02
 DE product:similar to CDNA: FLJ22800 FIS, CLONE KAI2630).
 GN Name=TM4sf20;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

[1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikolaio I., Pesole G., Quackenbush J.,
 RA Straub L.M., Straubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
 RX MEDLINE=22346683; PubMed=12468851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmer S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawaasa Y., Kedzierki R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).

[5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Ogawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
 RA Adachi T., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK017195; BAB30629.1; -; mRNA.
 DR EMBL; AK007532; BAB25093.1; -; mRNA.
 DR EMBL; ENSMUSG0000026149; Mus musculus.
 DR MGI; MGI:1913511; Tm48f20.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR InterPro; IPR008661; L6 membrane.
 DR Pfam; PF05805; L6 membrane; 1.
 SQ SEQUENCE 226 AA; 24760 MW; 3FE6BA1C6A335EAD CRC64;
 Query Match 75.3%; Score 70; DB 2; Length 226;
 Best Local Similarity 72.2%; Pred. No. 0.00094;
 Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 VSLVESDQFSQNPISCFE 18
 Db :||||| :||||| :|
 32 ISLVESDQFSQNPISCFE 49
 RESULT 6
 Q9D3R0 MOUSE PRELIMINARY; PRT; 226 AA.
 AC Q9D3R0;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mus musculus 11 days pregnant adult female ovary and uterus cDNA,
 DE RIKEN full-length enriched library, clone:5033405M13 product:similar
 DE to CDNA: FLJ22800 FIS, CLONE KAIJA2630.
 GN Name=Tm4sf20; Synonyms=1810018L02Rik;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 [2]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Peole G., Quackenbush J.,
 RA Schriml L.M., Staubli P., Furuno M., Aono H., Baldarelli R., Barch G.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barch G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
 RA The FANTOM Consortium;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1611-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamanoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori P.,
 RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito R., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Teima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2000) to the ENBL/GenBank/DBJ databases.
 DR ENBL; AK017154; BAB30618.1; -; mRNA.
 DR Ensembl; ENSMUSG00000026149; Mus musculus.
 DR MGI; MGI:1913511; 1810018L02Rik.
 DR MGI; MGI:1913511; Tm4sf20.
 GO; GO:0005615; C:extracellular space; TAS.

DR GO; GO:0016021; C:integral to membrane; TAS.
 DR InterPro; IPR008661; L6 membrane.
 DR Pfam; PF05805; L6 membrane; 1.
 SQ SEQUENCE 226 AA; 24714 MW; 8BE6B5EC2D1EDDC0 CRC64;
 Query Match 75.3%; Score 70; DB 2; Length 226;
 Best Local Similarity 72.2%; Pred. No. 0.00094;
 Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 VSLVERDQFSONDISCFE 18
 Db 32 ISLVADSTSQNPISCYE 49
 RESULT 7
 Q9D3Q0_MOUSE
 ID Q9D3Q0_MOUSE PRELIMINARY; PRT; 226 AA.
 AC Q9D3Q0;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mus musculus 11 days pregnant adult female ovary and uterus cDNA.
 DE RIKEN full-length enriched library, clone:5033430P14 product:similar
 DE to cDNA: FLJ22800 FIS, CLONE KAJA2630.
 GN Name=Tm4sf20; Synonym=1810018L02Rik;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
 RX MEDLINE=99275253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Peole G., Quackenbush J.,
 RA Schriml L.M., Staubli P., Furuno M., Aono H., Baldarelli R., Barch G.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barch G.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
 RA The FANTOM Consortium;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
[5]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
[6]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Akakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Segabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi P., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK017209; BAB30635.1; -; mRNA.
DR Ensembl; ENSMUSG00000026149; Mus musculus.
DR MGI; MGI:1913511; 1810018L02Rik.
DR MGI; MGI:1913511; T48f20.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR008661; L6 membrane.
DR Pfam; PF05805; L6 membrane; 1.
SQ SEQUENCE 226 AA; 24786 MW; 3FE6BA06703344B7 CRC64;

Query Match 75.3%; Score 70; DB 2; Length 226;
Best Local Similarity 72.2%; Pred. No. 0.00094;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VSLVEEDQFSQNPFISCF 18
:|||||:|||||:
DB 32 ISLVEADSTSQNPISCF 49

RESULT 8
Q9C252_NEUCR PRELIMINARY; PRT; 126 AA.
AC Q9C252;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Probable small nuclear ribonucleoprotein chain D2.
GN Name=B18D24.220;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
[1]
RN NUCLEOTIDE SEQUENCE.
RP Schulte U., Aign V., Hoheisel J., Brandt P., Partmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.

RA German Neurospora genome project;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL513466; CAC28820.1; -; Genomic_DNA.
DR HSP; P62316; 1B34.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005732; C:small nucleolar ribonucleoprotein complex; IEA.
DR GO; GO:0006397; P:mRNA processing; IEA.
DR InterPro; IPR006649; snRNP.
DR Pfam; PF01423; LSM; 1.
DR ProDom; PD020287; snRNP; 1.
DR SMART; SM00651; Sm; 1.
KW Ribonucleoprotein.
SQ SEQUENCE 126 AA; 14372 MW; 5DD84379C2316C86 CRC64;

Query Match 50.5%; Score 47; DB 2; Length 126;
Best Local Similarity 50.0%; Pred. No. 5.7;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 VSLVEEDQFSQNPFISCF 18
:|||||:|||||:
DB 24 VSLLEHBFSGPLSLIQ 41

RESULT 9
Q7V7K2_PROMM PRELIMINARY; PRT; 601 AA.
AC Q7V7K2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein precursor.
GN OrderedLocustNames=PMT0742;
OS Prochlorococcus marinus (strain MIT 9313).
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=74547;
[1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
RA Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
RA Algren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA Johnson Z.I., Land M.L., Lindell D., Post A.E., Regala W., Shah M.,
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb B.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT niche differentiation.";
RL Nature 424:1042-1047(2003).
DR EMBL; BX572097; CAE20917.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein; Signal.
FT SIGNAL 1 28 Potential.
SQ SEQUENCE 601 AA; 66706 MW; AF953044BEB36E3B CRC64;

Query Match 49.5%; Score 46; DB 2; Length 601;
Best Local Similarity 47.1%; Pred. No. 50;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 VSLVEEDQFSQNPFISCF 17
:|||||:|||||:
DB 78 IAKVEQDGLDQNWVSCF 94

RESULT 10
Q4N5J1_THEPA PRELIMINARY; PRT; 143 AA.
AC Q4N5J1;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN OSFNames=TP02_0299;
OS Theileria parva.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;

OC Theileria.
 OX NCBI_TaxID=5875;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Muga;
 RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
 RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M.,
 RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallow S.J., Weidman J.,
 RA Jiang L., Lynn J., Weaver B., Shoabi A., Wasawo D., Crabtree J.,
 RA Wortman J.R., Haas B., Angioli S.V., Creasy T.H., Lu C., Suh B.,
 RA Silva J.C., Uterback T.R., Feldblyum T.V., Perteau M., Allen J.,
 RA Taracha E.L.N., Salzberg S.L., White O.R., Fitzhugh H.A., Morzaria S.,
 RA Venter J.C., Fraser C.M., Nene V.;
 RT "Genome sequence of Theileria parva, a bovine pathogen that transforms
 RT lymphocytes";
 RL Science 309:134-137(2005).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Muga;
 RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
 RA Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
 RA Ralph S.A., Mann D.J., Xiong Z., Shallow S.J., Weidman J., Jiang L.,
 RA Lynn J., Weaver B., Shoabi A., Wasawo D., Crabtree J., Wortman J.R.,
 RA Haas B., Angioli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
 RA Uterback T., Feldblyum T., Perteau M., Allen J., Taracha E.L.,
 RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
 RA Fraser C.M., Nene V.;
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL: AAGK01000002; EMBL: EMBL32582.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 143 AA; 16977 MW; 500D0921D3856550 CRC64;
 Query Match 48.4%; Score 45; DB 2; Length 143;
 Best Local Similarity 50.0%; Pred. No. 15;
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 3 LVEDQFQNPISCPE 18
 Db 39 LVDDQFPRNDIYE 54
 RESULT 11
 Q7T301_BRARE PRELIMINARY; PRT; 238 AA.
 AC Q7T301;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Basic helix-loop-helix domain containing, class B, 5.
 GN Names=bhlhb5;
 OS Brachydanio rerio (zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauber R.L., Feingold E.A., Grouse L.H., Derge J.G.
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Iqbalano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.U.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RG NIH MGC Project;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 DR EMBL: BC053312; AHS3312.1; -; mRNA.
 DR ZFIN; ZDB-GENE-040426-1411; bhlhb5.
 DR Ensembl; ENSDARG0000025861; Danio rerio.
 DR ZFIN; ZDB-GENE-040426-1411; bhlhb5.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0030528; F:transcription regulator activity; IEA.
 DR GO; GO:0045449; P:regulation of transcription; IEA.
 DR InterPro; IPR001092; HLH_basic.
 DR Pfam; PF00010; HLH; 1.
 DR SMART; SM00353; HLH; 1.
 DR PROSITE; PS00888; HLH; 1.
 SQ SEQUENCE 238 AA; 25499 MW; 4F3D0949829EBF99 CRC64;
 Query Match 48.4%; Score 45; DB 2; Length 238;
 Best Local Similarity 88.9%; Pred. No. 26;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 10 SQNPISCPE 18
 Db 17 SQSPISCPE 25
 RESULT 12
 Q9VDK6_DROME PRELIMINARY; PRT; 410 AA.
 AC Q9VDK6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE CG4159-PA.
 GN Name=CG4159; ORFNames=CG4159;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
 RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brattler P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foeller C., Gabrieli A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Moutouf G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426085; PubMed=12537558;
RA Ceiniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
RT *melanogaster* euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celnikier S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomic perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bennett B.R., Celnikier S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX Berkeley *Drosophila* Genome Project;
RA Ceiniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX FlyBase;
RG Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -1- INTERACTION;
CC Q95T20:CG10494; NSEXP=1; InAct=EBI-156238, EBI-104332;
DR EMBL; AE003731; AAF5785.1; -; Genomic_DNA.
DR IntAct; Q9VDK6; -;
DR Ensembl; CG4159; *Drosophila melanogaster*.
DR FlyBase; FBgn0038811; CG4159.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0016829; P:lyase activity; IEA.
DR GO; GO:0004730; P:pseudouridylyate synthase activity; IEA.

DR GO; GO:0008033; P:tRNA processing; IEA.
DR InterPro; IPR001406; Pseudou synth 1.
DR PANTHER; PTHR11142; Pseudou synth 1.
DR Pfam; PF01416; Pseudou synth 1; 1.
DR TIGRFAMs; TIGR00071; hist trua; 1.
SQ SEQUENCE 410 AA; 47224 MW; 573D418102C16BBA CRC64;
Query Match 48.4%; Score 45; DB 2; Length 410;
Best Local Similarity 53.3%; Pred. No. 49;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 4 VERDQFSQNPISCFE 18
Db 109 ITEDSFEQIQISCFQ 123
RESULT 13
Q61CF7 CAEBR
ID Q61CF7 CAEBR PRELIMINARY; PRT; 575 AA.
AC Q61CF7
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG12934.
GN Names=CBG12934;
OS *Caenorhabditis briggsae*.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; *Caenorhabditis*.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAC0100061; CAE67442.1; -; Genomic DNA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0010181; F:FMN binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR003097; FAD binding.
DR InterPro; IPR001094; Flavodoxin-like.
DR InterPro; IPR008254; Flav_nitox synth.
DR InterPro; IPR001709; FPN_cyt reductase.
DR InterPro; IPR001433; Oxred FAD/NAD(P).
DR InterPro; IPR001221; Phe hydroxylase.
DR Pfam; PF00667; FAD binding 1; 1.
DR Pfam; PF00258; Flavodoxin 1; 1.
DR Pfam; PF00175; NAD binding 1; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; PFNCR.
DR PROSITE; PS50902; FLAVODOXIN-LIKE; 1.
KW Hypothetical protein.
SQ SEQUENCE 575 AA; 65274 MW; 39B9E967BF535ECB CRC64;
Query Match 48.4%; Score 45; DB 2; Length 575;
Best Local Similarity 61.5%; Pred. No. 72;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 VSLVERDQFSQNP 13
Db 269 VKVKNDQFSKNP 281
RESULT 14
Q55DX2 DICDI
ID Q55DX2 DICDI PRELIMINARY; PRT; 805 AA.
AC Q55DX2
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

DE Hypothetical protein.
GN ORFNames=DD50201744;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sungang R., Beriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Karhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Louesged H., Mungall K., Oliver K., Price C., Quail M.A., Sanders M.,
RA Urushihara H., Hernandez J., Rabinowitch E., Steffen D.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstein G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.,
RT "The genome of the social amoeba Dictyostelium discoideum";
RL Nature 010-0(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR ENBL; AAF10100011; EAL72619.1; -; Genomic_DNA.
DR InterPro; IPR000221; Protamine_P1.
DR InterPro; IPR001440; TPR.
DR InterPro; IPR011990; TPR-like_helical.
DR Pfam; PF00515; TPR.1; 1.
DR SMART; SM00028; TPR; 2.
DR PROSITE; PS00048; PROTAMINE_P1; UNKNOWN_1.
DR PROSITE; PS00005; TPR; 2.
DR PROSITE; PS0293; TPR_REGION; 1.
DR PROSITE; PS0293; TPR_REGION; 1.
KW Hypothetical protein; Repeat; TPR repeat.
SQ SEQUENCE 805 AA; 93914 MW; 6BE015F294B8C17 CRC64;

Query Match 48.48; Score 45; DB 2; Length 805;
Best Local Similarity 50.08; Pred. No. 1.1e+02;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 VSLVEEDQFQSNPTSC 16
DB 424 VNMLEDQLFSNWSC 439

RESULT 15
GYRA_MYCLE STANDARD; PRT; 1273 AA.
AC Q57532; Q50209; Q9CDF2;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE DNA gyrase subunit A (BC 5.99.1.3) [Contains: Mle gyra intein].
GN Namegyra; OrderedLocName=Mle0006;
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP NUCLEOTIDE SEQUENCE
RX MEDLINE=36194983; PubMed=8622949; DOI=10.1073/pnas.93.8.3410;
RA Fahi H., Vincent V., Cole S.T.;
RT "Homolog events in the gyra gene of some mycobacteria";
RL Proc. Natl. Acad. Sci. U.S.A. 93:3410-3415(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=TN;
RX MEDLINE=21128732; PubMed=11234002; DOI=10.1038/35059006;
RA Cole S.T., Eigmeier K., Parthill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C.M., Harris D.E.,
RA Mungall K.L., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L.D., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus";
RL Nature 409:1007-1011(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE OF 75-114.
RX MEDLINE=96050760; PubMed=8540734;
RA Guillemin I., Cambau E., Jarlier V.;
RT "Sequences of conserved region in the A subunit of DNA gyrase from
RT nine species of the genus Mycobacterium: phylogenetic analysis and
RT implication for intrinsic susceptibility to quinolones";
RL Antimicrob. Agents Chemother. 39:2145-2149(1995).
CC -1- FUNCTION: DNA gyrase negatively supercoils closed circular double-
CC stranded DNA in an ATP-dependent manner and also catalyzes the
CC interconversion of other topological isomers of double-stranded
CC DNA rings, including catenanes and knotted rings.
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -1- SUBUNIT: Made up of two chains. The A chain is responsible for DNA
CC breakage and rejoining; the B chain catalyzes ATP hydrolysis. The
CC enzyme forms an A2B2 tetramer.
CC -1- PTM: This protein undergoes a protein self splicing that involves
CC a post-translational excision of the intervening region (intein)
CC followed by peptide ligation (Potential).
CC -1- SIMILARITY: Belongs to the topoisomerase gyra/parC subunit family.
CC -1- SIMILARITY: Contains 1 DOD-type homing endonuclease domain.
CC -1- CAUTION: Ref.2 sequence differs from that shown due to a
CC frameshift in position 1247.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

DR ENBL; Z70722; CAA94713.1; -; Genomic_DNA.
DR ENBL; Z68206; CAA92430.1; -; Genomic_DNA.
DR ENBL; AL583917; CAC29514.1; ALT_FRAME; Genomic_DNA.
DR ENBL; X87124; CAA60608.1; -; Genomic_DNA.
DR PIR; T10006; T10006.
DR HGSP; P72065; IAM2.
DR SMR; Q57532; 494-550.
DR Leproma; ML0006; -.
DR InterPro; IPR005743; DNA_gyrase.
DR InterPro; IPR006691; DNA_gyraseA_C.
DR InterPro; IPR002205; DNA_topoisomV.
DR InterPro; IPR003586; Hedgehog_hint_C.
DR InterPro; IPR003587; Hedgehog_hint_N.
DR InterPro; IPR006142; INTEIN.
DR InterPro; IPR004042; Intein_endonuc.
DR InterPro; IPR006141; Intein_S.
DR Pfam; PF03989; DNA_gyraseA_C; 6.
DR Pfam; PF00521; DNA_topoisomV; 2.
DR PRINTS; PR00379; INTEIN.
DR PRODOM; PD000742; DNA_topoisomV; 2.
DR SMART; SM00305; HintC; 1.
DR SMART; SM00306; HintN; 1.
DR SMART; SM00434; TOP4C; 1.
DR TIGRFAMs; TIGR01063; gyra; 1.
DR TIGRFAMs; TIGR01443; Intein_Cterm; 1.
DR TIGRFAMs; TIGR01445; Intein_Nterm; 1.
DR PROSITE; PS50818; INTEIN_C_TER; 1.
DR PROSITE; PS50819; INTEIN_ENDONUCLEASE; 1.
DR PROSITE; PS50817; INTEIN_N_TER; 1.

KW Autocatalytic cleavage; Complete proteome; DNA-binding; Isomerase;
KW Protein splicing; Topoisomerase.
FT CHAIN 1 130 DNA gyrase subunit A, 1st part (By
FT similarity).
FT CHAIN 131 550 Mle gyrA intein (By similarity).
FT CHAIN 551 1273 DNA gyrase subunit A, 2nd part (By
FT similarity).
FT DOMAIN 256 396 DOD-type homing endonuclease.
FT ACT_SITE 130 130 O-(5'-phospho-DNA)-tyrosine intermediate
FT CONFLICT 267 267 (By similarity).
FT F -> S (in Ref. 1).
SQ SEQUENCE 1273 AA; 141218 MW; 4B6FFBB5BD7AEF53 CRC64;

Query Match 47.3%; Score 44; DB 1; Length 1273;
Best Local Similarity 46.7%; Pred. No. 2.7e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 VEEDQFSQNPISCPE 18
||| | : : :
Db 469 VEEDSFNQHNVDVQ 483

Search completed: December 22, 2005, 03:00:16
Job time : 128 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 22, 2005, 02:46:28 ; Search time 12.4898 Seconds
(without alignments)
119.150 Million cell updates/sec

Title: US-10-063-553-48_COPY_32_49

Perfect score: 93

Sequence: 1 VSLVEEDQFSQNPISCFE 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Issued Patents AA:**

- 1: /cgm2_6/ptodata/1/iaa/5_COMB.pep:**
- 2: /cgm2_6/ptodata/1/iaa/6_COMB.pep:**
- 3: /cgm2_6/ptodata/1/iaa/H_COMB.pep:**
- 4: /cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep:**
- 5: /cgm2_6/ptodata/1/iaa/RG_COMB.pep:**
- 6: /cgm2_6/ptodata/1/iaa/backfile1.pep:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	93	100.0	229	2	US-09-991-181-258
2	93	100.0	229	2	US-09-990-444-258
3	93	100.0	229	2	US-09-997-333-258
4	93	100.0	229	2	US-09-992-598-258
5	43	46.2	1110	1	US-08-118-441-29
6	43	46.2	1110	2	US-08-338-579A-29
7	43	46.2	1110	4	PCT-US94-09851-29
8	42	45.2	676	1	US-08-398-590A-40
9	42	45.2	676	2	US-08-894-997-40
10	42	45.2	676	2	US-09-873-155A-40
11	42	45.2	976	2	US-08-894-997-50
12	42	45.2	976	2	US-09-873-155A-50
13	42	45.2	1147	2	US-09-949-016-8616
14	42	45.2	1464	1	US-08-231-193A-11
15	42	45.2	1464	1	US-08-486-273A-11
16	42	45.2	1464	2	US-08-940-086A-11
17	42	45.2	1464	2	US-08-436-332B-10
18	42	45.2	1464	2	US-08-940-035A-11
19	42	45.2	1464	2	US-08-935-105A-11
20	42	45.2	1464	2	US-08-648-797-11
21	42	45.2	1464	2	US-08-217-704C-2
22	42	45.2	1464	2	US-09-386-123-11
23	42	45.2	1464	2	US-09-949-016-8311
24	42	45.2	1464	2	US-10-038-937-11
25	42	45.2	1464	2	US-10-007-747-11
26	42	45.2	1464	2	US-09-945-901-11
27	41	44.1	117	2	US-08-965-903B-6

28	41	44.1	139	2	US-08-965-903B-20	Sequence 20, Appl
29	41	44.1	139	2	US-09-370-398-4	Sequence 4, Appl
30	41	44.1	139	2	US-10-090-190-4	Sequence 4, Appl
31	41	44.1	139	2	US-10-082-902-4	Sequence 4, Appl
32	40.5	43.5	797	2	US-09-198-452A-636	Sequence 636, App
33	40.5	43.5	814	2	US-09-438-185A-596	Sequence 596, App
34	40	43.0	158	2	US-10-104-047-3221	Sequence 3221, Ap
35	40	43.0	305	2	US-09-248-796A-17837	Sequence 17837, A
36	40	43.0	789	2	US-09-949-016-7164	Sequence 7164, Ap
37	40	43.0	1500	2	US-09-949-016-5878	Sequence 5878, Ap
38	40	43.0	1620	2	US-09-949-016-7242	Sequence 7242, Ap
39	39	41.9	238	2	US-08-858-207A-420	Sequence 420, App
40	39	41.9	320	2	US-09-330-970-3	Sequence 3, Appli
41	39	41.9	390	2	US-09-949-016-10020	Sequence 10020, A
42	39	41.9	502	2	US-09-330-970-1	Sequence 1, Appli
43	39	41.9	659	2	US-09-583-110-4043	Sequence 4043, Ap
44	39	41.9	661	2	US-09-107-433-3700	Sequence 3700, Ap
45	39	41.9	741	2	US-08-943-956A-2	Sequence 2, Appli
46	38.5	41.4	355	2	US-09-498-520A-8	Sequence 8, Appli
47	38.5	41.4	355	2	US-09-498-520A-48	Sequence 48, Appl
48	38.5	41.4	393	2	US-08-956-171B-5248	Sequence 5248, Ap
49	38.5	41.4	393	2	US-08-781-986A-5248	Sequence 5248, Ap
50	38	40.9	193	2	US-09-949-016-10446	Sequence 10446, A
51	38	40.9	197	2	US-09-270-767-47012	Sequence 47012, A
52	38	40.9	291	2	US-09-198-452A-624	Sequence 624, App
53	38	40.9	291	2	US-09-438-185A-584	Sequence 584, App
54	38	40.9	339	2	US-08-758-280-1	Sequence 1, Appli
55	38	40.9	339	2	US-08-758-280-2	Sequence 2, Appli
56	38	40.9	339	2	US-08-964-614A-1	Sequence 1, Appli
57	38	40.9	339	2	US-08-964-614A-2	Sequence 2, Appli
58	38	40.9	339	2	US-09-538-092-1274	Sequence 1274, Ap
59	38	40.9	349	2	US-09-270-767-43051	Sequence 43051, A
60	38	40.9	395	2	US-09-949-016-8564	Sequence 8564, Ap
61	38	40.9	400	2	US-09-107-532A-4562	Sequence 4562, Ap
62	38	40.9	448	2	US-08-476-509B-2	Sequence 2, Appli
63	38	40.9	486	2	US-08-348-518C-2	Sequence 2, Appli
64	38	40.9	498	1	US-07-688-352C-20	Sequence 20, Appl
65	38	40.9	498	1	US-08-474-379C-20	Sequence 20, Appl
66	38	40.9	498	2	US-09-146-249A-20	Sequence 20, Appl
67	38	40.9	498	2	US-08-206-188B-20	Sequence 20, Appl
68	38	40.9	700	2	US-09-252-991A-23746	Sequence 23746, A
69	38	40.9	757	2	US-09-538-092-520	Sequence 520, App
70	38	40.9	772	2	US-10-148-806-37	Sequence 37, Appl
71	38	40.9	852	2	US-09-248-796A-14890	Sequence 14890, A
72	38	40.9	940	2	US-09-252-991A-24639	Sequence 24639, A
73	38	40.9	981	2	US-09-902-540-9848	Sequence 9848, Ap
74	38	40.9	1068	2	US-09-538-092-1111	Sequence 1111, Ap
75	38	40.9	1069	1	US-08-162-081B-37	Sequence 37, Appl
76	38	40.9	1069	1	US-08-780-872-37	Sequence 37, Appl
77	38	40.9	1069	2	US-09-085-957-37	Sequence 37, Appl
78	38	40.9	1080	1	US-08-162-081B-36	Sequence 36, Appl
79	38	40.9	1080	1	US-08-780-872-36	Sequence 36, Appl
80	38	40.9	1080	2	US-09-085-957-36	Sequence 36, Appl
81	37.5	40.3	15	1	US-08-522-326-6	Sequence 6, Appli
82	37.5	40.3	375	2	US-09-270-767-39877	Sequence 39877, A
83	37.5	40.3	375	2	US-09-270-767-55094	Sequence 55094, A
84	37	39.8	75	2	US-09-248-796A-24305	Sequence 24305, A
85	37	39.8	104	2	US-09-634-238-312	Sequence 312, App
86	37	39.8	116	2	US-08-965-903B-9	Sequence 9, Appli
87	37	39.8	191	2	US-09-270-767-35892	Sequence 35892, A
88	37	39.8	191	2	US-09-270-767-51109	Sequence 51109, A
89	37	39.8	277	2	US-09-328-352-7936	Sequence 7936, Ap
90	37	39.8	315	2	US-08-965-903B-8	Sequence 8, Appli
91	37	39.8	315	2	US-09-370-398-3	Sequence 3, Appli
92	37	39.8	315	2	US-09-370-398-6	Sequence 6, Appli
93	37	39.8	315	2	US-10-090-190-3	Sequence 3, Appli
94	37	39.8	315	2	US-10-090-190-6	Sequence 6, Appli
95	37	39.8	315	2	US-10-082-902-3	Sequence 3, Appli
96	37	39.8	315	2	US-10-082-902-6	Sequence 6, Appli
97	37	39.8	326	2	US-09-520-781-75	Sequence 75, Appl
98	37	39.8	326	2	US-09-957-187-75	Sequence 75, Appl
99	37	39.8	326	2	US-09-957-187-75	Sequence 75, Appl
100	37	39.8	339	2	US-09-134-000C-5209	Sequence 5209, Ap

101	37	39.8	363	2	US-09-205-258-278	Sequence 278, App	174	36	38.7	478	2	US-09-867-521-2	Sequence 2, Appli
102	37	39.8	363	2	US-10-004-860-278	Sequence 278, App	175	36	38.7	490	2	US-09-667-135-28	Sequence 28, Appl
103	37	39.8	370	2	US-09-205-258-558	Sequence 558, App	176	36	38.7	558	2	US-09-667-135-31	Sequence 31, Appl
104	37	39.8	370	2	US-10-004-860-558	Sequence 558, App	177	36	38.7	594	1	US-08-592-696-2	Sequence 2, Appli
105	37	39.8	380	2	US-09-248-796A-14486	Sequence 14486, A	178	36	38.7	594	1	US-08-592-696-4	Sequence 4, Appli
106	37	39.8	393	1	US-08-933-750C-11	Sequence 11, Appl	179	36	38.7	594	1	US-09-027-536-2	Sequence 2, Appli
107	37	39.8	393	2	US-09-234-613-11	Sequence 11, Appl	180	36	38.7	594	1	US-09-027-536-4	Sequence 4, Appli
108	37	39.8	393	2	US-09-663-600A-199	Sequence 199, App	181	36	38.7	594	2	US-09-028-148-2	Sequence 2, Appli
109	37	39.8	416	2	US-09-205-258-461	Sequence 461, App	182	36	38.7	594	2	US-09-028-148-4	Sequence 4, Appli
110	37	39.8	416	2	US-10-004-860-461	Sequence 461, App	183	36	38.7	594	2	US-09-124-141-15	Sequence 15, Appl
111	37	39.8	494	2	US-10-290-579A-175	Sequence 175, App	184	36	38.7	594	2	US-09-124-141-23	Sequence 23, Appl
112	37	39.8	510	2	US-09-370-368-5	Sequence 5, Appli	185	36	38.7	625	1	US-08-442-689-2	Sequence 2, Appli
113	37	39.8	549	2	US-09-107-532A-6840	Sequence 6840, Ap	186	36	38.7	625	1	US-08-468-583-2	Sequence 2, Appli
114	37	39.8	579	1	US-08-448-196A-8	Sequence 8, Appli	187	36	38.7	640	2	US-09-134-000C-5035	Sequence 5035, Ap
115	36.5	39.2	291	2	US-09-489-039A-8172	Sequence 8172, Ap	188	36	38.7	640	2	US-09-710-279-676	Sequence 676, App
116	36.5	39.2	657	2	US-09-653-465B-2	Sequence 2, Appli	189	36	38.7	648	2	US-09-949-016-11296	Sequence 11296, A
117	36.5	39.2	672	2	US-09-949-016-8895	Sequence 8895, Ap	190	36	38.7	741	1	US-08-462-481-2	Sequence 2, Appli
118	36	38.7	70	2	US-09-513-999C-6629	Sequence 6629, Ap	191	36	38.7	741	1	US-08-436-771-2	Sequence 2, Appli
119	36	38.7	90	2	US-09-188-930-134	Sequence 134, App	192	36	38.7	741	1	US-08-436-771-4	Sequence 4, Appli
120	36	38.7	90	2	US-09-312-283C-134	Sequence 134, App	193	36	38.7	741	1	US-08-434-998-2	Sequence 2, Appli
121	36	38.7	101	1	US-08-670-354-4	Sequence 4, Appli	194	36	38.7	741	1	US-08-434-998-4	Sequence 4, Appli
122	36	38.7	101	2	US-09-320-424-4	Sequence 4, Appli	195	36	38.7	741	1	US-08-487-797-2	Sequence 2, Appli
123	36	38.7	101	2	US-09-374-454-17	Sequence 17, Appl	196	36	38.7	741	1	US-08-487-797-4	Sequence 4, Appli
124	36	38.7	101	2	US-09-825-563-4	Sequence 4, Appli	197	36	38.7	741	1	US-08-701-005A-2	Sequence 2, Appli
125	36	38.7	101	4	PCT-US96-10895-4	Sequence 4, Appli	198	36	38.7	741	1	US-08-479-895-2	Sequence 2, Appli
126	36	38.7	120	2	US-09-513-999C-7833	Sequence 32, Appl	199	36	38.7	741	4	US-09-949-016-6997	Sequence 2, Appli
127	36	38.7	120	2	US-09-569-611C-32	Sequence 32, Appl	200	36	38.7	741	4	PCT-US95-02058-2	Sequence 2, Appli
128	36	38.7	122	2	US-09-569-611C-31	Sequence 31, Appl	201	36	38.7	741	4	PCT-US95-02058-4	Sequence 4, Appli
129	36	38.7	125	2	US-09-198-452A-1172	Sequence 1172, Ap	202	36	38.7	747	2	US-09-949-016-7955	Sequence 7955, Ap
130	36	38.7	157	2	US-09-270-767-40741	Sequence 40741, A	203	36	38.7	870	1	US-08-785-241-6	Sequence 4, Appli
131	36	38.7	157	2	US-09-270-767-55957	Sequence 55957, A	204	36	38.7	870	1	US-09-374-454-6	Sequence 6, Appli
132	36	38.7	161	2	US-09-270-767-48702	Sequence 48702, A	205	36	38.7	2789	2	US-09-949-016-8208	Sequence 8208, Ap
133	36	38.7	169	2	US-09-569-611C-29	Sequence 29, Appl	206	35	37.6	28	2	US-09-406-781-12	Sequence 12, Appl
134	36	38.7	185	2	US-10-104-047-1972	Sequence 1972, Ap	207	35	37.6	28	2	US-09-880-132-12	Sequence 12, Appl
135	36	38.7	208	2	US-09-521-335-11	Sequence 11, Appl	208	35	37.6	81	2	US-09-513-999C-6796	Sequence 6796, Ap
136	36	38.7	225	2	US-09-949-016-11297	Sequence 11297, A	209	35	37.6	92	2	US-09-248-796A-27911	Sequence 27911, A
137	36	38.7	225	2	US-09-949-016-11298	Sequence 11298, A	210	35	37.6	93	2	US-09-248-796A-25316	Sequence 25316, A
138	36	38.7	241	2	US-09-915-789A-11	Sequence 11, Appl	211	35	37.6	136	2	US-09-621-976-4705	Sequence 4705, Ap
139	36	38.7	250	2	US-08-124-141-17	Sequence 17, Appl	212	35	37.6	157	2	US-09-306-454-7	Sequence 7, Appli
140	36	38.7	250	2	US-09-902-540-13813	Sequence 13813, A	213	35	37.6	157	2	US-09-306-454-9	Sequence 9, Appli
141	36	38.7	252	1	US-08-834-655-7	Sequence 7, Appli	214	35	37.6	178	1	US-07-996-772A-6	Sequence 6, Appli
142	36	38.7	252	2	US-08-834-033A-8	Sequence 8, Appli	215	35	37.6	178	1	US-08-446-822-6	Sequence 6, Appli
143	36	38.7	252	2	US-09-363-574-7	Sequence 7, Appli	216	35	37.6	178	2	US-09-328-314-6	Sequence 6, Appli
144	36	38.7	252	2	US-09-363-526-7	Sequence 7, Appli	217	35	37.6	178	4	PCT-US93-12586-6	Sequence 6, Appli
145	36	38.7	261	2	US-09-270-767-47059	Sequence 47059, A	218	35	37.6	199	2	US-09-232-200-85	Sequence 85, Appl
146	36	38.7	266	2	US-09-645-415A-10	Sequence 10, Appl	219	35	37.6	199	2	US-09-232-197-85	Sequence 85, Appl
147	36	38.7	271	2	US-09-569-611C-30	Sequence 30, Appl	220	35	37.6	199	2	US-09-232-201-85	Sequence 85, Appl
148	36	38.7	279	2	US-09-072-993C-3	Sequence 3, Appli	221	35	37.6	199	2	US-09-232-195-85	Sequence 85, Appl
149	36	38.7	281	1	US-08-670-354-2	Sequence 2, Appli	222	35	37.6	202	2	US-09-543-681A-6592	Sequence 6592, Ap
150	36	38.7	281	2	US-08-584-031-1	Sequence 1, Appli	223	35	37.6	203	2	US-09-124-141-9	Sequence 9, Appli
151	36	38.7	281	2	US-08-780-496-1	Sequence 1, Appli	224	35	37.6	253	2	US-09-248-796A-14363	Sequence 14363, A
152	36	38.7	281	2	US-08-883-086-10	Sequence 10, Appl	225	35	37.6	254	2	US-10-126-279-27	Sequence 27, Appl
153	36	38.7	281	2	US-09-320-424-2	Sequence 2, Appli	226	35	37.6	254	2	US-10-286-606-27	Sequence 27, Appl
154	36	38.7	281	2	US-09-333-593A-6	Sequence 6, Appli	227	35	37.6	261	1	US-08-446-822-15	Sequence 15, Appl
155	36	38.7	281	2	US-09-157-864-11	Sequence 11, Appl	228	35	37.6	261	2	US-09-328-314-15	Sequence 15, Appl
156	36	38.7	281	2	US-09-825-563-2	Sequence 2, Appli	229	35	37.6	261	4	PCT-US93-12586-15	Sequence 15, Appl
157	36	38.7	281	2	US-09-919-039-118	Sequence 118, App	230	35	37.6	264	2	US-09-270-767-44841	Sequence 44841, A
158	36	38.7	281	2	US-09-582-450-1	Sequence 1, Appli	231	35	37.6	281	2	US-09-489-039A-10009	Sequence 10009, A
159	36	38.7	281	2	US-09-934-465-1	Sequence 1, Appli	232	35	37.6	309	2	US-09-248-796A-20432	Sequence 20432, A
160	36	38.7	281	2	US-10-011-125A-4	Sequence 4, Appli	233	35	37.6	311	2	US-09-270-767-42099	Sequence 42099, A
161	36	38.7	281	4	PCT-US96-10895-2	Sequence 2, Appli	234	35	37.6	331	2	US-09-711-681-4	Sequence 4, Appli
162	36	38.7	302	2	US-09-915-789A-18	Sequence 18, Appl	235	35	37.6	331	2	US-10-274-266-4	Sequence 4, Appli
163	36	38.7	309	2	US-09-667-135-6	Sequence 6, Appli	236	35	37.6	336	1	US-07-904-073-2	Sequence 2, Appli
164	36	38.7	309	2	US-09-910-174B-7	Sequence 7, Appli	237	35	37.6	336	1	US-07-904-071-2	Sequence 2, Appli
165	36	38.7	309	2	US-09-620-461-7	Sequence 7, Appli	238	35	37.6	336	1	US-08-442-043A-16	Sequence 16, Appl
166	36	38.7	352	2	US-09-710-279-216	Sequence 216, App	239	35	37.6	336	2	US-08-441-893A-16	Sequence 16, Appl
167	36	38.7	359	2	US-09-949-016-5912	Sequence 15912, Ap	240	35	37.6	352	2	US-09-248-796A-18408	Sequence 18408, A
168	36	38.7	377	2	US-09-489-039A-12546	Sequence 12546, A	241	35	37.6	360	2	US-09-555-313B-4	Sequence 4, Appli
169	36	38.7	403	2	US-09-540-236-2573	Sequence 2573, Ap	242	35	37.6	360	2	US-09-826-509-443	Sequence 443, App
170	36	38.7	411	2	US-09-188-930-302	Sequence 302, App	243	35	37.6	362	2	US-09-146-980-2	Sequence 2, Appli
171	36	38.7	411	2	US-09-312-283C-302	Sequence 302, App	244	35	37.6	362	2	US-09-270-767-4337	Sequence 4337, A
172	36	38.7	450	2	US-09-949-016-8496	Sequence 8496, Ap	245	35	37.6	377	2	US-10-164-595-64	Sequence 64, Appl
173	36	38.7	478	2	US-09-570-454-2	Sequence 2, Appli	246	35	37.6	378	2	US-09-826-509-445	Sequence 445, App

247	35	37.6	380	2	US-09-555-113B-24	Sequence 24, Appl	320	34	36.6	120	2	US-09-248-796A-16151	Sequence 16151, A
248	35	37.6	380	2	US-09-826-509-441	Sequence 441, App	321	34	36.6	130	2	US-09-621-976-4013	Sequence 4013, A
249	35	37.6	387	2	US-09-826-509-436	Sequence 436, App	322	34	36.6	141	2	US-09-489-039A-11896	Sequence 11896, A
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251	35	37.6	388	2	US-09-328-314-8	Sequence 8, Appl	324	34	36.6	154	2	US-08-845-623-22	Sequence 22, Appl
252	35	37.6	388	2	US-09-826-509-439	Sequence 439, App	325	34	36.6	154	2	US-08-815-927-22	Sequence 22, Appl
253	35	37.6	388	4	PCT-US93-12586-8	Sequence 8, Appl	326	34	36.6	154	2	US-09-103-330-22	Sequence 22, Appl
254	35	37.6	454	2	US-08-348-518C-4	Sequence 4, Appl	327	34	36.6	154	2	US-09-435-242-22	Sequence 22, Appl
255	35	37.6	454	2	US-08-476-509B-4	Sequence 4, Appl	328	34	36.6	154	2	US-09-270-767-43857	Sequence 43857, A
256	35	37.6	461	2	US-09-919-039-180	Sequence 180, App	329	34	36.6	156	2	US-09-543-681A-5954	Sequence 5954, A
257	35	37.6	466	2	US-09-949-016-7543	Sequence 7543, App	330	34	36.6	173	2	US-09-533-029-36	Sequence 36, Appl
258	35	37.6	466	2	US-09-270-767-34576	Sequence 34576, A	331	34	36.6	183	4	PCT-US95-03236-37	Sequence 37, Appl
259	35	37.6	548	2	US-09-270-767-49793	Sequence 49793, A	332	34	36.6	188	2	US-09-710-279-152	Sequence 152, App
260	35	37.6	569	1	US-07-821-716-2	Sequence 2, Appl	333	34	36.6	208	2	US-09-830-230A-350	Sequence 350, App
261	35	37.6	569	1	US-08-381-603-2	Sequence 2, Appl	334	34	36.6	224	2	US-09-270-767-33261	Sequence 33261, A
262	35	37.6	569	2	US-08-924-376-2	Sequence 2, Appl	335	34	36.6	224	2	US-09-830-230A-349	Sequence 349, App
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264	35	37.6	569	2	US-09-173-151A-31	Sequence 31, Appl	337	34	36.6	246	2	US-09-107-532A-5040	Sequence 5040, App
265	35	37.6	569	2	US-08-466-932A-2	Sequence 2, Appl	338	34	36.6	254	2	US-09-248-796A-21484	Sequence 21484, A
266	35	37.6	569	2	US-08-406-824A-6	Sequence 6, Appl	339	34	36.6	260	2	US-09-482-273-202	Sequence 202, App
267	35	37.6	569	2	US-09-949-016-6000	Sequence 6000, App	340	34	36.6	308	2	US-09-134-000C-6494	Sequence 6494, App
268	35	37.6	569	4	PCT-US94-02414-2	Sequence 2, Appl	341	34	36.6	309	1	US-08-078-683A-5	Sequence 5, Appl
269	35	37.6	569	4	PCT-US96-08899-2	Sequence 2, Appl	342	34	36.6	309	2	US-08-471-970A-5	Sequence 5, Appl
270	35	37.6	580	2	US-09-367-583-2	Sequence 2, Appl	343	34	36.6	309	2	US-09-723-677B-5	Sequence 5, Appl
271	35	37.6	588	2	US-09-949-016-8572	Sequence 8572, App	344	34	36.6	315	2	US-09-252-991A-24352	Sequence 24352, A
272	35	37.6	593	2	US-09-124-141-7	Sequence 7, Appl	345	34	36.6	317	2	US-09-949-016-8193	Sequence 8193, App
273	35	37.6	594	2	US-09-949-016-5996	Sequence 5996, App	346	34	36.6	323	1	US-08-044-812A-4	Sequence 4, Appl
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275	35	37.6	616	2	US-09-396-149-7	Sequence 7, Appl	348	34	36.6	323	2	US-08-706-281A-12	Sequence 12, Appl
276	35	37.6	652	2	US-09-134-001C-3517	Sequence 3517, App	349	34	36.6	323	2	US-09-191-359-4	Sequence 4, Appl
277	35	37.6	758	2	US-09-138-452A-996	Sequence 996, App	350	34	36.6	323	2	US-09-097-231-12	Sequence 12, Appl
278	35	37.6	758	2	US-09-438-185A-926	Sequence 926, App	351	34	36.6	323	2	US-09-353-099-12	Sequence 12, Appl
279	35	37.6	760	2	US-09-555-113B-2	Sequence 2, Appl	352	34	36.6	330	2	US-09-709-066-2	Sequence 2, Appl
280	35	37.6	826	2	US-09-252-991A-22143	Sequence 22143, A	353	34	36.6	330	2	US-09-301-666A-10	Sequence 10, Appl
281	35	37.6	856	2	US-09-248-796A-16089	Sequence 16089, A	354	34	36.6	330	2	US-09-301-217-10	Sequence 10, Appl
282	35	37.6	900	2	US-10-282-162-34	Sequence 34, Appl	355	34	36.6	352	2	US-09-107-532A-6703	Sequence 6703, App
283	35	37.6	900	2	US-10-282-162-40	Sequence 40, Appl	356	34	36.6	384	2	US-09-248-796A-18132	Sequence 18132, A
284	35	37.6	902	2	US-10-282-162-36	Sequence 36, Appl	357	34	36.6	390	2	US-08-492-459-2	Sequence 2, Appl
285	35	37.6	902	2	US-10-282-162-38	Sequence 38, Appl	358	34	36.6	422	2	US-08-492-459-2	Sequence 2, Appl
286	35	37.6	902	2	US-10-282-162-42	Sequence 42, Appl	359	34	36.6	422	2	US-08-423-752-2	Sequence 2, Appl
287	35	37.6	902	2	US-10-282-162-44	Sequence 44, Appl	360	34	36.6	422	2	US-08-423-752-2	Sequence 2, Appl
288	35	37.6	910	2	US-09-313-942-28	Sequence 28, Appl	361	34	36.6	422	2	US-08-423-752-4	Sequence 4, Appl
289	35	37.6	910	2	US-10-282-162-28	Sequence 28, Appl	362	34	36.6	422	2	US-08-716-873-7	Sequence 7, Appl
290	35	37.6	959	2	US-09-248-796A-20776	Sequence 20776, A	363	34	36.6	422	2	US-08-716-873-16	Sequence 16, Appl
291	35	37.6	1070	2	US-10-164-595-18	Sequence 18, Appl	364	34	36.6	422	2	US-08-716-873-18	Sequence 18, Appl
292	35	37.6	1073	2	US-10-164-595-22	Sequence 22, Appl	365	34	36.6	422	2	US-09-368-431-7	Sequence 7, Appl
293	35	37.6	1092	2	US-09-543-681A-7058	Sequence 7058, App	366	34	36.6	422	2	US-09-368-431-16	Sequence 16, Appl
294	35	37.6	1107	2	US-09-358-383C-16	Sequence 16, Appl	367	34	36.6	422	2	US-09-368-431-18	Sequence 18, Appl
295	35	37.6	1175	1	US-08-598-305A-36	Sequence 36, Appl	368	34	36.6	422	2	US-09-414-006-2	Sequence 2, Appl
296	35	37.6	1175	1	US-08-639-923A-36	Sequence 36, Appl	369	34	36.6	422	2	US-09-414-006-4	Sequence 4, Appl
297	35	37.6	1279	2	US-09-170-496D-293	Sequence 293, App	370	34	36.6	422	2	US-09-447-223-2	Sequence 2, Appl
298	35	37.6	1279	2	US-09-364-425B-58	Sequence 58, Appl	371	34	36.6	422	2	US-09-447-223-4	Sequence 4, Appl
299	35	37.6	1372	2	US-09-902-540-14099	Sequence 14099, A	372	34	36.6	422	2	US-09-951-217-7	Sequence 7, Appl
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301	35	37.6	1464	1	US-09-922-011-1	Sequence 1, Appl	374	34	36.6	422	2	US-09-951-217-18	Sequence 18, Appl
302	35	37.6	2368	1	US-08-198-446B-15	Sequence 15, Appl	375	34	36.6	449	2	US-09-134-000C-5444	Sequence 5444, App
303	35	37.6	2368	1	US-08-870-693-15	Sequence 15, Appl	376	34	36.6	451	2	US-08-996-139-4	Sequence 4, Appl
304	34.5	37.1	536	2	US-09-270-767-43553	Sequence 43553, A	377	34	36.6	451	2	US-08-995-659-4	Sequence 4, Appl
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306	34.5	37.1	826	2	US-09-949-016-9213	Sequence 9213, App	379	34	36.6	451	2	US-09-577-80-4	Sequence 4, Appl
307	34.5	37.1	826	2	US-09-949-016-9214	Sequence 9214, App	380	34	36.6	451	2	US-09-577-800-4	Sequence 4, Appl
308	34.5	37.1	903	2	US-09-328-352-4668	Sequence 4668, App	381	34	36.6	451	2	US-09-466-496-4	Sequence 4, Appl
309	34.5	37.1	1073	2	US-09-134-000C-6356	Sequence 6356, App	382	34	36.6	451	2	US-09-871-856-4	Sequence 4, Appl
310	34.5	37.1	1297	1	US-08-290-731C-4	Sequence 4, Appl	383	34	36.6	451	2	US-09-871-291-4	Sequence 4, Appl
311	34	36.6	21	1	US-09-555-113B-6	Sequence 6, Appl	384	34	36.6	451	2	US-09-107-532A-6652	Sequence 6652, App
312	34	36.6	43	1	US-08-882-083-16	Sequence 16, Appl	385	34	36.6	451	2	US-09-877-650-4	Sequence 4, Appl
313	34	36.6	43	1	US-08-558-107-16	Sequence 16, Appl	386	34	36.6	451	2	US-09-865-459-4	Sequence 4, Appl
314	34	36.6	43	2	US-09-243-539-16	Sequence 16, Appl	387	34	36.6	451	2	US-09-688-453-4	Sequence 4, Appl
315	34	36.6	75	2	US-09-248-796A-24803	Sequence 24803, A	388	34	36.6	502	2	US-09-252-991A-27020	Sequence 27020, A
316	34	36.6	79	2	US-09-248-796A-21828	Sequence 21828, A	389	34	36.6	521	2	US-09-413-814-106	Sequence 106, App
317	34	36.6	99	2	US-09-489-039A-7903	Sequence 7903, App	390	34	36.6	547	2	US-09-543-681A-5969	Sequence 5969, App
318	34	36.6	107	2	US-09-248-796A-20800	Sequence 20800, A	391	34	36.6	547	2	US-09-178-252-11	Sequence 11, Appl
319	34	36.6	117	2	US-09-248-796A-19723	Sequence 19723, A	392	34	36.6	547	2	US-09-826-660-11	Sequence 11, Appl

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394	34	36.6	569	1	US-09-350-729A-8	Sequence 8, Appli	467	34	36.6	1150	4	PCT-US95-05431-21	Sequence 21, Appl
395	34	36.6	574	1	US-08-756-317-4	Sequence 4, Appli	468	34	36.6	1155	1	US-08-349-867-19	Sequence 19, Appl
396	34	36.6	591	2	US-08-986-139-2	Sequence 2, Appli	469	34	36.6	1155	1	US-08-349-867-33	Sequence 33, Appl
397	34	36.6	591	2	US-08-995-659-2	Sequence 2, Appli	470	34	36.6	1155	1	US-08-239-476-19	Sequence 19, Appl
398	34	36.6	591	2	US-09-215-649A-2	Sequence 2, Appli	471	34	36.6	1155	1	US-08-446-486-2	Sequence 2, Appli
399	34	36.6	591	2	US-09-577-780-2	Sequence 2, Appli	472	34	36.6	1155	1	US-07-951-715A-9	Sequence 9, Appli
400	34	36.6	591	2	US-09-577-800-2	Sequence 2, Appli	473	34	36.6	1155	1	US-08-463-308-2	Sequence 2, Appli
401	34	36.6	591	2	US-09-466-496-2	Sequence 2, Appli	474	34	36.6	1155	1	US-08-598-305A-19	Sequence 19, Appl
402	34	36.6	591	2	US-08-871-856-2	Sequence 2, Appli	475	34	36.6	1155	1	US-08-598-305A-33	Sequence 33, Appl
403	34	36.6	591	2	US-09-871-291-2	Sequence 2, Appli	476	34	36.6	1155	1	US-08-639-923A-19	Sequence 19, Appl
404	34	36.6	591	2	US-09-877-650-2	Sequence 2, Appli	477	34	36.6	1155	1	US-08-459-448A-9	Sequence 9, Appli
405	34	36.6	591	2	US-09-865-363-2	Sequence 2, Appli	478	34	36.6	1155	1	US-08-459-595A-9	Sequence 9, Appli
406	34	36.6	591	2	US-09-688-317-3	Sequence 3, Appli	479	34	36.6	1155	2	US-09-021-203-2	Sequence 2, Appli
407	34	36.6	600	1	US-08-756-317-3	Sequence 3, Appli	480	34	36.6	1155	2	US-08-459-504B-9	Sequence 9, Appli
408	34	36.6	616	2	US-08-986-139-6	Sequence 6, Appli	481	34	36.6	1155	2	US-08-459-44A-9	Sequence 9, Appli
409	34	36.6	616	2	US-08-995-659-6	Sequence 6, Appli	482	34	36.6	1155	2	US-09-053-549-4	Sequence 4, Appli
410	34	36.6	616	2	US-09-215-649A-6	Sequence 6, Appli	483	34	36.6	1155	2	US-09-053-549-6	Sequence 6, Appli
411	34	36.6	616	2	US-09-577-800-6	Sequence 6, Appli	484	34	36.6	1155	2	US-09-547-422-9	Sequence 9, Appli
412	34	36.6	616	2	US-09-577-800-6	Sequence 6, Appli	485	34	36.6	1155	2	US-09-988-462-9	Sequence 9, Appli
413	34	36.6	616	2	US-09-466-496-6	Sequence 6, Appli	486	34	36.6	1155	4	PCT-US95-05431-19	Patent No. 5254799
414	34	36.6	616	2	US-08-871-856-6	Sequence 6, Appli	487	34	36.6	1155	6	5254799-4	Sequence 15, Appl
415	34	36.6	616	2	US-09-871-291-6	Sequence 6, Appli	488	34	36.6	1156	2	US-09-178-252-15	Sequence 15, Appl
416	34	36.6	616	2	US-09-877-650-6	Sequence 6, Appli	489	34	36.6	1156	2	US-09-826-660-15	Sequence 15, Appl
417	34	36.6	616	2	US-09-865-363-6	Sequence 6, Appli	490	34	36.6	1162	2	US-09-134-001C-4008	Sequence 4008, Ap
418	34	36.6	616	2	US-09-949-016-6421	Sequence 6421, Ap	491	34	36.6	1163	1	US-08-239-474A-11	Sequence 11, Appl
419	34	36.6	616	2	US-09-688-459-6	Sequence 6, Appli	492	34	36.6	1163	1	US-08-732-495-11	Sequence 11, Appl
420	34	36.6	616	2	US-09-957-344-2	Sequence 2, Appli	493	34	36.6	1163	2	US-09-178-252-21	Sequence 21, Appl
421	34	36.6	616	2	US-10-104-047-2497	Sequence 2497, Ap	494	34	36.6	1163	2	US-09-826-660-21	Sequence 21, Appl
422	34	36.6	620	2	US-09-134-000C-5867	Sequence 5867, Ap	495	34	36.6	1165	1	US-07-828-788A-14	Sequence 14, Appl
423	34	36.6	622	2	US-09-957-944-10	Sequence 10, Appl	496	34	36.6	1165	1	US-08-239-476-33	Sequence 33, Appl
424	34	36.6	632	2	US-09-328-352-5495	Sequence 5495, Ap	497	34	36.6	1165	1	US-08-356-034-4	Sequence 4, Appli
425	34	36.6	638	1	US-08-756-317-2	Sequence 2, Appli	498	34	36.6	1165	1	US-08-639-923A-33	Sequence 33, Appl
426	34	36.6	647	1	US-08-218-943-1	Sequence 1, Appli	499	34	36.6	1165	2	US-08-933-891-4	Sequence 4, Appli
427	34	36.6	672	2	US-09-363-708-2	Sequence 2, Appli	500	34	36.6	1165	2	US-09-176-320-6	Sequence 6, Appli
428	34	36.6	672	2	US-09-083-587-2	Sequence 2, Appli	501	34	36.6	1165	2	US-09-521-344-4	Sequence 4, Appli
429	34	36.6	719	1	US-08-082-849B-31	Sequence 31, Appl	502	34	36.6	1165	2	US-09-837-961A-4	Sequence 4, Appli
430	34	36.6	719	1	PCT-US94-01624-31	Sequence 31, Appl	503	34	36.6	1165	2	US-09-661-016-6	Sequence 6, Appli
431	34	36.6	735	1	US-08-021-601-4	Sequence 4, Appli	504	34	36.6	1165	4	PCT-US92-11337-14	Sequence 14, Appl
432	34	36.6	735	1	US-08-082-849B-4	Sequence 4, Appli	505	34	36.6	1165	6	PCT-US95-05431-33	Sequence 33, Appl
433	34	36.6	735	1	PCT-US94-01624-4	Sequence 4, Appli	506	34	36.6	1165	6	518960-4	Patent No. 518960
434	34	36.6	735	2	US-09-350-729A-7	Sequence 7, Appli	507	34	36.6	1171	1	US-07-828-788A-6	Sequence 6, Appli
435	34	36.6	736	2	US-09-823-038A-52	Sequence 52, Appl	508	34	36.6	1171	1	US-08-278-685-2	Sequence 2, Appli
436	34	36.6	757	2	US-09-350-729A-5	Sequence 5, Appli	509	34	36.6	1171	1	US-08-277-721-2	Sequence 2, Appli
437	34	36.6	763	2	US-09-350-729A-6	Sequence 6, Appli	510	34	36.6	1171	1	US-08-277-721-4	Sequence 4, Appli
438	34	36.6	764	2	US-08-021-601-12	Sequence 12, Appl	511	34	36.6	1171	1	US-08-602-737-4	Sequence 4, Appli
439	34	36.6	903	1	US-08-082-849B-12	Sequence 12, Appl	512	34	36.6	1171	2	US-09-001-982-4	Sequence 4, Appli
440	34	36.6	903	1	PCT-US94-01624-12	Sequence 12, Appl	513	34	36.6	1171	4	US-09-668-650-4	Sequence 4, Appli
441	34	36.6	924	2	US-09-489-039A-8842	Sequence 8842, Ap	514	34	36.6	1171	4	PCT-US92-11337-6	Sequence 6, Appli
442	34	36.6	1046	2	US-09-199-637A-13	Sequence 13, Appl	515	34	36.6	1174	1	US-07-828-788A-10	Sequence 10, Appl
443	34	36.6	1049	2	US-09-232-991A-26475	Sequence 26475, A	516	34	36.6	1174	1	US-08-349-867-25	Sequence 25, Appl
444	34	36.6	1129	6	5164180-6	Patent No. 5164180	517	34	36.6	1174	1	US-08-349-867-29	Sequence 29, Appl
445	34	36.6	1148	1	US-08-349-867-23	Sequence 23, Appl	518	34	36.6	1174	1	US-08-349-867-32	Sequence 32, Appl
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449	34	36.6	1148	1	US-08-598-305A-23	Sequence 23, Appl	522	34	36.6	1174	1	US-08-598-305A-25	Sequence 25, Appl
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452	34	36.6	1148	1	US-08-598-305A-37	Sequence 37, Appl	525	34	36.6	1174	1	US-08-639-923A-25	Sequence 25, Appl
453	34	36.6	1148	1	US-08-598-305A-38	Sequence 38, Appl	526	34	36.6	1174	1	US-08-639-923A-29	Sequence 29, Appl
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455	34	36.6	1148	1	US-08-639-923A-27	Sequence 27, Appl	528	34	36.6	1174	2	US-09-178-252-6	Sequence 6, Appli
456	34	36.6	1148	1	US-08-639-923A-35	Sequence 35, Appl	529	34	36.6	1174	2	US-09-521-344-8	Sequence 8, Appli
457	34	36.6	1148	1	US-08-639-923A-38	Sequence 38, Appl	530	34	36.6	1174	2	US-09-826-660-6	Sequence 6, Appli
458	34	36.6	1148	1	US-08-639-923A-38	Sequence 38, Appl	531	34	36.6	1174	2	US-09-837-961A-8	Sequence 8, Appli
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462	34	36.6	1148	4	PCT-US95-05431-27	Sequence 27, Appl	535	34	36.6	1174	4	PCT-US95-05431-29	Sequence 29, Appl
463	34	36.6	1150	1	US-08-349-867-21	Sequence 21, Appl	536	34	36.6	1174	6	518960-8	Patent No. 518960
464	34	36.6	1150	1	US-08-239-476-21	Sequence 21, Appl	537	34	36.6	1176	1	US-07-828-788A-12	Sequence 12, Appl
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539	34	36.6	1176	1	US-08-356-034-2	Sequence 2, Appli	612	34	36.6	1189	1	US-08-757-536-10	Sequence 10, Appl
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543	34	36.6	1176	2	US-09-521-344-2	Sequence 2, Appli	616	34	36.6	1189	2	US-09-314-093-6	Sequence 6, Appli
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546	34	36.6	1179	1	US-08-040-751-1	Sequence 1, Appli	619	34	36.6	1189	2	US-09-314-093-12	Sequence 12, Appli
547	34	36.6	1179	6	5188960-2	Patent No. 5188960	620	34	36.6	1189	2	US-09-314-093-51	Sequence 59, Appl
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564	34	36.6	1181	2	US-08-459-504B-13	Sequence 13, Appl	637	34	36.6	1189	2	US-09-337-635-2	Sequence 2, Appli
565	34	36.6	1181	2	US-08-459-504B-15	Sequence 15, Appl	638	34	36.6	1189	2	US-09-337-635-4	Sequence 4, Appli
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567	34	36.6	1181	2	US-08-459-504B-28	Sequence 28, Appl	640	34	36.6	1189	2	US-09-337-635-8	Sequence 8, Appli
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569	34	36.6	1181	2	US-08-459-444-13	Sequence 13, Appl	642	34	36.6	1189	2	US-09-337-635-12	Sequence 12, Appl
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574	34	36.6	1181	2	US-09-547-422-13	Sequence 13, Appl	647	34	36.6	1189	2	US-09-337-280-6	Sequence 6, Appli
575	34	36.6	1181	2	US-09-547-422-15	Sequence 15, Appl	648	34	36.6	1189	2	US-09-337-280-8	Sequence 8, Appli
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582	34	36.6	1181	2	US-09-988-462-28	Sequence 28, Appl	655	34	36.6	1189	2	US-09-668-650-2	Sequence 2, Appli
583	34	36.6	1182	1	US-08-349-867-34	Sequence 34, Appl	656	34	36.6	1189	2	US-09-972-175-2	Sequence 2, Appli
584	34	36.6	1182	1	US-08-598-305A-34	Sequence 34, Appl	657	34	36.6	1189	2	US-09-972-175-4	Sequence 4, Appli
585	34	36.6	1184	1	US-08-239-476-32	Sequence 32, Appl	658	34	36.6	1189	2	US-09-972-175-6	Sequence 6, Appli
586	34	36.6	1184	1	US-08-639-923A-32	Sequence 32, Appl	659	34	36.6	1189	2	US-09-972-175-8	Sequence 8, Appli
587	34	36.6	1184	4	PCT-US95-05431-32	Sequence 32, Appl	660	34	36.6	1189	2	US-09-972-175-10	Sequence 10, Appl
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590	34	36.6	1186	2	US-09-178-252-23	Sequence 23, Appl	663	34	36.6	1189	2	US-09-972-175-61	Sequence 61, Appl
591	34	36.6	1186	2	US-09-826-660-23	Sequence 23, Appl	664	34	36.6	1189	2	US-10-200-522-2	Sequence 2, Appli
592	34	36.6	1186	2	US-09-668-650-6	Sequence 6, Appli	665	34	36.6	1189	2	US-10-200-522-4	Sequence 4, Appli
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594	34	36.6	1188	1	US-08-639-923A-34	Sequence 34, Appl	667	34	36.6	1189	2	US-10-200-522-8	Sequence 8, Appli
595	34	36.6	1188	4	PCT-US95-05431-34	Sequence 34, Appl	668	34	36.6	1189	2	US-10-200-522-12	Sequence 12, Appl
596	34	36.6	1188	6	5254799-7	Patent No. 5254799	669	34	36.6	1189	2	US-10-200-522-59	Sequence 59, Appl
597	34	36.6	1189	1	US-07-828-788A-16	Sequence 16, Appl	670	34	36.6	1189	2	US-10-200-522-61	Sequence 61, Appl
598	34	36.6	1189	1	US-08-356-034-6	Sequence 6, Appli	671	34	36.6	1189	2	US-10-200-522-61	Sequence 61, Appl
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603	34	36.6	1189	1	US-08-980-071-8	Sequence 8, Appli	676	34	36.6	1190	1	US-08-732-495-12	Sequence 12, Appl
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605	34	36.6	1189	1	US-08-980-071-12	Sequence 12, Appl	678	34	36.6	1193	2	US-08-954-490-30	Sequence 30, Appl
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687	34	36.6	1193	2	US-09-873-873-30	Sequence 30, Appl	760	33	35.5	192	2	US-09-828-310-11	Sequence 11, Appl
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689	34	36.6	1193	2	US-09-636-746B-30	Sequence 30, Appl	762	33	35.5	193	2	US-09-540-236-2960	Sequence 2960, Ap
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693	34	36.6	1193	2	US-10-071-900-4	Sequence 4, Appli	766	33	35.5	215	2	US-09-270-767-62476	Sequence 62476, A
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707	33.5	36.0	838	2	US-09-315-794-52	Sequence 52, Appl	780	33	35.5	260	2	US-09-989-903-2	Sequence 2, Appli
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711	33.5	36.0	1942	2	US-09-949-016-8135	Sequence 8135, Ap	784	33	35.5	291	2	US-09-107-532A-4763	Sequence 4763, Ap
712	33	35.5	27	2	US-09-406-781-14	Sequence 14, Appl	785	33	35.5	294	2	US-09-949-016-6097	Sequence 6097, Ap
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715	33	35.5	28	2	US-09-880-132-11	Sequence 11, Appl	788	33	35.5	302	2	US-09-270-767-44347	Sequence 44347, A
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722	33	35.5	56	2	US-09-270-767-57450	Sequence 57450, A	795	33	35.5	329	2	US-09-107-433-4603	Sequence 4603, Ap
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724	33	35.5	73	2	US-09-949-016-9293	Sequence 9293, Ap	797	33	35.5	336	2	US-09-248-796A-20058	Sequence 20058, A
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1153	32	34.4	414	2	US-09-399-913-55	Sequence 55, Appli	1226	32	34.4	565	2	US-09-716-964B-154	Sequence 154, App
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RESULT 1

US-09-991-181-258
; Sequence 258, Application US/09991181
; Patent No. 6913919
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Garber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey J.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavins, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P27301C53
; CURRENT APPLICATION NUMBER: US/09/991,181
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607

ALIGNMENTS


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; PRIOR FILING DATE: 1998-07-09
Query Match      100.0%; Score 93; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 8.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C19
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Db 32 VSLVEEDQFSQNPISCPE 49
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 US-09-997-333-258
 ; Sequence 258, Application US/09997333
 ; Patent No. 6953836
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
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 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730P1C27
 ; CURRENT APPLICATION NUMBER: US/09/997,333
 ; CURRENT FILING DATE: 2001-11-15
 ; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
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; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 93; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. NO. 8.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSLVEEDQFSQNPISCFE 18
| | | | | | | | | | | | | | | | | |

Db 32 VSLVEEDQFSQNPISCFE 49
| | | | | | | | | | | | | | | | | |

RESULT 4
US-09-992-598-258
; Sequence 258, Application US/09992598

Patent No. 6956108
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: P2730FIC20
FILE REFERENCE: P2730FIC20
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1997-11-13
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PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429

; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435
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; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 93; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 8.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSLVEEDQFSQNPISCFE 18
Db 32 VSLVEEDQFSQNPISCFE 49

RESULT 5
US-08-118-441-29
; Sequence 29, Application US/08118441
; Patent No. 5578493
; GENERAL INFORMATION:
; APPLICANT: Gilliam, T. Conrad
; APPLICANT: Tanzi, Rudolph E.
; TITLE OF INVENTION: ISOLATION AND USES OF A WILSON'S DISEASE
; TITLE OF INVENTION: GENE
; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,441
; FILING DATE: June 17, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/44011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-118-441-29

Query Match 46.2%; Score 43; DB 1; Length 1110;
Best Local Similarity 69.2%; Pred. No. 1.2e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VSLVEEDQFSQNP 13
Db 590 VKLVEEAQMSKNP 602

RESULT 6
US-08-338-579A-29
; Sequence 29, Application US/08338579A
; Patent No. 6068975
; GENERAL INFORMATION:
; APPLICANT: Gilliam, T. Conrad
; APPLICANT: Tanzi, Rudolph E.
; TITLE OF INVENTION: ISOLATION AND USES OF A WILSON'S
; TITLE OF INVENTION: DISEASE GENE
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/338,579A
; FILING DATE: June 17, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/44011-A-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400

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; TELEFAX: (212) 391-0525
; TELEX:
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1110 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-338-579A-29

Query Match          46.2%; Score 43; DB 2; Length 1110;
Best Local Similarity 69.2%; Pred. No. 1.2e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 VSLVEEDQFSQNP 13
Db      590 VKLVEEAQMSKNP 602

RESULT 7
PCT-US94-09851-29
; Sequence 29, Application PC/TUS9409851
; GENERAL INFORMATION:
; APPLICANT: Gilliam, T. Conrad
; APPLICANT: Tanzi, Rudolph E.
; TITLE OF INVENTION: ISOLATION AND USES OF A WILSON'S
; TITLE OF INVENTION: DISEASE GENE
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09851
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/44011-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1110 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-09851-29

Query Match          46.2%; Score 43; DB 4; Length 1110;
Best Local Similarity 69.2%; Pred. No. 1.2e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 VSLVEEDQFSQNP 13
Db      590 VKLVEEAQMSKNP 602

RESULT 8
US-08-398-590A-40
; Sequence 40, Application US/08398590A
; Patent No. 5935811

; TELEFAX: (212) 391-0525
; TELEX:
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1110 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-398-590A-40

Query Match          45.2%; Score 42; DB 1; Length 676;
Best Local Similarity 53.3%; Pred. No. 98;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy      2 SLVEEDQFSQNPISC 16
Db      284 STAEEDGFSKGPIRC 298

RESULT 9
US-08-894-997-40
; Sequence 40, Application US/08894997A
; Patent No. 6270990
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J
; APPLICANT: Schoenherr, Christopher J
; TITLE OF INVENTION: NEURON-RESTRICTIVE SILENCER FACTOR
; FILE REFERENCE: 17810-502 NRSF
; CURRENT APPLICATION NUMBER: US/08/894,997A
; CURRENT FILING DATE: 1998-01-06
; EARLIER APPLICATION NUMBER: PCT/US96/02817
; EARLIER FILING DATE: 1996-03-01
; EARLIER APPLICATION NUMBER: 08/398,590
; EARLIER FILING DATE: 1995-03-03
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
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; LOCATION: (1)..(676)
; OTHER INFORMATION: Human NSRF (partial)
US-08-894-997-40

Query Match      45.2%; Score 42; DB 2; Length 676;
Best Local Similarity 53.3%; Pred. No. 98;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      2 SLVEEDQFSQNPISC 16
DB      284 STAEEDGFSKGPISC 298

RESULT 10
US-09-873-155A-40
; Sequence 40, Application US/09873155A
; Patent No. 6824774
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J
; APPLICANT: Schoenherr, Christopher J
; TITLE OF INVENTION: Antibodies That Bind Neuron Restrictive Silencer Factor
; FILE OF INVENTION: Proteins
; FILE REFERENCE: 17810-502 CIPCON
; CURRENT APPLICATION NUMBER: US/09/873,155A
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 08/894,997
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: PCT/US96/02817
; PRIOR FILING DATE: 1996-03-01
; PRIOR APPLICATION NUMBER: 08/398,590
; PRIOR FILING DATE: 1995-03-03
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (1)..(676)
; OTHER INFORMATION: Human NSRF (partial)
US-09-873-155A-40

Query Match      45.2%; Score 42; DB 2; Length 676;
Best Local Similarity 53.3%; Pred. No. 98;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      2 SLVEEDQFSQNPISC 16
DB      284 STAEEDGFSKGPISC 298

RESULT 11
US-08-894-997-50
; Sequence 50, Application US/08894997A
; Patent No. 6270990
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J
; APPLICANT: Schoenherr, Christopher J
; TITLE OF INVENTION: NEURON-RESTRICTIVE SILENCER FACTOR
; FILE REFERENCE: 17810-502 NSRF
; CURRENT APPLICATION NUMBER: US/08/894,997A
; CURRENT FILING DATE: 1998-01-06
; EARLIER APPLICATION NUMBER: PCT/US96/02817
; EARLIER FILING DATE: 1996-03-01
; EARLIER APPLICATION NUMBER: 08/398,590
; EARLIER FILING DATE: 1995-03-03
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 976
; TYPE: PRT
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(976)
; OTHER INFORMATION: Human NSRF
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (1)..(976)
; OTHER INFORMATION: Human NSRF
US-08-894-997-50

Query Match      45.2%; Score 42; DB 2; Length 976;
Best Local Similarity 53.3%; Pred. No. 1.5e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      2 SLVEEDQFSQNPISC 16
DB      199 SPAEEGEGFSKGPISC 213

RESULT 12
US-09-873-155A-50
; Sequence 50, Application US/09873155A
; Patent No. 6824774
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J
; APPLICANT: Schoenherr, Christopher J
; TITLE OF INVENTION: Antibodies That Bind Neuron Restrictive Silencer Factor
; FILE OF INVENTION: Proteins
; FILE REFERENCE: 17810-502 CIPCON
; CURRENT APPLICATION NUMBER: US/09/873,155A
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 08/894,997
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: PCT/US96/02817
; PRIOR FILING DATE: 1996-03-01
; PRIOR APPLICATION NUMBER: 08/398,590
; PRIOR FILING DATE: 1995-03-03
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 976
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(976)
; OTHER INFORMATION: Human NSRF
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (1)..(976)
; OTHER INFORMATION: Human NSRF
US-09-873-155A-50

Query Match      45.2%; Score 42; DB 2; Length 976;
Best Local Similarity 53.3%; Pred. No. 1.5e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      2 SLVEEDQFSQNPISC 16
DB      199 SPAEEGEGFSKGPISC 213

RESULT 13
US-09-949-016-8616
; Sequence 8616, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
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;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 8616
;; LENGTH: 1147
;; TYPE: PRT
;; ORGANISM: Human
US-09-949-016-8616

Query Match 45.2%; Score 42; DB 2; Length 1147;
Best Local Similarity 53.3%; Pred. No. 1.8e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 2 SLVEEDQFSQNPISC 16
Db 254 STAEEDFSKQPIRC 268

RESULT 14
US-08-231-193A-11
; Sequence 11, Application US/08231193A
; Patent No. 5849895
; GENERAL INFORMATION:
; APPLICANT: Daggett, Lorrie P.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lu, Chin-Chun
; TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
; TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,193A
; FILING DATE: 20-APR-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/052,459
; FILING DATE: 20-APR-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1464 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-231-193A-11

Query Match 45.2%; Score 42; DB 1; Length 1464;
Best Local Similarity 46.7%; Pred. No. 2.3e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VSLVEEDQFSQNPIS 15
Db 1018 VDSIRQDSLSONPVS 1032

RESULT 15
US-08-486-273A-11
; Sequence 11, Application US/08486273A
; Patent No. 5985586
; GENERAL INFORMATION:
; APPLICANT: Daggett, Lorrie P.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lu, Chin-Chun
; TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA
; TITLE OF INVENTION: ENCODING SAME AND USES THEREFOR
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,273A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/231,193
; FILING DATE: 20-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9383B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1464 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-486-273A-11

Query Match 45.2%; Score 42; DB 1; Length 1464;
Best Local Similarity 46.7%; Pred. No. 2.3e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

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Db 1018 VDSIRQDSLSONPVS 1032

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Job time : 26.4898 secs

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OM protein - protein search, using sw model

Run on: December 22, 2005, 03:01:15 ; Search time 21.6735 Seconds
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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Listing first 1500 summaries

Database : Published Applications AA.Main.*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1159	36	38.7	281	4	US-10-151-882-41	Sequence 41, Appl	1232	36	38.7	344	3	US-09-764-853-812	Sequence 812, App
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1194	36	38.7	281	5	US-10-986-349-66	Sequence 66, Appl	1267	36	38.7	473	4	US-10-051-874-48	Sequence 48, Appl
1195	36	38.7	281	5	US-10-986-376-66	Sequence 66, Appl	1268	36	38.7	473	4	US-10-250-533-4	Sequence 4, Appl
1196	36	38.7	281	6	US-11-019-829-113	Sequence 113, App	1269	36	38.7	478	3	US-09-867-521-2	Sequence 2, Appl
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1198	36	38.7	281	6	US-11-088-459-2	Sequence 2, Appl	1271	36	38.7	490	4	US-10-318-855-28	Sequence 28, Appl
1199	36	38.7	281	6	US-11-142-736-17	Sequence 17, Appl	1272	36	38.7	513	4	US-10-369-493-2090	Sequence 2090, App
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Sequence 2139, Ap

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OM protein - protein search, using sw model

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(without alignments)
77.661 Million cell updates/sec

Perfect score: 93
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 53982 seqs, 7132107 residues

Total number of hits satisfying chosen parameters: 53982

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1500 summaries

Database : Published Applications AA New:

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	39	41.9	1001	6	US-10-467-562B-81
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4	36	38.7	266	7	US-11-082-544-10
5	36	38.7	281	6	US-10-821-234-1288
6	36	38.7	281	7	US-11-077-272-2
7	36	38.7	335	6	US-10-467-557-3818
8	36	38.7	352	6	US-10-793-626-216
9	36	38.7	573	6	US-10-467-657-684
10	36	38.7	646	6	US-10-793-626-676
11	36	38.7	892	7	US-11-082-389-396
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17	35	37.6	902	7	US-11-144-987-6
18	35	37.6	902	7	US-11-144-987-8
19	35	37.6	902	7	US-11-144-987-12
20	35	37.6	902	7	US-11-144-987-14
21	35	37.6	910	7	US-11-144-987-2
22	34.5	37.1	463	7	US-11-000-463-872
23	34	36.6	188	6	US-10-793-626-152
24	34	36.6	383	7	US-11-129-143-76
25	34	36.6	388	6	US-10-467-657-786
26	34	36.6	449	7	US-11-112-882-71
27	34	36.6	764	7	US-11-022-562-209
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552	27	29.0	273	6	US-10-353-783-54	Sequence 54, Appl	627	27	29.0	751	6	US-11-012-762-26	Sequence 26, Appl
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557	27	29.0	301	7	US-11-055-822-1062	Sequence 1062, App	631	27	29.0	771	7	US-11-147-047-34	Sequence 34, Appl
558	27	29.0	307	6	US-10-793-626-522	Sequence 522, App	632	27	29.0	799	7	US-11-074-176-348	Sequence 348, App
559	27	29.0	315	6	US-10-467-657-7848	Sequence 7848, App	633	27	29.0	805	7	US-11-074-176-172	Sequence 172, App
560	27	29.0	317	6	US-10-821-234-1529	Sequence 1529, App	634	27	29.0	829	7	US-11-090-739-122	Sequence 122, App
561	27	29.0	319	6	US-10-467-657-3252	Sequence 3252, App	635	27	29.0	839	7	US-11-186-284-18	Sequence 18, Appl
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579	27	29.											

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699	26.5	28.5	1142	7	US-11-109-156-22	Sequence 22, Appl	773	26	28.0	302	6	US-10-793-626-1552	Sequence 1552, Ap
700	26.5	28.5	1210	7	US-11-108-172-692	Sequence 692, Appl	774	26	28.0	303	6	US-10-770-726-52	Sequence 52, Appl
701	26.5	28.5	1548	7	US-11-108-172-1095	Sequence 1095, Ap	775	26	28.0	304	6	US-10-467-657-506	Sequence 506, App
702	26.5	28.5	1554	7	US-11-186-284-93	Sequence 93, Appl	776	26	28.0	305	6	US-11-113-424-58	Sequence 58, Appl
703	26	28.0	13	6	US-10-511-559-410	Sequence 410, App	777	26	28.0	306	6	US-10-467-657-7672	Sequence 7672, Ap
704	26	28.0	31	6	US-10-467-657-8808	Sequence 808, Ap	778	26	28.0	308	6	US-11-055-822-822	Sequence 822, App
705	26	28.0	42	6	US-10-656-894-6	Sequence 6, Appl	779	26	28.0	312	6	US-10-793-626-2186	Sequence 2186, Ap
706	26	28.0	42	6	US-10-656-894-22	Sequence 22, Appl	780	26	28.0	314	6	US-10-793-626-2552	Sequence 2552, Ap
707	26	28.0	42	6	US-10-656-894-23	Sequence 23, Appl	781	26	28.0	314	7	US-11-129-143-86	Sequence 86, Appl
708	26	28.0	43	6	US-10-467-657-2656	Sequence 2656, Ap	782	26	28.0	319	6	US-10-793-626-1040	Sequence 1040, Ap
709	26	28.0	45	7	US-11-198-847-280	Sequence 280, App	783	26	28.0	332	7	US-11-113-424-55	Sequence 55, Appl
710	26	28.0	46	6	US-10-467-657-4096	Sequence 4096, Ap	784	26	28.0	334	7	US-11-055-822-24	Sequence 24, Appl
711	26	28.0	54	6	US-10-467-657-7188	Sequence 718, Ap	785	26	28.0	341	7	US-11-069-642-4	Sequence 4, Appl
712	26	28.0	57	7	US-11-082-389-370	Sequence 370, App	786	26	28.0	343	7	US-11-000-463-936	Sequence 936, App
713	26	28.0	60	6	US-10-467-657-6136	Sequence 6136, Ap	788	26	28.0	349	6	US-10-485-517-417	Sequence 417, App
714	26	28.0	69	6	US-10-467-657-1680	Sequence 1680, Ap	789	26	28.0	353	6	US-10-667-295-113	Sequence 113, App
715	26	28.0	71	6	US-10-467-657-5618	Sequence 5618, Ap	790	26	28.0	354	7	US-11-064-769-4	Sequence 4, Appl
716	26	28.0	77	6	US-10-467-657-3496	Sequence 3496, Ap	791	26	28.0	354	7	US-11-064-774A-119	Sequence 119, App
717	26	28.0	77	7	US-11-006-119-23	Sequence 23, Appl	792	26	28.0	354	7	US-11-090-439-60	Sequence 60, Appl
718	26	28.0	79	7	US-11-077-386-21	Sequence 21, Appl	793	26	28.0	354	7	US-11-090-439-62	Sequence 62, Appl
719	26	28.0	95	7	US-11-198-847-89	Sequence 89, Appl	794	26	28.0	356	7	US-11-012-762-46	Sequence 46, Appl
720	26	28.0	98	6	US-10-467-657-6988	Sequence 6988, Ap	795	26	28.0	358	6	US-10-793-626-2136	Sequence 2136, Ap
721	26	28.0	105	6	US-10-467-657-1678	Sequence 1678, Ap	796	26	28.0	365	6	US-10-793-626-470	Sequence 470, App
722	26	28.0	107	6	US-10-467-657-3832	Sequence 3832, Ap	797	26	28.0	368	7	US-11-053-185-12	Sequence 12, Appl
723	26	28.0	116	6	US-10-793-626-136	Sequence 136, App	798	26	28.0	369	7	US-11-055-822-116	Sequence 116, App
724	26	28.0	123	6	US-10-467-657-4690	Sequence 4690, Ap	799	26	28.0	369	7	US-11-055-822-486	Sequence 486, App
725	26	28.0	124	6	US-10-467-657-294	Sequence 294, App	800	26	28.0	373	7	US-11-149-349-2	Sequence 2, Appl
726	26	28.0	124	6	US-10-467-657-5944	Sequence 5944, Ap	801	26	28.0	376	7	US-11-055-822-152	Sequence 152, App
727	26	28.0	128	6	US-10-467-657-5268	Sequence 5268, Ap	802	26	28.0	380	6	US-10-793-626-1402	Sequence 1402, App
728	26	28.0	135	6	US-10-467-657-5364	Sequence 5364, Ap	803	26	28.0	386	7	US-11-012-762-44	Sequence 44, Appl
729	26	28.0	135	6	US-10-467-657-8348	Sequence 8348, Ap	804	26	28.0	387	7	US-11-060-008-10	Sequence 10, Appl
730	26	28.0	136	6	US-10-793-626-1852	Sequence 1852, Ap	805	26	28.0	389	6	US-10-979-821-2	Sequence 2, Appl
731	26	28.0	156	6	US-10-467-657-2864	Sequence 2864, Ap	806	26	28.0	389	7	US-11-012-762-72	Sequence 72, Appl
732	26	28.0	160	6	US-10-846-172A-10	Sequence 10, Appl	807	26	28.0	391	6	US-10-821-234-1487	Sequence 1487, Ap
733	26	28.0	163	7	US-11-102-240-160	Sequence 160, App	808	26	28.0	391	7	US-11-105-172-4	Sequence 4, Appl
734	26	28.0	165	6	US-10-454-437-58	Sequence 58, Appl	809	26	28.0	394	6	US-10-793-626-552	Sequence 552, App
735	26	28.0	174	6	US-10-485-517-301	Sequence 301, App	810	26	28.0	394	6	US-10-873-528-41	Sequence 41, Appl
736	26	28.0	177	7	US-11-088-717-8	Sequence 8, Appl	811	26	28.0	401	6	US-10-793-626-836	Sequence 836, App
737	26	28.0	178	7	US-11-055-822-118	Sequence 118, App	812	26	28.0	404	6	US-10-667-295-112	Sequence 112, App
738	26	28.0	178	7	US-11-055-822-488	Sequence 488, App	813	26	28.0	413	6	US-10-967-648A-8	Sequence 8, Appl
739	26	28.0	181	7	US-11-000-463-890	Sequence 890, App	814	26	28.0	421	6	US-11-082-389-70	Sequence 70, Appl
740	26	28.0	182	7	US-11-000-463-418	Sequence 418, App	815	26	28.0	422	6	US-10-821-234-1313	Sequence 1313, Ap
741	26	28.0	195	6	US-10-467-657-8594	Sequence 8594, Ap	816	26	28.0	422	7	US-11-186-284-75	Sequence 75, Appl
742	26	28.0	195	7	US-11-055-822-914	Sequence 914, App	817	26	28.0	423	7	US-11-074-176-4	Sequence 4, Appl
743	26	28.0	196	6	US-10-467-657-8288	Sequence 8288, Ap	818	26	28.0	428	7	US-11-055-822-606	Sequence 606, App
744	26	28.0	200	6	US-10-118-590-32	Sequence 32, Appl	819	26	28.0	430	7	US-11-055-822-412	Sequence 412, App
745	26	28.0	206	6	US-10-467-657-2550	Sequence 2550, Ap	820	26	28.0	431	6	US-10-467-657-202	Sequence 202, App
746	26	28.0	216	6	US-10-118-590-2	Sequence 2, Appl	821	26	28.0	431	6	US-10-467-657-6310	Sequence 6310, Ap
747	26	28.0	217	7	US-11-170-653-48	Sequence 48, Appl	822	26	28.0	437	7	US-11-088-634A-4	Sequence 4, Appl
748	26	28.0	220	7	US-11-082-389-72	Sequence 72, Appl	823	26	28.0	440	6	US-10-606-302-9	Sequence 9, Appl
749	26	28.0	225	6	US-10-793-626-1452	Sequence 1452, Ap	824	26	28.0	442	7	US-11-055-822-402	Sequence 402, App
750	26	28.0	226	6	US-10-467-657-2162	Sequence 2162, Ap	825	26	28.0	445	6	US-10-873-528-30	Sequence 30, Appl
751	26	28.0	232	6	US-10-467-657-4338	Sequence 4338, Ap	826	26	28.0	446	6	US-10-667-295-111	Sequence 111, App
752	26	28.0	234	7	US-11-102-240-14	Sequence 14, Appl	827	26	28.0	448	6	US-10-467-657-4416	Sequence 4416, Ap
753	26	28.0	236	6	US-10-878-556A-96	Sequence 96, Appl	828	26	28.0	449	7	US-11-071-062-1	Sequence 1, Appl
754	26	28.0	237	6	US-10-793-626-162	Sequence 162, App	829	26	28.0	449	7	US-11-196-459-1	Sequence 1, Appl
755	26	28.0	244	6	US-10-434-437-238	Sequence 238, App	830	26	28.0	449	7	US-11-196-459-2	Sequence 2, Appl
756	26	28.0	244	6	US-10-454-437-240	Sequence 240, App	831	26	28.0	450	7	US-11-074-176-212	Sequence 212, App
757	26	28.0	251	7	US-11-054-515-151	Sequence 151, App	832	26	28.0	461	7	US-11-054-385-6	Sequence 6, Appl
758	26	28.0	252	6	US-10-510-386-104	Sequence 104, App	833	26	28.0	464	6	US-10-763-712A-46	Sequence 46, Appl
759	26	28.0	255	7	US-11-054-515-863	Sequence 863, App	834	26	28.0	468	6	US-10-763-712A-3	Sequence 3, Appl
760	26	28.0	255	7	US-11-054-515-866	Sequence 866, App	835	26	28.0	481	7	US-11-090-439-16	Sequence 16, Appl
761	26	28.0	256	6	US-10-118-590-36	Sequence 36, Appl	836	26	28.0	482	6	US-10-878-556A-30	Sequence 30, Appl
762	26	28.0	257	6	US-10-663-794-2	Sequence 2, Appl	837	26	28.0	482	6	US-10-878-556A-139	Sequence 139, App
763	26	28.0	259	7	US-11-182-946-2	Sequence 2, Appl	838	26	28.0	487	7	US-11-113-424-56	Sequence 56, Appl
764	26	28.0	266	7	US-11-000-463-464	Sequence 464, App	839	26	28.0	487	7	US-11-113-424-57	Sequence 57, Appl
765	26	28.0	267	6	US-10-467-657-5806	Sequence 5806, Ap	840	26	28.0	491	7	US-11-053-185-22	Sequence 22, Appl
766	26	28.0	270	6	US-10-467-657-5806	Sequence 85, Appl	841	26	28.0	492	6	US-10-148-606-1	Sequence 1, Appl
767	26	28.0	277	6	US-10-667-295-85	Sequence 310, App	842	26	28.0	500	6	US-10-467-657-48	Sequence 48, Appl
768	26	28.0	280	6	US-11-000-463-310	Sequence 1806, Ap	843	26	28.0	500	7	US-11-087-100-24	Sequence 24, Appl
769	26	28.0	280	6	US-10-467-657-1806	Sequence 1118, Ap	844	26	28.0	500	7	US-11-087-084-24	Sequence 24, Appl
770	26	28.0	288	6	US-10-793-626-1118	Sequence 316, App	845	26	28.0	500	7	US-11-087-085-24	Sequence 24, Appl
771	26	28.0	292	7	US-11-194-246-316								

846	26	28.0	501	6	US-10-467-657-7682	Sequence 7682, Ap	922	26	28.0	1142	7	US-11-044-051-73	Sequence 73, Appl
847	26	28.0	509	6	US-10-508-263-18	Sequence 18, Appl	923	26	28.0	1145	6	US-10-793-626-1432	Sequence 1432, Ap
849	26	28.0	513	6	US-11-102-240-124	Sequence 124, App	924	26	28.0	1163	7	US-11-044-899-2	Sequence 2, Appli
850	26	28.0	530	6	US-11-088-634A-2	Sequence 2, Appli	925	26	28.0	1163	7	US-11-044-899-30	Sequence 30, Appl
851	26	28.0	537	6	US-10-719-311-10	Sequence 10, Appl	926	26	28.0	1167	7	US-11-097-125-2	Sequence 2, Appli
852	26	28.0	539	6	US-10-467-657-7736	Sequence 7736, Ap	927	26	28.0	1176	6	US-10-821-234-897	Sequence 897, App
853	26	28.0	544	6	US-10-719-311-178	Sequence 18, Appl	928	26	28.0	1176	7	US-11-044-899-29	Sequence 29, Appl
854	26	28.0	545	6	US-11-102-240-110	Sequence 110, App	929	26	28.0	1179	7	US-11-097-125-1	Sequence 1, Appli
855	26	28.0	548	6	US-10-467-657-7704	Sequence 7704, Ap	930	26	28.0	1186	7	US-11-053-100-46	Sequence 46, Appl
856	26	28.0	548	6	US-11-119-769-3	Sequence 3, Appli	931	26	28.0	1186	6	US-10-995-561-921	Sequence 921, App
857	26	28.0	550	6	US-10-467-657-234	Sequence 234, App	932	26	28.0	1234	6	US-10-995-561-870	Sequence 870, App
858	26	28.0	550	6	US-10-467-657-924	Sequence 924, App	933	26	28.0	1236	6	US-11-080-991-68	Sequence 68, Appl
859	26	28.0	593	7	US-11-194-246-317	Sequence 317, App	934	26	28.0	1238	7	US-11-078-735-21	Sequence 21, Appl
860	26	28.0	596	7	US-11-090-878-22	Sequence 22, Appl	935	26	28.0	1255	7	US-11-022-562-235	Sequence 235, App
861	26	28.0	598	6	US-10-719-311-16	Sequence 16, Appl	936	26	28.0	1360	7	US-11-188-743-22	Sequence 22, Appl
862	26	28.0	598	7	US-11-090-878-8	Sequence 8, Appli	937	26	28.0	1365	6	US-10-995-561-867	Sequence 867, App
863	26	28.0	598	7	US-11-090-878-10	Sequence 10, Appl	938	26	28.0	1366	6	US-10-995-561-868	Sequence 868, App
864	26	28.0	598	7	US-11-090-878-12	Sequence 12, Appl	939	26	28.0	1400	6	US-10-821-234-1045	Sequence 1045, Ap
865	26	28.0	598	7	US-11-055-822-820	Sequence 820, App	940	26	28.0	1402	6	US-10-971-982-2	Sequence 2, Appli
866	26	28.0	600	6	US-10-467-657-4866	Sequence 4866, Ap	941	26	28.0	1411	6	US-10-995-561-869	Sequence 869, App
867	26	28.0	600	6	US-10-606-302-3	Sequence 3, Appli	942	26	28.0	1663	6	US-10-982-545-6	Sequence 6, Appli
868	26	28.0	616	6	US-10-982-545-5	Sequence 5, Appli	943	26	28.0	1960	7	US-11-069-834-48	Sequence 48, Appl
869	26	28.0	616	7	US-11-090-878-20	Sequence 20, Appl	944	26	28.0	2059	7	US-11-087-100-4	Sequence 4, Appli
870	26	28.0	617	7	US-11-090-878-18	Sequence 18, Appl	945	26	28.0	2059	7	US-11-087-084-4	Sequence 4, Appli
871	26	28.0	621	7	US-11-184-380-26	Sequence 26, Appl	946	26	28.0	2059	7	US-11-087-085-4	Sequence 4, Appli
872	26	28.0	623	6	US-10-719-311-2	Sequence 2, Appli	947	26	28.0	2087	7	US-11-075-185-28	Sequence 28, Appl
873	26	28.0	623	6	US-10-719-311-11	Sequence 11, Appl	948	26	28.0	2096	6	US-10-995-561-606	Sequence 606, App
874	26	28.0	624	7	US-11-090-878-2	Sequence 2, Appli	949	26	28.0	2107	6	US-10-995-561-827	Sequence 827, App
875	26	28.0	624	7	US-11-090-878-4	Sequence 4, Appli	950	26	28.0	2261	6	US-10-995-561-600	Sequence 600, App
876	26	28.0	624	7	US-11-090-878-6	Sequence 6, Appli	951	26	28.0	2351	6	US-10-995-561-608	Sequence 608, App
877	26	28.0	633	7	US-11-063-343-26	Sequence 26, Appl	952	26	28.0	2480	6	US-10-995-561-825	Sequence 825, App
878	26	28.0	637	7	US-11-090-878-24	Sequence 24, Appl	953	26	28.0	2725	7	US-11-113-424-52	Sequence 52, Appl
879	26	28.0	642	6	US-10-467-657-5900	Sequence 5900, Ap	954	26	28.0	3116	6	US-10-995-561-826	Sequence 826, App
881	26	28.0	653	7	US-11-135-855-25	Sequence 25, Appl	955	26	28.0	4374	7	US-11-128-572-2	Sequence 2, Appli
882	26	28.0	657	7	US-11-110-082-37	Sequence 37, Appl	956	25.5	27.4	33	7	US-11-121-301-48	Sequence 48, Appl
883	26	28.0	659	6	US-10-661-966-14	Sequence 14, Appl	957	25.5	27.4	143	6	US-10-995-951A-30	Sequence 30, Appl
885	26	28.0	695	7	US-11-038-284-34	Sequence 34, Appl	958	25.5	27.4	186	6	US-11-067-425A-65	Sequence 65, Appl
886	26	28.0	696	7	US-11-029-003-8	Sequence 8, Appli	959	25.5	27.4	203	6	US-10-467-657-5598	Sequence 5598, Ap
887	26	28.0	715	7	US-11-089-551A-47	Sequence 47, Appl	960	25.5	27.4	286	6	US-10-467-657-8012	Sequence 8012, Ap
888	26	28.0	718	7	US-11-074-176-306	Sequence 306, App	961	25.5	27.4	213	6	US-11-102-621-135	Sequence 135, App
889	26	28.0	723	7	US-11-074-176-18	Sequence 18, Appl	962	25.5	27.4	223	6	US-10-793-626-2824	Sequence 2824, Ap
890	26	28.0	732	7	US-11-078-189-14	Sequence 14, Appl	963	25.5	27.4	236	6	US-11-140-965-4	Sequence 4, Appli
891	26	28.0	734	6	US-10-719-311-4	Sequence 4, Appli	964	25.5	27.4	263	6	US-10-873-528-68	Sequence 68, Appl
892	26	28.0	736	6	US-11-053-100-45	Sequence 45, Appl	965	25.5	27.4	283	7	US-11-080-991-80	Sequence 80, Appl
893	26	28.0	745	7	US-11-147-109-8	Sequence 8, Appli	966	25.5	27.4	332	7	US-11-102-240-10	Sequence 10, Appl
894	26	28.0	756	7	US-11-113-837-20	Sequence 20, Appl	967	25.5	27.4	331	7	US-11-105-268-59	Sequence 59, Appl
895	26	28.0	762	6	US-11-055-822-912	Sequence 912, App	968	25.5	27.4	364	7	US-11-067-884-2	Sequence 2, Appli
896	26	28.0	767	6	US-10-467-962B-91	Sequence 91, Appl	969	25.5	27.4	368	6	US-10-689-742-100	Sequence 100, App
897	26	28.0	779	7	US-11-128-420-12	Sequence 12, Appl	970	25.5	27.4	384	7	US-11-120-543-2	Sequence 2, Appli
898	26	28.0	786	7	US-11-070-627-9	Sequence 9, Appli	971	25.5	27.4	384	7	US-11-120-543-4	Sequence 4, Appli
899	26	28.0	794	6	US-10-793-626-1050	Sequence 1050, Ap	972	25.5	27.4	384	7	US-11-120-543-6	Sequence 6, Appli
900	26	28.0	803	6	US-10-821-234-1643	Sequence 1643, Ap	973	25.5	27.4	384	7	US-11-120-543-8	Sequence 8, Appli
901	26	28.0	825	6	US-10-995-561-679	Sequence 679, App	974	25.5	27.4	384	7	US-11-120-543-14	Sequence 14, Appl
902	26	28.0	832	7	US-11-108-172-1081	Sequence 1081, Ap	975	25.5	27.4	384	7	US-11-120-543-22	Sequence 22, Appl
903	26	28.0	843	6	US-10-645-441-8	Sequence 8, Appli	976	25.5	27.4	396	7	US-11-120-543-10	Sequence 10, Appl
904	26	28.0	849	6	US-10-467-962B-53	Sequence 53, Appl	977	25.5	27.4	400	7	US-11-120-543-12	Sequence 12, Appl
905	26	28.0	852	7	US-11-104-923A-5	Sequence 5, Appli	978	25.5	27.4	416	6	US-10-467-657-5284	Sequence 5284, Ap
906	26	28.0	879	7	US-11-022-562-340	Sequence 340, App	979	25.5	27.4	421	7	US-11-120-543-16	Sequence 16, Appl
907	26	28.0	902	7	US-11-057-058-64	Sequence 64, Appl	980	25.5	27.4	422	7	US-11-120-543-20	Sequence 20, Appl
908	26	28.0	943	6	US-10-475-204-34	Sequence 34, Appl	981	25.5	27.4	441	6	US-10-821-234-1668	Sequence 1668, Ap
909	26	28.0	958	7	US-11-108-172-1087	Sequence 1087, Ap	982	25.5	27.4	477	6	US-10-763-712A-57	Sequence 57, Appl
910	26	28.0	963	6	US-10-467-962B-2	Sequence 2, Appli	983	25.5	27.4	477	6	US-10-467-657-4870	Sequence 4870, Ap
911	26	28.0	977	7	US-11-093-274-39	Sequence 39, Appl	986	25.5	27.4	521	7	US-11-109-156-34	Sequence 34, Appl
912	26	28.0	1005	7	US-11-113-424-63	Sequence 63, Appl	987	25.5	27.4	521	7	US-11-105-268-58	Sequence 58, Appl
913	26	28.0	1023	6	US-10-995-561-968	Sequence 968, App	988	25.5	27.4	532	6	US-10-857-780-18	Sequence 18, Appl
914	26	28.0	1032	6	US-10-835-475-1	Sequence 1, Appli	989	25.5	27.4	532	7	US-10-995-561-897	Sequence 897, App
915	26	28.0	1032	6	US-11-014-367-1	Sequence 1, Appli	990	25.5	27.4	532	7	US-11-104-812-2	Sequence 2, Appli
916	26	28.0	1062	7	US-11-137-465-43	Sequence 43, Appl	991	25.5	27.4	532	7	US-11-105-279-2	Sequence 2, Appli
917	26	28.0	1076	6	US-11-089-551A-23	Sequence 23, Appl	992	25.5	27.4	532	7	US-11-107-028-22	Sequence 22, Appl
918	26	28.0	1076	6	US-10-467-657-5708	Sequence 5708, Ap	993	25.5	27.4	546	6	US-10-661-966-18	Sequence 18, Appl
919	26	28.0	1087	7	US-11-117-169-10	Sequence 10, Appl	994	25.5	27.4	712	6	US-10-995-561-984	Sequence 984, App
920	26	28.0	1092	6	US-10-821-234-999	Sequence 999, App	995	25.5	27.4	752	6	US-10-793-626-1036	Sequence 1036, App
921	26	28.0	1124	7	US-11-195-197-9	Sequence 9, Appli	996	25.5	27.4	769	6	US-10-995-561-985	Sequence 985, App

997	25.5	27.4	769	6	US-10-995-561-986	Sequence 986, App	1070	25	26.9	168	6	US-10-467-657-268	Sequence 268, App
998	25.5	27.4	769	7	US-11-107-028-5	Sequence 5, Appli	1071	25	26.9	168	6	US-10-467-657-3658	Sequence 3658, Ap
999	25.5	27.4	858	6	US-10-878-556A-113	Sequence 113, App	1072	25	26.9	173	6	US-10-984-376-13	Sequence 13, Appl
1000	25.5	27.4	1206	6	US-10-995-561-709	Sequence 709, App	1073	25	26.9	174	6	US-10-984-376-14	Sequence 14, Appl
1001	25.5	27.4	1907	7	US-11-039-398-25	Sequence 45, Appl	1074	25	26.9	177	6	US-10-980-388-94	Sequence 94, Appl
1002	25.5	27.4	7968	7	US-11-143-980-49	Sequence 49, Appl	1075	25	26.9	181	6	US-10-467-657-278	Sequence 278, App
1003	25	26.9	14	7	US-11-054-515-2506	Sequence 2506, Ap	1076	25	26.9	181	6	US-10-467-657-4306	Sequence 4306, Ap
1004	25	26.9	15	7	US-11-045-024-13379	Sequence 13379, A	1077	25	26.9	181	6	US-10-746-959C-10	Sequence 10, Appl
1005	25	26.9	19	6	US-10-503-575-155	Sequence 155, App	1078	25	26.9	182	6	US-10-467-657-2626	Sequence 2626, Ap
1006	25	26.9	25	6	US-10-986-501-238	Sequence 238, App	1079	25	26.9	189	6	US-10-467-657-2688	Sequence 2688, Ap
1007	25	26.9	27	6	US-10-723-207-66	Sequence 66, Appl	1080	25	26.9	190	7	US-11-055-822-538	Sequence 538, App
1008	25	26.9	42	6	US-10-467-657-1670	Sequence 1670, Ap	1081	25	26.9	192	6	US-10-821-234-1299	Sequence 1299, Ap
1009	25	26.9	42	6	US-10-656-894-7	Sequence 7, Appli	1082	25	26.9	197	6	US-11-013-247A-10	Sequence 10, Appl
1010	25	26.9	42	6	US-10-656-894-8	Sequence 8, Appli	1083	25	26.9	199	6	US-10-647-072-2	Sequence 2, Appli
1011	25	26.9	42	6	US-10-656-894-9	Sequence 9, Appli	1084	25	26.9	206	7	US-11-036-797-34	Sequence 34, Appl
1012	25	26.9	42	6	US-10-656-894-10	Sequence 10, Appl	1085	25	26.9	208	6	US-10-467-657-3098	Sequence 3098, Ap
1013	25	26.9	42	6	US-10-656-894-11	Sequence 11, Appl	1086	25	26.9	210	6	US-10-454-437-302	Sequence 302, App
1014	25	26.9	42	6	US-10-656-894-12	Sequence 12, Appl	1087	25	26.9	210	7	US-11-055-822-1026	Sequence 1026, Ap
1015	25	26.9	42	6	US-10-656-894-13	Sequence 13, Appl	1088	25	26.9	219	6	US-10-793-626-22	Sequence 22, Appl
1016	25	26.9	42	6	US-10-656-894-14	Sequence 14, Appl	1089	25	26.9	223	6	US-10-793-626-2884	Sequence 2884, Ap
1017	25	26.9	48	6	US-10-467-657-8368	Sequence 8368, Ap	1091	25	26.9	225	6	US-10-485-517-143	Sequence 143, App
1018	25	26.9	53	6	US-10-656-894-21	Sequence 21, Appl	1092	25	26.9	227	6	US-10-948-429A-6	Sequence 6, Appli
1019	25	26.9	54	6	US-10-656-894-17	Sequence 17, Appl	1093	25	26.9	227	7	US-11-000-463-301	Sequence 301, App
1020	25	26.9	64	6	US-10-467-657-3224	Sequence 3224, Ap	1094	25	26.9	232	6	US-10-793-626-2194	Sequence 2194, Ap
1021	25	26.9	65	6	US-10-467-657-5106	Sequence 5106, Ap	1095	25	26.9	239	7	US-11-170-653-40	Sequence 40, Appl
1022	25	26.9	67	6	US-10-467-657-8858	Sequence 8858, Ap	1096	25	26.9	241	6	US-10-987-663-8	Sequence 8, Appli
1023	25	26.9	75	6	US-10-667-295-53	Sequence 53, Appl	1097	25	26.9	244	6	US-10-467-657-3662	Sequence 3662, Ap
1024	25	26.9	79	6	US-10-467-657-1888	Sequence 1888, Ap	1098	25	26.9	244	6	US-10-467-657-6684	Sequence 6684, Ap
1025	25	26.9	80	6	US-10-952-535A-27	Sequence 27, Appl	1099	25	26.9	247	7	US-11-054-515-2124	Sequence 2124, Ap
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1027	25	26.9	83	6	US-10-746-959C-2	Sequence 2, Appli	1101	25	26.9	249	7	US-11-054-515-632	Sequence 632, App
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1031	25	26.9	94	7	US-11-126-126-14	Sequence 14, Appl	1105	25	26.9	284	6	US-10-793-626-1112	Sequence 1112, Ap
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1033	25	26.9	101	7	US-11-126-126-12	Sequence 12, Appl	1107	25	26.9	264	7	US-11-053-185-10	Sequence 10, Appl
1034	25	26.9	102	6	US-10-467-657-5146	Sequence 5146, Ap	1108	25	26.9	270	6	US-10-821-234-1348	Sequence 1348, Ap
1035	25	26.9	103	7	US-11-053-076-103	Sequence 109, App	1109	25	26.9	277	6	US-10-878-556A-4	Sequence 4, Appli
1036	25	26.9	104	7	US-11-000-463-939	Sequence 939, App	1110	25	26.9	286	7	US-11-089-551A-27	Sequence 27, Appl
1037	25	26.9	106	7	US-11-126-126-8	Sequence 4, Appli	1111	25	26.9	287	6	US-10-793-626-468	Sequence 468, App
1038	25	26.9	106	7	US-11-126-126-8	Sequence 8, Appli	1112	25	26.9	289	6	US-10-987-663-2	Sequence 2, Appli
1039	25	26.9	106	7	US-11-000-463-467	Sequence 467, App	1113	25	26.9	290	6	US-10-793-626-214	Sequence 214, App
1040	25	26.9	109	7	US-11-126-126-6	Sequence 6, Appli	1114	25	26.9	290	6	US-10-793-626-758	Sequence 758, App
1041	25	26.9	122	6	US-10-467-657-4042	Sequence 4042, Ap	1115	25	26.9	291	6	US-10-793-626-1690	Sequence 1690, Ap
1042	25	26.9	123	6	US-10-467-657-4920	Sequence 4920, Ap	1116	25	26.9	295	6	US-10-987-663-10	Sequence 10, Appl
1043	25	26.9	125	6	US-10-986-501-198	Sequence 198, App	1117	25	26.9	286	7	US-11-074-176-166	Sequence 166, App
1044	25	26.9	125	6	US-11-194-246-395	Sequence 395, App	1118	25	26.9	300	7	US-11-179-977-4	Sequence 4, Appli
1045	25	26.9	126	6	US-10-821-234-1318	Sequence 1318, Ap	1119	25	26.9	301	6	US-10-793-626-1826	Sequence 1826, Ap
1046	25	26.9	126	7	US-11-084-508-25	Sequence 25, Appl	1120	25	26.9	301	7	US-11-147-047-37	Sequence 37, Appl
1047	25	26.9	127	6	US-10-467-657-1320	Sequence 1320, Ap	1121	25	26.9	302	6	US-10-878-556A-61	Sequence 61, Appl
1048	25	26.9	127	6	US-10-467-657-5548	Sequence 5548, Ap	1122	25	26.9	303	7	US-11-186-284-193	Sequence 193, App
1049	25	26.9	127	6	US-10-467-657-5606	Sequence 5606, Ap	1123	25	26.9	306	6	US-10-467-657-4304	Sequence 4304, Ap
1050	25	26.9	127	6	US-10-467-657-7500	Sequence 7500, Ap	1124	25	26.9	309	6	US-10-793-626-936	Sequence 936, App
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1052	25	26.9	127	6	US-10-467-657-8312	Sequence 8312, Ap	1126	25	26.9	310	7	US-11-092-168-9	Sequence 9, Appli
1053	25	26.9	132	6	US-10-793-626-1058	Sequence 1058, Ap	1127	25	26.9	311	7	US-11-000-463-345	Sequence 345, App
1054	25	26.9	137	6	US-10-821-234-1242	Sequence 1242, Ap	1128	25	26.9	311	7	US-11-000-463-829	Sequence 829, App
1055	25	26.9	139	6	US-10-878-556A-117	Sequence 117, App	1129	25	26.9	312	6	US-10-793-626-3104	Sequence 3104, Ap
1056	25	26.9	141	6	US-10-467-657-4110	Sequence 4110, Ap	1130	25	26.9	313	6	US-10-723-207-4	Sequence 4, Appli
1057	25	26.9	144	7	US-11-174-398-10	Sequence 10, Appl	1131	25	26.9	314	7	US-11-143-980-56	Sequence 56, Appl
1058	25	26.9	146	7	US-11-034-569-14	Sequence 14, Appl	1132	25	26.9	317	7	US-11-129-143-85	Sequence 85, Appl
1059	25	26.9	148	6	US-10-467-657-5478	Sequence 5478, Ap	1133	25	26.9	317	6	US-10-793-626-1600	Sequence 1600, Ap
1060	25	26.9	149	6	US-10-986-501-231	Sequence 231, App	1134	25	26.9	318	7	US-11-000-463-432	Sequence 432, App
1061	25	26.9	151	6	US-10-467-657-244	Sequence 244, App	1135	25	26.9	318	7	US-11-000-463-904	Sequence 904, App
1062	25	26.9	152	7	US-11-069-642-7	Sequence 7, Appli	1136	25	26.9	321	6	US-10-485-517-133	Sequence 133, App
1063	25	26.9	158	6	US-10-821-234-1294	Sequence 1294, Ap	1137	25	26.9	323	6	US-10-485-517-251	Sequence 251, App
1064	25	26.9	161	6	US-10-467-657-1786	Sequence 1786, Ap	1138	25	26.9	326	7	US-11-102-621-33	Sequence 33, Appl
1065	25	26.9	161	7	US-11-126-126-2	Sequence 2, Appli	1139	25	26.9	328	6	US-10-485-517-268	Sequence 268, App
1066	25	26.9	162	7	US-11-089-642-6	Sequence 6, Appli	1140	25	26.9	333	7	US-10-467-657-6450	Sequence 6450, Ap
1067	25	26.9	163	6	US-10-467-657-2662	Sequence 2662, Ap	1141	25	26.9	333	7	US-11-074-176-32	Sequence 32, Appl
1068	25	26.9	164	6	US-10-467-657-232	Sequence 232, App	1142	25	26.9	333	7	US-11-050-440-2	Sequence 2, Appli
1069	25	26.9	164	6	US-10-467-657-664	Sequence 664, App	1143	25	26.9	334	6	US-10-793-626-10	Sequence 10, Appl

1144	25	26.9	334	7	US-11-140-417-8	Sequence 8, Appli	1218	25	26.9	457	6	US-10-763-712A-61	Sequence 61, Appli
1145	25	26.9	335	6	US-10-985-561-704	Sequence 704, App	1219	25	26.9	458	7	US-10-618-320A-1	Sequence 1, Appli
1146	25	26.9	335	7	US-11-141-947-2	Sequence 2, Appli	1220	25	26.9	462	7	US-11-132-142-10	Sequence 10, Appli
1147	25	26.9	337	6	US-10-980-388-115	Sequence 115, App	1221	25	26.9	463	6	US-10-467-657-6352	Sequence 6352, Ap
1148	25	26.9	341	6	US-10-467-657-62	Sequence 62, Appl	1222	25	26.9	463	6	US-10-467-657-7604	Sequence 7604, Ap
1149	25	26.9	341	6	US-10-467-657-2166	Sequence 2166, Ap	1223	25	26.9	465	6	US-11-186-284-197	Sequence 197, App
1150	25	26.9	341	7	US-11-092-168-4	Sequence 4, Appli	1224	25	26.9	465	6	US-10-957-569-28	Sequence 28, Appl
1151	25	26.9	343	7	US-11-080-591-86	Sequence 86, Appl	1225	25	26.9	468	7	US-11-167-273-1	Sequence 1, Appli
1152	25	26.9	343	7	US-11-092-168-3	Sequence 3, Appli	1226	25	26.9	469	7	US-11-186-284-119	Sequence 119, App
1153	25	26.9	344	6	US-10-467-657-6546	Sequence 6546, Ap	1227	25	26.9	484	7	US-11-051-568-13	Sequence 13, Appl
1154	25	26.9	344	6	US-11-102-240-42	Sequence 42, Appl	1228	25	26.9	489	6	US-10-467-657-6158	Sequence 6158, Ap
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1156	25	26.9	350	6	US-10-878-556A-66	Sequence 66, Appl	1230	25	26.9	494	7	US-11-165-697-48	Sequence 48, Appl
1157	25	26.9	350	6	US-10-873-528-89	Sequence 89, Appl	1231	25	26.9	494	7	US-11-165-697-49	Sequence 49, Appl
1158	25	26.9	351	7	US-11-132-142-13	Sequence 13, Appl	1232	25	26.9	497	6	US-10-984-376-3	Sequence 3, Appli
1159	25	26.9	351	7	US-11-132-142-14	Sequence 14, Appl	1233	25	26.9	501	7	US-11-013-247A-2	Sequence 2, Appli
1160	25	26.9	352	6	US-10-926-709-18	Sequence 18, Appl	1234	25	26.9	502	6	US-10-821-234-1554	Sequence 1554, Ap
1161	25	26.9	353	7	US-11-132-142-11	Sequence 11, Appl	1235	25	26.9	509	6	US-10-793-626-98	Sequence 98, Appl
1162	25	26.9	360	6	US-10-467-657-2796	Sequence 2796, Ap	1236	25	26.9	511	6	US-10-510-947-3	Sequence 3, Appli
1163	25	26.9	362	7	US-11-013-247A-7	Sequence 7, Appli	1237	25	26.9	513	7	US-11-055-822-348	Sequence 348, App
1164	25	26.9	363	6	US-10-793-626-302	Sequence 302, App	1238	25	26.9	513	7	US-11-149-349-6	Sequence 6, Appli
1165	25	26.9	364	6	US-10-510-947-2	Sequence 2, Appli	1239	25	26.9	515	6	US-10-821-234-1411	Sequence 1411, Ap
1166	25	26.9	364	6	US-11-013-247A-6	Sequence 6, Appli	1240	25	26.9	519	6	US-10-485-517-220	Sequence 220, App
1167	25	26.9	365	6	US-10-467-657-3846	Sequence 3846, Ap	1241	25	26.9	522	6	US-10-467-657-7238	Sequence 7238, Ap
1168	25	26.9	366	6	US-11-000-463-457	Sequence 457, App	1242	25	26.9	526	7	US-11-054-168B-19	Sequence 19, Appl
1169	25	26.9	366	6	US-10-467-657-1336	Sequence 1336, Ap	1243	25	26.9	529	7	US-11-013-247A-17	Sequence 17, Appl
1170	25	26.9	371	6	US-10-467-962B-41	Sequence 41, Appl	1244	25	26.9	542	7	US-11-074-176-30	Sequence 30, Appl
1171	25	26.9	371	6	US-10-467-657-1166	Sequence 1166, Ap	1245	25	26.9	543	6	US-11-087-227-16	Sequence 16, Appl
1172	25	26.9	371	6	US-11-137-671-16	Sequence 16, Appl	1246	25	26.9	545	6	US-10-858-730-90	Sequence 90, Appl
1173	25	26.9	372	7	US-11-143-980-37	Sequence 37, Appl	1247	25	26.9	548	6	US-10-858-730-68	Sequence 68, Appl
1174	25	26.9	372	6	US-10-467-657-7508	Sequence 7508, Ap	1248	25	26.9	548	7	US-11-132-142-5	Sequence 5, Appli
1175	25	26.9	379	6	US-10-858-730-24	Sequence 24, Appl	1249	25	26.9	558	6	US-10-467-657-4258	Sequence 4258, Ap
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1177	25	26.9	379	6	US-10-858-730-285	Sequence 285, App	1251	25	26.9	574	6	US-10-821-234-1624	Sequence 1624, Ap
1178	25	26.9	379	6	US-10-858-730-290	Sequence 290, App	1252	25	26.9	574	7	US-11-102-240-164	Sequence 164, App
1179	25	26.9	385	6	US-10-873-528-144	Sequence 144, App	1253	25	26.9	575	7	US-11-131-212-23	Sequence 23, Appl
1180	25	26.9	388	7	US-11-186-284-169	Sequence 169, App	1254	25	26.9	575	7	US-11-131-212-24	Sequence 24, Appl
1181	25	26.9	389	6	US-10-467-657-4468	Sequence 4468, Ap	1255	25	26.9	585	6	US-10-878-556A-42	Sequence 42, Appl
1182	25	26.9	391	6	US-10-770-726-59	Sequence 59, Appl	1256	25	26.9	588	6	US-10-763-712A-95	Sequence 95, Appl
1183	25	26.9	393	6	US-10-821-234-1043	Sequence 1043, Ap	1257	25	26.9	595	7	US-11-102-476-33	Sequence 33, Appl
1184	25	26.9	394	6	US-10-793-626-58	Sequence 58, Appl	1258	25	26.9	607	7	US-11-096-051-14	Sequence 14, Appl
1185	25	26.9	395	7	US-11-132-142-12	Sequence 12, Appl	1259	25	26.9	612	6	US-10-821-234-1101	Sequence 1101, Ap
1186	25	26.9	399	6	US-10-362-772-4	Sequence 4, Appli	1260	25	26.9	612	6	US-10-467-657-764	Sequence 764, App
1187	25	26.9	402	7	US-11-055-822-778	Sequence 778, App	1261	25	26.9	626	7	US-11-082-389-392	Sequence 392, App
1188	25	26.9	402	7	US-11-055-822-780	Sequence 780, App	1262	25	26.9	628	7	US-11-074-176-244	Sequence 244, App
1189	25	26.9	402	7	US-11-000-463-449	Sequence 449, App	1263	25	26.9	634	7	US-11-082-389-390	Sequence 390, App
1190	25	26.9	405	6	US-10-467-657-1048	Sequence 1048, Ap	1264	25	26.9	636	6	US-10-763-712A-29	Sequence 29, Appl
1191	25	26.9	408	7	US-11-051-568-15	Sequence 15, Appl	1265	25	26.9	636	6	US-10-763-712A-93	Sequence 93, Appl
1192	25	26.9	414	6	US-10-873-528-76	Sequence 76, Appl	1266	25	26.9	648	6	US-10-501-039-6	Sequence 6, Appli
1193	25	26.9	414	7	US-11-089-551A-28	Sequence 28, Appl	1267	25	26.9	649	7	US-11-102-240-132	Sequence 132, App
1194	25	26.9	425	7	US-11-096-276-2	Sequence 2, Appli	1268	25	26.9	654	6	US-10-528-031-1	Sequence 1, Appli
1195	25	26.9	428	6	US-11-000-463-448	Sequence 448, App	1269	25	26.9	654	6	US-10-770-726-82	Sequence 82, Appl
1196	25	26.9	430	6	US-10-821-234-1437	Sequence 1437, Ap	1270	25	26.9	656	6	US-10-821-234-1121	Sequence 1121, Ap
1197	25	26.9	430	7	US-10-650-326B-19	Sequence 19, Appl	1272	25	26.9	664	6	US-10-878-556A-44	Sequence 44, Appl
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1199	25	26.9	431	6	US-10-816-768-39	Sequence 39, Appl	1274	25	26.9	673	7	US-11-102-240-16	Sequence 16, Appl
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1465	24	25.8	107	6	US-10-467-657-1054	Sequence 1054, Ap
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1468	24	25.8	110	7	US-11-053-076-210	Sequence 210, App
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1473	24	25.8	118	6	US-10-467-657-1372	Sequence 1372, Ap
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1475	24	25.8	127	7	US-11-000-463-269	Sequence 269, App
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1494	24	25.8	183	6	US-10-467-657-5600	Sequence 5600, Ap
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1497	24	25.8	188	6	US-10-980-388-101	Sequence 101, App
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16	65.5	14.6	650	2	US-08-833-391-60
17	65.5	14.6	650	2	US-09-060-610-60
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21	63	14.0	1165	2	US-09-487-558B-76
22	62.5	13.9	152	2	US-09-270-767-47052
23	62.5	13.9	270	2	US-09-270-767-46312
24	62.5	13.9	416	2	US-09-949-016-7087
25	62.5	13.9	711	2	US-08-134-000C-5325
26	62	13.8	290	2	US-09-252-991A-18337
27	62	13.8	341	2	US-09-248-796A-20844

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30	61	13.6	296	2	US-09-270-767-53197	Sequence 53197, A
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32	61	13.6	715	2	US-09-792-024-85	Sequence 85, Appli
33	61	13.6	741	2	US-09-248-796A-18963	Sequence 18963, A
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36	61	13.6	1810	4	PCT-US95-11684-4	Sequence 4, Appli
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38	60	13.4	160	2	US-09-248-796A-24377	Sequence 24377, A
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42	59	13.1	153	2	US-09-640-211A-910	Sequence 910, App
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51	58.5	13.0	208	2	US-09-997-333-416	Sequence 416, App
52	58.5	13.0	208	2	US-09-992-598-416	Sequence 416, App
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76	58	12.9	486	2	US-09-879-957-26	Sequence 26, Appli
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85	57.5	12.8	896	2	US-09-357-914-33	Sequence 33, Appli
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87	57.5	12.8	896	2	US-10-095-929-10	Sequence 10, Appli
88	57.5	12.8	896	2	US-10-014-156-13	Sequence 13, Appli
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96	57.5	12.8	908	1	US-08-693-697-33	Sequence 33, Appli
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102	57.5	12.8	960	1	US-08-355-888A-8	Sequence 8, Appli	175	55	12.2	213	2	US-09-996-288-213	Sequence 213, App
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104	57.5	12.8	960	1	US-08-693-697-8	Sequence 8, Appli	177	55	12.2	213	2	US-09-996-288-217	Sequence 217, App
105	57.5	12.8	960	1	US-08-640-389A-3	Sequence 3, Appli	178	55	12.2	213	2	US-09-996-288-219	Sequence 219, App
106	57.5	12.8	960	2	US-08-693-696-8	Sequence 3, Appli	179	55	12.2	213	2	US-09-996-288-221	Sequence 221, App
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108	57.5	12.8	960	2	US-09-357-914-8	Sequence 8, Appli	181	55	12.2	213	2	US-09-996-288-225	Sequence 225, App
109	57.5	12.8	960	2	US-10-095-929-3	Sequence 3, Appli	182	55	12.2	213	2	US-09-996-288-227	Sequence 227, App
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111	57.5	12.8	1185	1	US-08-599-455B-4	Sequence 4, Appli	184	55	12.2	213	2	US-09-996-288-231	Sequence 231, App
112	57.5	12.8	1185	1	US-09-093-814-1	Sequence 1, Appli	185	55	12.2	213	2	US-09-996-288-233	Sequence 233, App
113	57.5	12.8	1185	2	US-09-069-781B-4	Sequence 4, Appli	186	55	12.2	213	2	US-09-996-288-235	Sequence 235, App
114	57.5	12.8	1185	2	US-08-618-957A-11	Sequence 11, Appl	187	55	12.2	213	2	US-09-996-288-237	Sequence 237, App
115	57.5	12.8	1185	2	US-09-137-132-4	Sequence 4, Appli	188	55	12.2	213	2	US-09-996-288-239	Sequence 239, App
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118	57.5	12.8	1185	2	US-08-708-123D-4	Sequence 4, Appli	191	55	12.2	213	2	US-09-996-288-247	Sequence 247, App
119	57.5	12.8	1185	2	US-08-583-153A-4	Sequence 4, Appli	192	55	12.2	213	2	US-09-996-288-251	Sequence 251, App
120	57.5	12.8	1185	2	US-08-570-142D-4	Sequence 4, Appli	193	55	12.2	213	2	US-09-996-288-253	Sequence 253, App
121	57.5	12.8	1185	2	US-08-780-562-2	Sequence 2, Appli	194	55	12.2	213	2	US-09-996-288-255	Sequence 255, App
122	57.5	12.8	1185	2	US-08-638-524B-4	Sequence 4, Appli	195	55	12.2	213	2	US-09-996-288-257	Sequence 257, App
123	57.5	12.8	1185	2	US-10-095-929-11	Sequence 11, Appl	196	55	12.2	213	2	US-09-996-265-209	Sequence 209, App
124	57.5	12.8	1221	2	US-08-982-430-2	Sequence 2, Appli	197	55	12.2	213	2	US-09-996-265-213	Sequence 213, App
125	57	12.7	136	2	US-09-615-192A-293	Sequence 293, App	198	55	12.2	213	2	US-09-996-265-215	Sequence 215, App
126	57	12.7	218	2	US-09-252-991A-22136	Sequence 22136, A	199	55	12.2	213	2	US-09-996-265-217	Sequence 217, App
127	57	12.7	576	2	US-09-252-991A-26023	Sequence 26023, A	200	55	12.2	213	2	US-09-996-265-219	Sequence 219, App
128	56.5	12.6	198	2	US-09-248-796A-18306	Sequence 18306, A	201	55	12.2	213	2	US-09-996-265-221	Sequence 221, App
129	56.5	12.6	235	2	US-09-252-991A-18300	Sequence 18300, A	202	55	12.2	213	2	US-09-996-265-223	Sequence 223, App
130	56.5	12.6	629	2	US-10-104-047-3405	Sequence 3405, Ap	203	55	12.2	213	2	US-09-996-265-225	Sequence 225, App
131	56.5	12.6	811	2	US-09-605-703B-1114	Sequence 1114, Ap	204	55	12.2	213	2	US-09-996-265-227	Sequence 227, App
132	56.5	12.6	811	2	US-09-605-703B-1116	Sequence 1116, Ap	205	55	12.2	213	2	US-09-996-265-229	Sequence 229, App
133	56.5	12.6	1912	1	US-08-409-995-4	Sequence 4, Appli	206	55	12.2	213	2	US-09-996-265-231	Sequence 231, App
134	56.5	12.6	1912	2	US-08-685-467-4	Sequence 4, Appli	207	55	12.2	213	2	US-09-996-265-233	Sequence 233, App
135	56.5	12.6	2353	2	US-09-377-155-33	Sequence 33, Appl	208	55	12.2	213	2	US-09-996-265-235	Sequence 235, App
136	56.5	12.6	2353	2	US-08-913-942-4	Sequence 4, Appli	209	55	12.2	213	2	US-09-996-265-237	Sequence 237, App
137	56.5	12.6	2353	2	US-09-669-974-33	Sequence 33, Appl	210	55	12.2	213	2	US-09-996-265-239	Sequence 239, App
138	56.5	12.6	2353	2	US-09-797-862-33	Sequence 33, Appl	211	55	12.2	213	2	US-09-996-265-243	Sequence 243, App
139	56.5	12.6	2353	2	US-09-684-707-4	Sequence 4, Appli	212	55	12.2	213	2	US-09-996-265-245	Sequence 245, App
140	56.5	12.6	2353	2	US-09-288-347-47	Sequence 47, Appl	213	55	12.2	213	2	US-09-996-265-247	Sequence 247, App
141	56.5	12.6	2411	2	US-09-268-347-36	Sequence 36, Appl	214	55	12.2	213	2	US-09-996-265-251	Sequence 251, App
142	56	12.5	137	2	US-09-252-991A-25510	Sequence 25510, A	215	55	12.2	213	2	US-09-996-265-253	Sequence 253, App
143	56	12.5	213	2	US-09-996-288-241	Sequence 241, App	216	55	12.2	213	2	US-09-996-265-255	Sequence 255, App
144	56	12.5	213	2	US-09-996-265-241	Sequence 241, App	217	55	12.2	213	2	US-09-996-265-257	Sequence 257, App
145	56	12.5	269	2	US-09-859-053-30	Sequence 30, Appl	218	55	12.2	213	2	US-10-135-636-7	Sequence 7, Appli
146	56	12.5	269	1	US-08-484-505-116	Sequence 116, App	219	55	12.2	213	2	US-09-996-288-249	Sequence 249, App
147	56	12.5	269	2	US-08-481-985B-116	Sequence 116, App	220	55	12.2	213	2	US-09-996-265-249	Sequence 249, App
148	56	12.5	269	2	US-08-370-476-116	Sequence 116, App	221	55	12.2	213	2	US-09-252-991A-19803	Sequence 19803, A
149	56	12.5	282	2	US-09-270-767-41535	Sequence 41535, A	222	55	12.2	253	2	US-09-310-463-36	Sequence 36, Appl
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151	56	12.5	481	2	US-09-002-361-5	Sequence 5, Appli	224	55	12.2	273	2	US-09-270-767-32843	Sequence 32843, A
152	56	12.5	631	2	US-09-310-463-20	Sequence 20, Appl	225	55	12.2	273	2	US-09-270-767-48060	Sequence 48060, A
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156	55.5	12.4	302	2	US-09-710-279-2980	Sequence 2980, Ap	229	55	12.2	332	2	US-09-170-354-6	Sequence 4, Appli
157	55.5	12.4	350	2	US-09-134-001C-3383	Sequence 3383, Ap	230	55	12.2	368	1	US-07-977-630-4	Sequence 4, Appli
158	55.5	12.4	441	1	US-08-121-713D-56	Sequence 56, Appl	231	55	12.2	451	2	US-09-270-767-40751	Sequence 40751, A
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161	55.5	12.4	441	2	US-08-833-391-56	Sequence 56, Appl	234	55	12.2	2842	1	US-07-741-940-7	Sequence 7, Appli
162	55.5	12.4	441	2	US-09-060-610-56	Sequence 56, Appl	235	55	12.2	2842	1	US-08-289-548A-7	Sequence 7, Appli
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164	55.5	12.4	704	2	US-09-487-558B-218	Sequence 218, App	237	55	12.2	2842	2	US-08-449-731-7	Sequence 7, Appli
165	55.5	12.4	920	2	US-09-538-092-1197	Sequence 1197, Ap	238	55	12.2	2843	1	US-07-741-940-2	Sequence 2, Appli
166	55.5	12.4	1068	1	US-08-537-210A-2	Sequence 2, Appli	239	55	12.2	2843	1	US-08-289-548A-2	Sequence 2, Appli
167	55.5	12.4	1068	2	US-09-113-825-2	Sequence 2, Appli	240	55	12.2	2843	1	US-08-452-654-2	Sequence 2, Appli
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169	55.5	12.4	2385	2	US-09-543-681A-6304	Sequence 6304, Ap	242	55	12.2	2843	1	US-08-452-655B-7	Sequence 7, Appli
170	55.5	12.4	2556	1	US-08-185-432-17	Sequence 17, Appl	243	55	12.2	2843	1	US-08-370-235A-2	Sequence 2, Appli
171	55.5	12.4	2556	2	US-08-899-232-2	Sequence 2, Appli	244	55	12.2	2843	2	US-08-450-582-2	Sequence 2, Appli
172	55.5	12.4	2556	2	US-09-121-457-2	Sequence 2, Appli	245	55	12.2	2843	2	US-08-450-582-7	Sequence 7, Appli
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248	55	12.2	2843	2	US-09-538-092-1007	Sequence 1007, Ap	321	53.5	11.9	743	2	US-08-270-767-41908	Sequence 41908, A
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251	55	12.2	2973	1	US-09-003-687A-7	Sequence 7, Appl	324	53.5	11.9	950	2	US-10-009-332-1	Sequence 1, Appl
252	55	12.2	2973	1	US-09-136-605-7	Sequence 7, Appl	325	53	11.8	43	1	US-08-332-562A-26	Sequence 26, Appl
253	54.5	12.1	108	2	US-09-281-760B-37	Sequence 37, Appl	326	53	11.8	73	2	US-09-621-976-6146	Sequence 6146, Ap
254	54.5	12.1	186	2	US-09-248-796A-18477	Sequence 18477, A	327	53	11.8	87	1	US-08-332-562A-90	Sequence 90, Appl
255	54.5	12.1	348	2	US-09-203-716-3	Sequence 3, Appl	328	53	11.8	88	2	US-08-311-731A-327	Sequence 327, App
256	54.5	12.1	348	2	US-09-684-254-3	Sequence 3, Appl	329	53	11.8	119	1	US-08-602-010A-12	Sequence 12, Appl
257	54.5	12.1	348	2	US-09-409-926-3	Sequence 3, Appl	330	53	11.8	119	1	US-08-680-726A-12	Sequence 12, Appl
258	54.5	12.1	377	2	US-09-248-796A-15498	Sequence 15498, A	331	53	11.8	119	2	US-09-092-409-12	Sequence 12, Appl
259	54.5	12.1	749	2	US-09-562-737-97	Sequence 97, Appl	332	53	11.8	136	2	US-09-647-224A-22	Sequence 22, Appl
260	54.5	12.1	2523	1	US-08-185-432-18	Sequence 18, Appl	333	53	11.8	170	2	US-09-245-764-5	Sequence 5, Appl
261	54.5	12.1	2523	2	US-08-899-232-6	Sequence 3, Appl	334	53	11.8	170	2	US-09-245-764-6	Sequence 6, Appl
262	54.5	12.1	2523	2	US-09-121-457-3	Sequence 3, Appl	335	53	11.8	170	2	US-09-245-764-10	Sequence 10, Appl
263	54.5	12.1	3542	2	US-10-087-013-2	Sequence 2, Appl	336	53	11.8	170	2	US-09-245-764-11	Sequence 11, Appl
264	54	12.0	221	2	US-08-228-208A-22	Sequence 22, Appl	337	53	11.8	170	2	US-09-245-764-12	Sequence 12, Appl
265	54	12.0	221	2	US-09-454-651B-22	Sequence 22, Appl	338	53	11.8	171	2	US-09-245-764-3	Sequence 3, Appl
266	54	12.0	226	1	US-08-505-058-6	Sequence 6, Appl	339	53	11.8	171	2	US-09-245-764-14	Sequence 14, Appl
267	54	12.0	226	1	US-08-459-818-26	Sequence 26, Appl	340	53	11.8	171	2	US-09-245-764-15	Sequence 15, Appl
268	54	12.0	226	1	US-08-889-666-26	Sequence 26, Appl	341	53	11.8	213	2	US-09-996-288-211	Sequence 211, App
269	54	12.0	226	1	US-08-465-078-26	Sequence 26, Appl	342	53	11.8	213	2	US-09-996-265-211	Sequence 211, App
270	54	12.0	226	1	US-08-725-776-26	Sequence 26, Appl	343	53	11.8	214	1	US-08-458-516-12	Sequence 12, Appl
271	54	12.0	226	1	US-08-488-062-26	Sequence 26, Appl	344	53	11.8	231	2	US-09-252-991A-26289	Sequence 26289, A
272	54	12.0	243	1	US-07-958-140-2	Sequence 2, Appl	345	53	11.8	237	2	US-08-308-469-100	Sequence 100, App
273	54	12.0	243	1	FCT-US93-09166-2	Sequence 2, Appl	346	53	11.8	262	2	US-09-248-796A-15919	Sequence 15919, A
274	54	12.0	299	1	US-08-872-437-2	Sequence 2, Appl	347	53	11.8	281	2	US-10-027-736A-67	Sequence 67, Appl
275	54	12.0	299	2	US-08-651-136C-12	Sequence 12, Appl	348	53	11.8	281	2	US-10-027-736A-19	Sequence 19, Appl
276	54	12.0	299	2	US-09-229-911A-12	Sequence 12, Appl	349	53	11.8	307	1	US-08-332-562A-83	Sequence 83, Appl
277	54	12.0	299	2	US-10-007-521-12	Sequence 12, Appl	350	53	11.8	315	2	US-09-949-016-7014	Sequence 7014, Ap
278	54	12.0	488	1	US-08-554-659-2	Sequence 2, Appl	351	53	11.8	315	2	US-09-949-016-11121	Sequence 11121, A
279	54	12.0	488	1	US-08-554-659-4	Sequence 4, Appl	352	53	11.8	316	2	US-10-027-736A-17	Sequence 17, Appl
280	54	12.0	621	2	US-09-949-016-11557	Sequence 11557, A	353	53	11.8	316	2	US-10-027-736A-16	Sequence 16, Appl
281	54	12.0	984	1	US-08-257-073-3	Sequence 3, Appl	354	53	11.8	317	2	US-10-027-736A-19	Sequence 19, Appl
282	54	12.0	984	1	US-08-184-009-120	Sequence 120, App	355	53	11.8	345	1	US-08-220-151-19	Sequence 19, Appl
283	54	12.0	984	1	US-08-458-356-120	Sequence 120, App	356	53	11.8	345	1	US-08-220-151-20	Sequence 20, Appl
284	54	12.0	984	2	US-08-460-736-120	Sequence 120, App	357	53	11.8	345	1	US-08-413-118-19	Sequence 19, Appl
285	54	12.0	984	2	US-09-535-370-120	Sequence 120, App	358	53	11.8	345	1	US-08-413-118-20	Sequence 20, Appl
286	54	12.0	984	2	US-09-663-667-120	Sequence 120, App	359	53	11.8	345	1	US-08-413-118-128	Sequence 128, App
287	54	12.0	989	2	US-08-213-419B-2	Sequence 2, Appl	360	53	11.8	345	1	US-08-680-726A-54	Sequence 54, Appl
288	54	12.0	989	2	US-08-213-419B-4	Sequence 4, Appl	361	53	11.8	345	1	US-08-332-562A-132	Sequence 132, App
289	53.5	11.9	113	2	US-09-232-290-25	Sequence 25, Appl	362	53	11.8	345	2	US-08-473-446-19	Sequence 19, Appl
290	53.5	11.9	141	2	US-09-248-796A-20650	Sequence 20650, A	363	53	11.8	345	2	US-08-473-446-20	Sequence 20, Appl
291	53.5	11.9	148	2	US-09-621-976-4783	Sequence 72, Ap	364	53	11.8	345	2	US-08-473-446-128	Sequence 128, App
292	53.5	11.9	226	2	US-09-456-090A-72	Sequence 72, Appl	365	53	11.8	345	2	US-09-092-409-54	Sequence 54, Appl
293	53.5	11.9	226	2	US-09-453-234-72	Sequence 72, Appl	366	53	11.8	379	2	US-09-949-016-10257	Sequence 10257, A
294	53.5	11.9	235	2	US-08-781-420-6	Sequence 6, Appl	367	53	11.8	467	2	US-09-002-361-3	Sequence 3, Appl
295	53.5	11.9	235	2	US-08-874-102-6	Sequence 6, Appl	368	53	11.8	481	4	PCT-US91-02166-13	Sequence 13, Appl
296	53.5	11.9	235	2	US-08-984-919A-6	Sequence 6, Appl	369	53	11.8	491	2	US-10-011-125A-2	Sequence 2, Appl
297	53.5	11.9	235	2	US-09-006-595A-6	Sequence 6, Appl	370	53	11.8	496	2	US-09-002-361-2	Sequence 2, Appl
298	53.5	11.9	268	2	US-09-647-224A-20	Sequence 20, Appl	371	53	11.8	686	2	US-09-248-796A-18636	Sequence 18636, A
299	53.5	11.9	297	2	US-09-252-991A-18764	Sequence 18764, A	372	53	11.8	742	2	US-09-107-532A-6890	Sequence 6890, Ap
300	53.5	11.9	342	2	US-10-104-047-2985	Sequence 2985, Ap	373	53	11.8	754	2	US-09-214-564A-2	Sequence 2, Appl
301	53.5	11.9	359	2	US-09-270-767-43751	Sequence 43751, A	374	53	11.8	808	2	US-10-104-047-3401	Sequence 3401, Ap
302	53.5	11.9	366	2	US-08-984-919A-11	Sequence 11, Appl	375	53	11.8	858	2	US-07-956-483-17	Sequence 17, Appl
303	53.5	11.9	368	2	US-09-000-092-2	Sequence 2, Appl	376	53	11.8	858	2	US-09-206-551-18	Sequence 18, Appl
304	53.5	11.9	368	2	US-09-000-092-4	Sequence 4, Appl	377	53	11.8	1337	2	US-08-854-585-2	Sequence 2, Appl
305	53.5	11.9	368	2	US-09-000-092-8	Sequence 8, Appl	378	53	11.8	1337	4	US-09-447-533-2	Sequence 2, Appl
306	53.5	11.9	368	2	US-09-000-092-10	Sequence 10, Appl	379	53	11.8	1337	4	PCT-US95-05512-2	Sequence 2, Appl
307	53.5	11.9	368	2	US-08-781-420-11	Sequence 11, Appl	380	52.5	11.7	99	2	US-09-073-009-141	Sequence 141, App
308	53.5	11.9	368	2	US-08-874-102-11	Sequence 11, Appl	381	52.5	11.7	99	2	US-09-073-010-141	Sequence 141, App
309	53.5	11.9	368	2	US-09-006-595A-11	Sequence 11, Appl	382	52.5	11.7	116	2	US-09-270-767-33915	Sequence 33915, A
310	53.5	11.9	466	2	US-08-984-919A-33	Sequence 33, Appl	383	52.5	11.7	116	2	US-09-270-767-49132	Sequence 49132, A
311	53.5	11.9	468	2	US-08-874-102-33	Sequence 33, Appl	384	52.5	11.7	172	2	US-09-270-767-37433	Sequence 37433, A
312	53.5	11.9	470	2	US-08-984-919A-55	Sequence 55, Appl	385	52.5	11.7	172	2	US-09-270-767-52650	Sequence 52650, A
313	53.5	11.9	472	2	US-08-874-102-55	Sequence 55, Appl	386	52.5	11.7	237	1	US-08-704-744-80	Sequence 80, Appl
314	53.5	11.9	482	2	US-09-252-991A-21327	Sequence 21327, A	387	52.5	11.7	237	1	US-08-469-537A-85	Sequence 85, Appl
315	53.5	11.9	495	2	US-08-984-919A-47	Sequence 47, Appl	388	52.5	11.7	251	4	PCT-US96-01314-59	Sequence 59, Appl
316	53.5	11.9	497	2	US-08-874-102-47	Sequence 47, Appl	389	52.5	11.7	288	2	US-09-818-247-22	Sequence 22, Appl
317	53.5	11.9	519	2	US-08-270-767-57156	Sequence 57156, A	390	52.5	11.7	290	2	US-09-643-596B-144	Sequence 144, App
318	53.5	11.9	615	1	US-08-752-307B-9	Sequence 9, Appl	391	52.5	11.7	305	2	US-09-270-767-59446	Sequence 59446, A
319	53.5	11.9	615	2	US-09-707-802-9	Sequence 9, Appl	392	52.5	11.7	318	1	US-07-704-288C-9	Sequence 9, Appl

393	52.5	11.7	318	1	US-08-379-259-9	Sequence 9, Appli	466	52	11.6	259	2	US-09-911-513-6	Sequence 6, Appli
394	52.5	11.7	319	2	US-09-270-767-44038	Sequence 44038, A	467	52	11.6	272	2	US-09-583-110-5240	Sequence 5240, Ap
395	52.5	11.7	328	2	US-07-791-931-7	Sequence 7, Appli	468	52	11.6	282	2	US-09-117-853-8	Sequence 8, Appli
396	52.5	11.7	370	2	US-08-857-076-107	Sequence 107, App	469	52	11.6	282	2	US-09-911-154-8	Sequence 8, Appli
397	52.5	11.7	370	2	US-09-205-658-107	Sequence 107, App	470	52	11.6	282	2	US-09-911-514-8	Sequence 8, Appli
398	52.5	11.7	387	2	US-09-563-569-2	Sequence 2, Appli	471	52	11.6	282	2	US-09-911-513-8	Sequence 8, Appli
399	52.5	11.7	387	2	US-09-643-596B-136	Sequence 136, App	472	52	11.6	287	2	US-09-107-433-5100	Sequence 5100, Ap
400	52.5	11.7	460	1	US-08-933-821-17	Sequence 17, Appl	473	52	11.6	317	1	US-08-619-362A-8	Sequence 8, Appli
401	52.5	11.7	460	2	US-08-934-494-6	Sequence 6, Appli	474	52	11.6	318	1	US-08-960-022-4	Sequence 4, Appli
402	52.5	11.7	460	2	US-08-960-507-17	Sequence 17, Appl	475	52	11.6	334	2	US-09-248-796A-16418	Sequence 16418, A
403	52.5	11.7	460	2	US-09-143-068-6	Sequence 6, Appli	476	52	11.6	418	2	US-09-019-095A-10	Sequence 10, Appl
404	52.5	11.7	460	2	US-09-143-707-6	Sequence 6, Appli	477	52	11.6	471	2	US-09-071-709-4	Sequence 4, Appli
405	52.5	11.7	460	2	US-09-202-089-6	Sequence 6, Appli	478	52	11.6	471	2	US-09-160-494-2	Sequence 2, Appli
406	52.5	11.7	460	2	US-09-136-828-17	Sequence 17, Appl	479	52	11.6	471	2	US-09-713-669-4	Sequence 4, Appli
407	52.5	11.7	460	2	US-09-332-928A-17	Sequence 17, Appl	480	52	11.6	491	2	US-09-710-279-2808	Sequence 2808, Ap
408	52.5	11.7	460	2	US-09-511-123-6	Sequence 6, Appli	481	52	11.6	494	2	US-09-477-962-104	Sequence 104, App
409	52.5	11.7	460	2	US-09-136-801-17	Sequence 17, Appl	482	52	11.6	517	2	US-09-487-558B-100	Sequence 100, App
410	52.5	11.7	460	2	US-09-332-929-17	Sequence 17, Appl	483	52	11.6	532	2	US-09-117-853-2	Sequence 2, Appli
411	52.5	11.7	460	2	US-09-690-169-6	Sequence 6, Appli	484	52	11.6	532	2	US-09-911-154-2	Sequence 2, Appli
412	52.5	11.7	460	2	US-09-511-631-6	Sequence 6, Appli	485	52	11.6	532	2	US-09-485-529-2	Sequence 2, Appli
413	52.5	11.7	460	2	US-09-333-075-17	Sequence 17, Appl	486	52	11.6	532	2	US-09-911-514-2	Sequence 2, Appli
414	52.5	11.7	460	2	US-09-690-189-6	Sequence 6, Appli	487	52	11.6	532	2	US-09-911-513-2	Sequence 2, Appli
415	52.5	11.7	460	2	US-09-202-088A-17	Sequence 17, Appl	488	52	11.6	534	2	US-09-248-796A-19568	Sequence 19568, A
416	52.5	11.7	460	2	US-09-333-077-17	Sequence 17, Appl	489	52	11.6	681	2	US-08-760-615-4	Sequence 4, Appli
417	52.5	11.7	475	2	US-09-949-016-7940	Sequence 7940, Ap	490	52	11.6	681	2	US-09-336-910A-2	Sequence 2, Appli
418	52.5	11.7	613	2	US-09-949-016-7353	Sequence 7353, Ap	491	52	11.6	2496	2	US-09-125-028-2	Sequence 2, Appli
419	52.5	11.7	651	2	US-09-949-016-8426	Sequence 8426, Ap	492	52	11.6	2958	2	US-08-894-344C-2	Sequence 2, Appli
420	52.5	11.7	788	1	US-07-728-215-30	Sequence 30, Appl	493	52	11.6	2958	2	US-09-678-023A-2	Sequence 2, Appli
421	52.5	11.7	798	2	US-08-938-085A-30	Sequence 30, Appl	494	52	11.6	3460	2	US-09-334-220-1	Sequence 1, Appli
422	52.5	11.7	798	2	US-10-072-844-30	Sequence 30, Appl	495	51.5	11.5	79	2	US-09-248-796A-21029	Sequence 21029, A
423	52.5	11.7	798	2	US-10-072-831A-30	Sequence 30, Appl	496	51.5	11.5	91	2	US-09-248-796A-22642	Sequence 22642, A
424	52.5	11.7	798	2	US-10-072-841A-30	Sequence 30, Appl	497	51.5	11.5	101	2	US-09-461-325-214	Sequence 214, App
425	52.5	11.7	798	2	US-10-219-631A-30	Sequence 30, Appl	498	51.5	11.5	101	2	US-10-012-542-214	Sequence 214, App
426	52.5	11.7	798	2	US-09-949-016-6193	Sequence 6193, Ap	499	51.5	11.5	101	2	US-10-115-123-214	Sequence 214, App
427	52.5	11.7	886	2	US-08-956-171B-5235	Sequence 5235, Ap	500	51.5	11.5	106	2	US-08-397-411-8	Sequence 8, Appli
428	52.5	11.7	886	2	US-08-781-986A-5235	Sequence 5235, Ap	501	51.5	11.5	107	2	US-09-438-954-1	Sequence 9, Appli
429	52.5	11.7	909	2	US-10-172-502-6	Sequence 6, Appli	502	51.5	11.5	142	2	US-09-380-882-9	Sequence 9, Appli
430	52.5	11.7	1041	1	US-08-494-714-2	Sequence 2, Appli	503	51.5	11.5	158	2	US-09-270-767-38728	Sequence 38728, A
431	52.5	11.7	1041	4	PCT-US96-10782-2	Sequence 2, Appli	504	51.5	11.5	158	2	US-09-270-767-53945	Sequence 53945, A
432	52.5	11.7	1367	1	US-08-249-687C-2	Sequence 2, Appli	505	51.5	11.5	153	2	US-09-252-991A-17451	Sequence 17451, A
433	52.5	11.7	1367	1	US-08-625-819-2	Sequence 2, Appli	506	51.5	11.5	171	2	US-09-248-796A-25024	Sequence 25024, A
434	52.5	11.7	1367	2	US-08-746-559A-2	Sequence 2, Appli	507	51.5	11.5	183	2	US-09-328-352-5634	Sequence 5634, Ap
435	52.5	11.7	1367	2	US-08-864-641B-18	Sequence 18, Appl	508	51.5	11.5	197	2	US-09-252-991A-28579	Sequence 28579, A
436	52.5	11.7	1367	2	US-09-343-551-2	Sequence 2, Appli	509	51.5	11.5	213	2	US-10-104-047-2722	Sequence 2722, Ap
437	52.5	11.7	1367	2	US-09-949-001-18	Sequence 18, Appl	510	51.5	11.5	226	2	US-09-456-090A-38	Sequence 38, Appl
438	52.5	11.7	1377	2	US-09-949-001-21	Sequence 21, Appl	511	51.5	11.5	226	2	US-09-456-090A-74	Sequence 74, Appl
439	52.5	11.7	3788	2	US-09-336-447A-76	Sequence 76, Appl	512	51.5	11.5	226	2	US-09-453-234-38	Sequence 38, Appl
440	52.5	11.7	3788	2	US-09-952-267B-76	Sequence 76, Appl	513	51.5	11.5	226	2	US-09-453-234-74	Sequence 74, Appl
441	52	11.6	76	2	US-09-252-991A-25030	Sequence 25030, A	514	51.5	11.5	258	2	US-09-248-796A-23723	Sequence 23723, A
442	52	11.6	83	2	US-09-270-767-38732	Sequence 38732, A	515	51.5	11.5	277	2	US-09-354-151-3	Sequence 3, Appli
443	52	11.6	83	2	US-09-270-767-53949	Sequence 53949, A	516	51.5	11.5	310	2	US-09-907-794A-423	Sequence 423, App
444	52	11.6	141	2	US-09-472-087-88	Sequence 88, Appl	517	51.5	11.5	310	2	US-09-905-125A-423	Sequence 423, App
445	52	11.6	144	2	US-09-949-016-11102	Sequence 1102, A	518	51.5	11.5	310	2	US-09-902-775A-423	Sequence 423, App
446	52	11.6	167	1	US-08-627-610-6	Sequence 6, Appli	519	51.5	11.5	310	2	US-09-906-700-423	Sequence 423, App
447	52	11.6	168	1	US-08-508-735-46	Sequence 46, Appl	520	51.5	11.5	310	2	US-09-903-603A-423	Sequence 423, App
448	52	11.6	168	2	US-09-201-139-46	Sequence 46, Appl	521	51.5	11.5	310	2	US-09-904-920A-423	Sequence 423, App
449	52	11.6	218	4	PCT-US96-13152-2	Sequence 2, Appli	522	51.5	11.5	310	2	US-09-909-064-423	Sequence 423, App
450	52	11.6	221	2	US-09-117-853-4	Sequence 4, Appli	523	51.5	11.5	310	2	US-09-905-381A-423	Sequence 423, App
451	52	11.6	221	2	US-09-911-154-4	Sequence 4, Appli	524	51.5	11.5	310	2	US-09-906-618-423	Sequence 423, App
452	52	11.6	221	2	US-09-911-514-4	Sequence 4, Appli	525	51.5	11.5	310	2	US-09-906-646-423	Sequence 423, App
453	52	11.6	221	2	US-09-911-513-4	Sequence 4, Appli	526	51.5	11.5	310	2	US-09-904-462-423	Sequence 423, App
454	52	11.6	233	1	US-08-792-824-6	Sequence 6, Appli	527	51.5	11.5	310	2	US-09-902-736A-423	Sequence 20, Appl
455	52	11.6	233	2	US-09-216-393B-110	Sequence 110, App	528	51.5	11.5	310	2	US-10-033-301-20	Sequence 20, Appl
456	52	11.6	235	2	US-09-472-087-14	Sequence 14, Appl	529	51.5	11.5	310	2	US-09-906-722A-423	Sequence 423, App
457	52	11.6	235	2	US-09-472-087-65	Sequence 65, Appl	530	51.5	11.5	376	2	US-09-404-296B-32	Sequence 32, Appl
458	52	11.6	236	1	US-08-792-824-3	Sequence 3, Appli	531	51.5	11.5	436	2	US-10-169-048-50	Sequence 50, Appl
459	52	11.6	236	1	US-08-792-824-9	Sequence 9, Appli	532	51.5	11.5	448	2	US-09-717-364A-7	Sequence 7, Appli
460	52	11.6	236	1	US-08-792-824-12	Sequence 12, Appl	533	51.5	11.5	511	2	US-08-646-695-5	Sequence 5, Appli
461	52	11.6	236	2	US-09-726-219A-188	Sequence 188, App	534	51.5	11.5	511	4	PCT-US96-06053-5	Sequence 5350, A
462	52	11.6	236	2	US-09-136-522-188	Sequence 188, App	535	51.5	11.5	668	2	US-09-248-796A-19350	Sequence 7610, Ap
463	52	11.6	259	2	US-09-117-853-6	Sequence 6, Appli	536	51.5	11.5	1676	2	US-09-949-016-7610	Sequence 2, Appli
464	52	11.6	259	2	US-09-911-154-6	Sequence 6, Appli	537	51.5	11.5	3635	2	US-09-845-583A-2	Sequence 47, Appl
465	52	11.6	259	2	US-09-911-514-6	Sequence 6, Appli	538	51.5	11.5	3635	2	US-10-037-417-47	Sequence 47, Appl

539	51.5	11.5	3635	2	US-10-037-182-4	Sequence 4, Appli	612	50.5	11.2	254	1	US-08-047-413-9	Sequence 9, Appli
540	51.5	11.5	3852	2	US-10-025-225-4	Sequence 4, Appli	613	50.5	11.2	254	2	US-08-229-050-9	Sequence 9, Appli
541	51.5	11.5	4585	2	US-10-025-225-6	Sequence 6, Appli	614	50.5	11.2	254	2	US-08-801-563-9	Sequence 9, Appli
542	51.5	11.5	4588	2	US-10-025-225-8	Sequence 8, Appli	615	50.5	11.2	281	2	US-09-270-767-58184	Sequence 58184, A
543	51.5	11.5	4599	2	US-10-025-225-2	Sequence 2, Appli	616	50.5	11.2	289	2	US-09-489-039A-12627	Sequence 12627, A
544	51	11.4	98	2	US-09-248-796A-18363	Sequence 18363, A	617	50.5	11.2	294	2	US-09-328-352-7430	Sequence 7430, Ap
545	51	11.4	96	2	US-09-270-767-48032	Sequence 48032, A	618	50.5	11.2	338	2	US-09-489-039A-12787	Sequence 12787, A
546	51	11.4	148	2	US-09-270-767-31975	Sequence 31975, A	619	50.5	11.2	361	2	US-09-032-372-12	Sequence 12, Appl
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548	51	11.4	151	1	US-08-387-942C-50	Sequence 50, Appl	621	50.5	11.2	418	2	US-09-328-352-4525	Sequence 4525, Ap
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550	51	11.4	195	2	US-09-134-001C-5045	Sequence 5045, Ap	623	50.5	11.2	486	2	US-09-270-767-42864	Sequence 42864, A
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553	51	11.4	218	2	US-09-328-352-7829	Sequence 7829, Ap	626	50.5	11.2	524	2	US-09-265-585C-35	Sequence 35, Appl
554	51	11.4	222	2	US-09-252-991A-26487	Sequence 26487, A	627	50.5	11.2	588	2	US-09-265-585C-34	Sequence 34, Appl
555	51	11.4	224	2	US-09-456-090A-46	Sequence 46, Appl	628	50.5	11.2	607	1	US-08-409-995-6	Sequence 6, Appli
556	51	11.4	224	2	US-09-453-234-46	Sequence 46, Appl	629	50.5	11.2	607	2	US-08-685-467-6	Sequence 6, Appli
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558	51	11.4	252	2	US-09-270-767-40634	Sequence 40634, A	631	50.5	11.2	607	2	US-09-684-707-6	Sequence 6, Appli
559	51	11.4	252	2	US-09-270-767-55850	Sequence 55850, A	632	50.5	11.2	722	2	US-09-198-452A-513	Sequence 513, App
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568	51	11.4	391	2	US-09-107-532A-4209	Sequence 4209, Ap	641	50.5	11.2	1292	2	US-08-569-214-5	Sequence 5, Appli
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570	51	11.4	545	2	US-10-067-422-11	Sequence 11, Appl	643	50.5	11.2	1292	2	US-08-337-236-5	Sequence 5, Appli
571	51	11.4	550	2	US-09-583-110-4871	Sequence 110, Ap	644	50.5	11.2	1374	2	US-09-900-425B-2	Sequence 2, Appli
572	51	11.4	550	2	US-09-107-433-3858	Sequence 3858, Ap	645	50.5	11.2	1752	2	US-09-949-002-294	Sequence 294, App
573	51	11.4	627	2	US-10-246-658-4	Sequence 4, Appli	646	50.5	11.2	1917	2	US-09-949-002-485	Sequence 485, App
574	51	11.4	627	2	US-10-843-131-4	Sequence 4, Appli	647	50.5	11.2	2167	2	US-09-487-558B-56	Sequence 56, Appl
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585	51	11.4	1097	1	US-08-347-003-6	Sequence 6, Appli	658	50	11.1	196	2	US-10-015-389A-216	Sequence 216, App
586	51	11.4	1097	1	US-09-949-016-6209	Sequence 6209, Ap	659	50	11.1	196	2	US-10-006-768A-216	Sequence 216, App
587	51	11.4	1119	2	US-09-949-016-10081	Sequence 10081, A	660	50	11.1	196	2	US-10-015-671A-216	Sequence 216, App
588	51	11.4	1148	2	US-09-949-016-8328	Sequence 8328, Ap	661	50	11.1	196	2	US-10-015-993A-216	Sequence 216, App
589	51	11.4	1187	1	US-08-357-598-8	Sequence 8, Appli	662	50	11.1	196	2	US-10-011-833A-216	Sequence 216, App
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591	51	11.4	1187	1	US-09-003-289-8	Sequence 8, Appli	664	50	11.1	196	2	US-10-012-064A-216	Sequence 216, App
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594	51	11.4	1187	2	US-09-972-800A-18	Sequence 18, Appl	667	50	11.1	221	1	US-08-659-235C-29	Sequence 29, Appl
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596	51	11.4	1302	2	US-09-949-016-10852	Sequence 10852, A	669	50	11.1	230	2	US-09-333-809-221	Sequence 221, App
597	51	11.4	1402	2	US-09-125-635-12	Sequence 12, Appl	670	50	11.1	230	2	US-09-333-809-222	Sequence 222, App
598	51	11.4	1402	2	US-09-445-553E-2	Sequence 2, Appli	671	50	11.1	230	2	US-09-333-809-223	Sequence 223, App
599	51	11.4	1420	2	US-09-125-635-4	Sequence 4, Appli	672	50	11.1	230	2	US-09-333-809-224	Sequence 224, App
600	51	11.4	1586	2	US-09-060-299-44	Sequence 44, Appl	673	50	11.1	230	2	US-09-333-809-225	Sequence 225, App
601	51	11.4	1586	2	US-09-402-923A-44	Sequence 44, Appl	674	50	11.1	230	2	US-09-333-809-226	Sequence 226, App
602	51	11.4	1614	2	US-09-060-299-42	Sequence 42, Appl	675	50	11.1	230	2	US-09-333-809-227	Sequence 227, App
603	51	11.4	1614	2	US-09-402-923A-42	Sequence 42, Appl	676	50	11.1	230	2	US-09-333-809-228	Sequence 228, App
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605	50.5	11.2	108	2	US-09-240-274-41	Sequence 41, Appl	678	50	11.1	230	2	US-09-746-311B-371	Sequence 371, App
606	50.5	11.2	108	2	US-09-848-798-41	Sequence 41, Appl	679	50	11.1	230	2	US-09-746-311B-373	Sequence 373, App
607	50.5	11.2	183	2	US-09-270-767-45510	Sequence 45510, A	680	50	11.1	230	2	US-09-746-311B-374	Sequence 374, App
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609	50.5	11.2	242	2	US-09-270-767-61432	Sequence 61432, A	682	50	11.1	230	2	US-09-746-311B-376	Sequence 376, App
610	50.5	11.2	248	2	US-09-248-796A-20545	Sequence 20545, A	683	50	11.1	230	2	US-09-746-311B-377	Sequence 377, App
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979	48.5	10.8	842	4	PCT-US96-02331-15	Sequence 15, Appl	1052	48	10.7	318	1	US-09-058-368-3	Sequence 3, Appl
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985	48.5	10.8	1249	2	US-09-964-899-33	Sequence 33, Appl	1058	48	10.7	332	2	US-09-934-868-50	Sequence 50, Appl
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991	48.5	10.8	1418	2	US-09-570-573-20	Sequence 20, Appl	1064	48	10.7	459	6	5210189-2	Patent No. 5210189
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997	48.5	10.8	2231	1	US-08-153-799-16	Sequence 16, Appl	1070	48	10.7	513	2	US-08-659-235C-14	Sequence 14, Appl
998	48.5	10.8	2324	1	US-08-283-857-1	Sequence 1, Appl	1071	48	10.7	513	2	US-09-071-035-68	Sequence 68, Appl
999	48.5	10.8	2324	1	PCT-US95-09819-1	Sequence 1, Appl	1072	48	10.7	513	2	US-10-206-576-68	Sequence 68, Appl
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1010	48	10.7	109	1	US-09-848-798-168	Sequence 168, App	1083	48	10.7	625	2	US-09-019-385-2	Sequence 2, Appl
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1018	48	10.7	135	2	US-09-270-767-54759	Sequence 54759, A	1091	48	10.7	832	2	US-10-015-389A-227	Sequence 227, App
1019	48	10.7	131	2	US-09-252-991A-23278	Sequence 23278, A	1092	48	10.7	832	2	US-10-006-768A-227	Sequence 227, App
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1036	48	10.7	237	1	US-08-463-587A-25	Sequence 25, Appl	1109	48	10.7	2813	2	US-09-132-652-2	Sequence 2, Appl
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1038	48	10.7	237	2	US-08-923-854-25	Sequence 25, Appl	1111	48	10.7	2813	2	US-09-662-478C-2	Sequence 2, Appl
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1044	48	10.7	289	2	US-09-949-016-10744	Sequence 10744, A	1117	47.5	10.6	51	2	US-09-732-210-1703	Sequence 1703 Ap
1045	48	10.7	294	2	US-10-027-736A-18	Sequence 18, Appl	1118	47.5	10.6	85	2	US-09-248-796A-21280	Sequence 21280, A
1046	48	10.7	300	2	US-09-248-796A-18445	Sequence 18445, A	1119	47.5	10.6	98	2	US-09-252-991A-28085	Sequence 28085, A
1047	48	10.7	309	2	US-09-270-767-44995	Sequence 44995, A	1120	47.5	10.6	102	2	US-09-771-415-17	Sequence 17, Appl
1048	48	10.7	317	1	US-08-790-572-3	Sequence 3, Appl	1121	47.5	10.6	106	2	US-09-771-415-21	Sequence 21, Appl
1049	48	10.7	317	1	US-09-213-398-3	Sequence 3, Appl	1122	47.5	10.6	106	2		

1123	47.5	10.6	106	2	US-09-771-415-23	Sequence 23, Appl	1196	47.5	10.6	530	2	US-09-222-817-12	Sequence 12, Appl
1124	47.5	10.6	106	2	US-09-771-415-25	Sequence 25, Appl	1197	47.5	10.6	530	2	US-09-222-817-14	Sequence 14, Appl
1125	47.5	10.6	106	2	US-09-996-288-60	Sequence 60, Appl	1198	47.5	10.6	530	2	US-09-222-786-12	Sequence 12, Appl
1126	47.5	10.6	106	2	US-09-996-265-60	Sequence 60, Appl	1199	47.5	10.6	530	2	US-09-222-786-14	Sequence 14, Appl
1127	47.5	10.6	107	2	US-09-240-374-158	Sequence 158, Appl	1200	47.5	10.6	532	2	US-09-828-302-12	Sequence 12, Appl
1128	47.5	10.6	107	2	US-09-848-798-158	Sequence 158, Appl	1201	47.5	10.6	533	2	US-08-941-445A-5	Sequence 5, Appl
1129	47.5	10.6	108	2	US-09-240-274-177	Sequence 177, Appl	1202	47.5	10.6	571	2	US-09-460-295B-13	Sequence 13, Appl
1130	47.5	10.6	108	2	US-09-848-798-177	Sequence 177, Appl	1203	47.5	10.6	572	2	US-09-543-681A-7137	Sequence 7137, Ap
1131	47.5	10.6	133	2	US-09-107-532A-1461	Sequence 4161, Ap	1204	47.5	10.6	594	2	US-09-117-415B-2	Sequence 2, Appl
1132	47.5	10.6	134	2	US-09-646-028-1	Sequence 1, Appl	1205	47.5	10.6	604	2	US-09-731-166-4	Sequence 4, Appl
1133	47.5	10.6	134	2	US-09-248-796A-22888	Sequence 22888, A	1206	47.5	10.6	610	1	US-08-455-073A-2	Sequence 2, Appl
1134	47.5	10.6	147	2	US-08-838-128B-49	Sequence 49, Appl	1207	47.5	10.6	613	2	US-09-117-415B-22	Sequence 22, Appl
1135	47.5	10.6	154	2	US-09-252-991A-24938	Sequence 24938, A	1208	47.5	10.6	631	2	US-09-117-415B-18	Sequence 18, Appl
1136	47.5	10.6	161	2	US-09-352-991A-25631	Sequence 25631, A	1209	47.5	10.6	631	2	US-09-117-415B-20	Sequence 20, Appl
1137	47.5	10.6	177	2	US-09-247-155-164	Sequence 164, Appl	1210	47.5	10.6	635	1	US-08-245-809-1	Sequence 1, Appl
1138	47.5	10.6	177	2	US-09-903-190-164	Sequence 164, Appl	1211	47.5	10.6	636	1	US-08-296-624-2	Sequence 2, Appl
1139	47.5	10.6	194	2	US-08-679-493A-215	Sequence 215, Appl	1212	47.5	10.6	649	2	US-09-117-415B-16	Sequence 16, Appl
1140	47.5	10.6	194	2	US-08-679-493A-216	Sequence 216, Appl	1213	47.5	10.6	657	2	US-07-705-490-14	Sequence 14, Appl
1141	47.5	10.6	225	2	US-09-589-733C-10	Sequence 10, Appl	1214	47.5	10.6	657	2	US-07-751-891B-14	Sequence 14, Appl
1142	47.5	10.6	236	1	US-08-642-846-3	Sequence 3, Appl	1215	47.5	10.6	673	2	US-09-949-016-11718	Sequence 11718, A
1143	47.5	10.6	236	2	US-09-264-604-3	Sequence 3, Appl	1216	47.5	10.6	676	2	US-08-760-615-2	Sequence 2, Appl
1144	47.5	10.6	236	2	US-09-978-343-3	Sequence 3, Appl	1217	47.5	10.6	676	2	US-09-650-086A-2	Sequence 2, Appl
1145	47.5	10.6	236	5	US-09-599-652-3	Sequence 3, Appl	1218	47.5	10.6	676	2	US-10-226-795-2	Sequence 2, Appl
1146	47.5	10.6	258	2	US-10-104-047-3034	Sequence 3034, Ap	1219	47.5	10.6	678	2	US-09-991-181-179	Sequence 179, App
1147	47.5	10.6	222	2	US-09-248-796A-21832	Sequence 21832, A	1220	47.5	10.6	678	2	US-09-990-444-179	Sequence 179, App
1148	47.5	10.6	273	2	US-09-248-796A-18140	Sequence 18140, A	1221	47.5	10.6	678	2	US-09-997-333-179	Sequence 179, App
1149	47.5	10.6	274	2	US-09-248-796A-21922	Sequence 21922, A	1222	47.5	10.6	678	2	US-09-992-598-179	Sequence 179, App
1150	47.5	10.6	282	2	US-09-907-794A-127	Sequence 127, App	1223	47.5	10.6	707	2	US-10-104-047-3162	Sequence 3162, Ap
1151	47.5	10.6	282	2	US-09-905-125A-127	Sequence 127, App	1224	47.5	10.6	724	2	US-08-914-999-4	Sequence 4, Appl
1152	47.5	10.6	282	2	US-09-902-775A-127	Sequence 127, App	1225	47.5	10.6	746	2	US-09-589-892B-2	Sequence 2, Appl
1153	47.5	10.6	282	2	US-09-906-700-127	Sequence 127, App	1226	47.5	10.6	760	2	US-09-248-796A-19620	Sequence 19620, A
1154	47.5	10.6	282	2	US-09-808-847-1	Sequence 1, Appl	1227	47.5	10.6	796	2	US-08-361-083-56	Sequence 56, Appl
1155	47.5	10.6	282	2	US-09-903-603A-127	Sequence 127, App	1228	47.5	10.6	796	2	US-09-536-784-56	Sequence 56, Appl
1156	47.5	10.6	282	2	US-09-904-920A-127	Sequence 127, App	1229	47.5	10.6	796	2	US-09-765-271-56	Sequence 56, Appl
1157	47.5	10.6	282	2	US-09-909-064-127	Sequence 127, App	1230	47.5	10.6	796	2	US-09-765-272A-56	Sequence 56, Appl
1158	47.5	10.6	282	2	US-09-905-381A-127	Sequence 127, App	1231	47.5	10.6	798	2	US-09-935-430-658	Sequence 658, App
1159	47.5	10.6	282	2	US-09-906-618-127	Sequence 127, App	1232	47.5	10.6	798	2	US-09-964-956-28	Sequence 28, Appl
1160	47.5	10.6	282	2	US-09-906-646-127	Sequence 127, App	1233	47.5	10.6	808	2	US-09-265-585C-112	Sequence 112, App
1161	47.5	10.6	282	2	US-09-904-462-127	Sequence 127, App	1234	47.5	10.6	809	2	US-09-186-276B-58	Sequence 58, Appl
1162	47.5	10.6	282	2	US-09-902-736A-127	Sequence 127, App	1235	47.5	10.6	809	2	US-08-842-445-58	Sequence 58, Appl
1163	47.5	10.6	282	2	US-09-906-722A-127	Sequence 127, App	1236	47.5	10.6	809	2	US-09-186-188B-58	Sequence 58, Appl
1164	47.5	10.6	284	2	US-09-248-796A-25423	Sequence 25423, A	1237	47.5	10.6	809	2	US-09-265-585C-58	Sequence 58, Appl
1165	47.5	10.6	285	2	US-09-248-796A-15972	Sequence 15972, A	1238	47.5	10.6	816	2	US-09-645-835A-7	Sequence 7, Appl
1166	47.5	10.6	287	1	US-08-433-783-37	Sequence 37, Appl	1239	47.5	10.6	819	2	US-09-468-656A-8	Sequence 8, Appl
1167	47.5	10.6	287	1	US-08-337-358-37	Sequence 37, Appl	1240	47.5	10.6	829	2	US-09-583-110-3851	Sequence 3851, Ap
1168	47.5	10.6	287	4	PCT-US95-07537A-37	Sequence 37, Appl	1241	47.5	10.6	830	4	PCT-US91-05059-2	Sequence 2, Appl
1169	47.5	10.6	287	4	PCT-US95-07537-37	Sequence 37, Appl	1242	47.5	10.6	830	6	5378464-2	Patent No. 5378464
1170	47.5	10.6	287	2	US-09-134-000C-3527	Sequence 3527, Ap	1243	47.5	10.6	837	2	US-09-964-956-5	Sequence 5, Appl
1171	47.5	10.6	318	2	US-09-248-796A-26749	Sequence 26749, A	1244	47.5	10.6	841	2	US-09-935-430-657	Sequence 657, App
1172	47.5	10.6	320	2	US-09-854-122-20	Sequence 20, Appl	1245	47.5	10.6	841	2	US-09-964-956-2	Sequence 2, Appl
1173	47.5	10.6	321	2	US-09-107-433-2993	Sequence 2993, Ap	1246	47.5	10.6	841	2	US-09-872-733A-16	Sequence 16, Appl
1174	47.5	10.6	325	2	US-08-829-402-2	Sequence 2, Appl	1247	47.5	10.6	879	2	US-09-248-796A-20328	Sequence 20328, A
1175	47.5	10.6	338	2	US-09-252-991A-16820	Sequence 16820, A	1248	47.5	10.6	879	2	US-09-954-987B-171	Sequence 171, Appl
1176	47.5	10.6	339	2	US-08-444-818-158	Sequence 158, App	1249	47.5	10.6	1036	2	US-10-104-047-2812	Sequence 2812, Ap
1177	47.5	10.6	345	2	US-09-222-817-2	Sequence 2, Appl	1250	47.5	10.6	1049	2	US-09-999-833A-496	Sequence 496, App
1178	47.5	10.6	345	2	US-09-222-786-2	Sequence 2, Appl	1251	47.5	10.6	1049	2	US-09-954-987B-170	Sequence 170, App
1179	47.5	10.6	365	2	US-09-270-767-58705	Sequence 58705, A	1252	47.5	10.6	1049	2	US-09-954-987B-170	Sequence 170, App
1180	47.5	10.6	366	2	US-09-270-767-35334	Sequence 35334, A	1253	47.5	10.6	1049	2	US-10-020-445A-496	Sequence 496, App
1181	47.5	10.6	366	2	US-09-270-767-50551	Sequence 50551, A	1254	47.5	10.6	1167	2	US-08-857-076-48	Sequence 48, Appl
1182	47.5	10.6	399	2	US-09-248-796A-15312	Sequence 15312, A	1255	47.5	10.6	1167	2	US-09-205-658-48	Sequence 48, Appl
1183	47.5	10.6	396	2	US-09-538-092-1303	Sequence 1303, Ap	1256	47.5	10.6	1167	2	US-09-206-942-37	Sequence 37, Appl
1184	47.5	10.6	397	2	US-09-270-767-43356	Sequence 43356, A	1257	47.5	10.6	1222	2	US-10-193-764-37	Sequence 37, Appl
1185	47.5	10.6	414	2	US-09-634-238-271	Sequence 271, App	1258	47.5	10.6	1222	2	US-09-206-942-34	Sequence 34, Appl
1186	47.5	10.6	415	2	US-09-935-430-659	Sequence 659, App	1259	47.5	10.6	1228	2	US-10-193-764-34	Sequence 34, Appl
1187	47.5	10.6	424	1	US-08-951-148-9	Sequence 9, Appl	1260	47.5	10.6	1276	2	US-08-937-236-3	Sequence 3, Appl
1188	47.5	10.6	424	1	US-09-165-234-9	Sequence 9, Appl	1261	47.5	10.6	1291	2	US-08-569-214-3	Sequence 3, Appl
1189	47.5	10.6	424	2	US-09-274-570-9	Sequence 9, Appl	1262	47.5	10.6	1291	2	US-08-337-236-2	Sequence 2, Appl
1190	47.5	10.6	424	2	US-09-538-092-1317	Sequence 1317, Ap	1263	47.5	10.6	1295	2	US-08-569-214-2	Sequence 2, Appl
1191	47.5	10.6	440	2	US-09-964-956-29	Sequence 29, Appl	1264	47.5	10.6	1433	2	US-09-487-558B-60	Sequence 60, Appl
1192	47.5	10.6	475	2	US-09-270-767-41691	Sequence 41691, A	1265	47.5	10.6	1602	2	US-09-269-874A-7	Sequence 7, Appl
1193	47.5	10.6	488	6	5223391-9	Patent No. 5223391	1266	47.5	10.6	1621	2	US-09-269-874A-5	Sequence 5, Appl
1194	47.5	10.6	524	2	US-09-171-553B-4	Sequence 4, Appl	1267	47.5	10.6	1639	2	US-09-269-874A-3	Sequence 3, Appl
1195	47.5	10.6	526	2	US-09-630-983A-7	Sequence 7, Appl	1268	47.5	10.6	1664	1	US-08-642-846-2	Sequence 2, Appl

1269	47.5	10.6	1664	2	US-09-264-604-2	Sequence 2, Appli	1342	47	10.5	224	2	US-09-456-090A-84	Sequence 84, Appl
1270	47.5	10.6	1664	2	US-09-978-343-2	Sequence 2, Appli	1343	47	10.5	224	2	US-09-456-090A-88	Sequence 88, Appl
1271	47.5	10.6	1664	5	US-09-599-652-2	Sequence 2, Appli	1344	47	10.5	224	2	US-09-456-090A-90	Sequence 90, Appl
1272	47.5	10.6	2391	1	US-08-446-855A-2	Sequence 2, Appli	1345	47	10.5	224	2	US-09-453-234-36	Sequence 36, Appl
1273	47.5	10.6	2391	2	US-09-150-741-2	Sequence 2, Appli	1346	47	10.5	224	2	US-09-453-234-82	Sequence 82, Appl
1274	47.5	10.6	3011	2	US-08-811-566-20	Sequence 20, Appl	1347	47	10.5	224	2	US-09-453-234-84	Sequence 84, Appl
1275	47.5	10.6	3011	2	US-09-034-756-20	Sequence 20, Appl	1348	47	10.5	224	2	US-09-453-234-88	Sequence 88, Appl
1276	47.5	10.6	3623	2	US-09-341-461-2	Sequence 2, Appli	1349	47	10.5	224	2	US-09-453-234-90	Sequence 90, Appl
1277	47	10.5	82	2	US-09-134-000C-5504	Sequence 5504, Ap	1350	47	10.5	225	2	US-09-270-767-40689	Sequence 40689, A
1278	47	10.5	103	2	US-09-248-796A-25804	Sequence 25804, A	1351	47	10.5	225	2	US-09-270-767-55905	Sequence 55905, A
1279	47	10.5	127	1	US-08-476-176B-6	Sequence 6, Appli	1352	47	10.5	228	1	US-08-442-248-4	Sequence 4, Appli
1280	47	10.5	127	1	US-08-476-176B-8	Sequence 8, Appli	1353	47	10.5	228	1	US-08-440-815-4	Sequence 4, Appli
1281	47	10.5	127	1	US-08-476-176B-10	Sequence 10, Appl	1354	47	10.5	228	1	US-08-379-802-2	Sequence 2, Appli
1282	47	10.5	127	2	US-08-127-721A-6	Sequence 6, Appli	1355	47	10.5	228	2	US-09-048-129-2	Sequence 2, Appli
1283	47	10.5	127	2	US-08-127-721A-8	Sequence 8, Appli	1356	47	10.5	228	2	US-09-048-129-2	Sequence 2, Appli
1284	47	10.5	127	2	US-08-127-721A-10	Sequence 10, Appl	1357	47	10.5	228	2	US-08-486-449-4	Sequence 4, Appli
1285	47	10.5	127	2	US-08-485-246A-6	Sequence 6, Appli	1358	47	10.5	228	2	US-09-214-631-9	Sequence 9, Appli
1286	47	10.5	127	2	US-08-485-246A-8	Sequence 8, Appli	1359	47	10.5	228	2	US-08-578-684-4	Sequence 4, Appli
1287	47	10.5	127	2	US-08-485-246A-10	Sequence 10, Appl	1360	47	10.5	228	4	PCT-US95-15781-5	Sequence 5, Appli
1288	47	10.5	139	2	US-09-472-087-22	Sequence 22, Appl	1361	47	10.5	230	2	US-09-248-796A-26509	Sequence 26509, A
1289	47	10.5	139	2	US-09-472-087-96	Sequence 96, Appl	1362	47	10.5	233	1	US-08-032-848C-12	Sequence 12, Appl
1290	47	10.5	146	2	US-09-252-991A-24346	Sequence 24346, A	1363	47	10.5	233	1	US-07-934-373C-25	Sequence 25, Appl
1291	47	10.5	150	2	US-09-252-991A-33012	Sequence 33012, A	1364	47	10.5	233	2	US-08-437-642B-25	Sequence 25, Appl
1292	47	10.5	152	2	US-09-252-991A-19284	Sequence 19284, A	1365	47	10.5	233	2	US-08-146-206C-25	Sequence 25, Appl
1293	47	10.5	160	2	US-09-252-991A-30765	Sequence 30765, A	1366	47	10.5	233	2	US-09-705-686-25	Sequence 25, Appl
1294	47	10.5	174	1	US-08-683-262B-38	Sequence 38, Appl	1367	47	10.5	233	2	US-09-705-392A-25	Sequence 25, Appl
1295	47	10.5	174	1	US-08-683-262B-39	Sequence 39, Appl	1368	47	10.5	233	2	US-09-705-398-25	Sequence 25, Appl
1296	47	10.5	174	1	US-08-683-262B-41	Sequence 41, Appl	1369	47	10.5	233	4	PCT-US93-07832-25	Sequence 25, Appl
1297	47	10.5	174	2	US-08-480-173A-44	Sequence 44, Appl	1370	47	10.5	234	2	US-09-740-002-24	Sequence 24, Appl
1298	47	10.5	174	2	US-08-484-408A-44	Sequence 44, Appl	1371	47	10.5	234	2	US-09-770-916-4	Sequence 4, Appli
1299	47	10.5	174	2	US-09-361-707-38	Sequence 38, Appl	1372	47	10.5	237	2	US-09-097-309-6	Sequence 6, Appli
1300	47	10.5	174	2	US-09-361-707-39	Sequence 39, Appl	1373	47	10.5	237	2	US-09-097-171A-10	Sequence 10, Appl
1301	47	10.5	174	2	US-09-361-707-41	Sequence 41, Appl	1374	47	10.5	237	2	US-09-422-712B-2	Sequence 2, Appli
1302	47	10.5	174	6	5204096-1	Patent No. 5204096	1375	47	10.5	237	2	US-09-607-756-2	Sequence 2, Appli
1303	47	10.5	181	2	US-09-270-767-35340	Sequence 35340, A	1376	47	10.5	237	2	US-09-460-587-6	Sequence 6, Appli
1304	47	10.5	181	2	US-09-270-767-50557	Sequence 50557, A	1377	47	10.5	237	2	US-09-940-166A-51	Sequence 51, Appl
1305	47	10.5	195	2	US-09-252-991A-21229	Sequence 21229, A	1378	47	10.5	242	2	US-09-027-449-51	Sequence 51, Appl
1306	47	10.5	198	2	US-08-737-248-6	Sequence 6, Appli	1379	47	10.5	242	2	US-09-027-449-56	Sequence 56, Appl
1307	47	10.5	211	2	US-09-170-769A-8	Sequence 8, Appli	1380	47	10.5	242	2	US-09-027-449-62	Sequence 62, Appl
1308	47	10.5	212	2	US-08-811-463-39	Sequence 39, Appl	1381	47	10.5	242	2	US-08-804-444A-51	Sequence 51, Appl
1309	47	10.5	212	2	US-09-252-991A-29138	Sequence 29138, A	1382	47	10.5	242	2	US-08-804-444A-56	Sequence 56, Appl
1310	47	10.5	212	2	US-09-933-497B-39	Sequence 39, Appl	1383	47	10.5	242	2	US-09-026-985-51	Sequence 51, Appl
1311	47	10.5	212	2	US-10-011-125A-5	Sequence 5, Appli	1384	47	10.5	242	2	US-09-026-985-56	Sequence 56, Appl
1312	47	10.5	213	2	US-09-270-767-33023	Sequence 33023, A	1385	47	10.5	242	2	US-09-026-985-62	Sequence 62, Appl
1313	47	10.5	213	2	US-09-270-767-48240	Sequence 48240, A	1386	47	10.5	242	2	US-09-121-952A-51	Sequence 51, Appl
1314	47	10.5	214	1	US-08-253-877C-5	Sequence 5, Appli	1387	47	10.5	242	2	US-09-121-952A-56	Sequence 56, Appl
1315	47	10.5	214	1	US-07-934-373C-39	Sequence 39, Appl	1388	47	10.5	242	2	US-09-121-952A-62	Sequence 62, Appl
1316	47	10.5	214	1	US-07-934-373C-40	Sequence 40, Appl	1389	47	10.5	242	2	US-09-234-340A-51	Sequence 51, Appl
1317	47	10.5	214	1	US-08-452-164A-5	Sequence 5, Appli	1390	47	10.5	242	2	US-09-234-340A-56	Sequence 56, Appl
1318	47	10.5	214	1	US-08-788-800-11	Sequence 11, Appl	1391	47	10.5	242	2	US-09-234-340A-62	Sequence 62, Appl
1319	47	10.5	214	2	US-08-437-642B-39	Sequence 39, Appl	1392	47	10.5	242	2	US-09-355-014-51	Sequence 51, Appl
1320	47	10.5	214	2	US-08-437-642B-40	Sequence 40, Appl	1393	47	10.5	242	2	US-09-355-014-56	Sequence 56, Appl
1321	47	10.5	214	2	US-09-097-309-2	Sequence 2, Appli	1394	47	10.5	242	2	US-09-355-014-62	Sequence 62, Appl
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; Sequence 258, Application US/09990444
; Patent No. 6930170
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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
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; APPLICANT: Gurney, Austin L.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C19
; CURRENT APPLICATION NUMBER: US/09/990,444
; PRIOR FILING DATE: 2001-11-14
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APPLICANT: Ashkenazi, Avi J.
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C27
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 449; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.9e-48;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGFLMCMSPNSNANCFSLKNISDIHPESFNQLQWFFNDSCAPPTGFKPKFTSNDTWSGW 60
Db 111 KGFLMCMSPNSNANCFSLKNISDIHPESFNQLQWFFNDSCAPPTGFKPKFTSNDTWSGW 170
QY 61 RASSFHPDSEKRLIHPS 80
Db 171 RASSFHPDSEKRLIHPS 190

RESULT 4

US-09-992-598-258
Sequence 258, Application US/09992598
Patent No. 6956108
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730F1C20
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
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PRIOR FILING DATE: 1998-06-10
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PRIOR APPLICATION NUMBER: 60/088826
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PRIOR FILING DATE: 1998-06-11
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PRIOR FILING DATE: 1998-06-11
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PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952

1 PRIOR FILING DATE: 1998-06-19
2 PRIOR APPLICATION NUMBER: 60/090246
3 PRIOR FILING DATE: 1998-06-22
4 PRIOR APPLICATION NUMBER: 60/090252
5 PRIOR FILING DATE: 1998-06-22
6 PRIOR APPLICATION NUMBER: 60/090254
7 PRIOR FILING DATE: 1998-06-22
8 PRIOR APPLICATION NUMBER: 60/090349
9 PRIOR FILING DATE: 1998-06-23
10 PRIOR APPLICATION NUMBER: 60/090355
11 PRIOR FILING DATE: 1998-06-23
12 PRIOR APPLICATION NUMBER: 60/090429
13 PRIOR FILING DATE: 1998-06-24
14 PRIOR APPLICATION NUMBER: 60/090431
15 PRIOR FILING DATE: 1998-06-24
16 PRIOR APPLICATION NUMBER: 60/090435
17 PRIOR FILING DATE: 1998-06-24
18 PRIOR APPLICATION NUMBER: 60/090444
19 PRIOR FILING DATE: 1998-06-24
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21 PRIOR FILING DATE: 1998-06-24
22 PRIOR APPLICATION NUMBER: 60/090472
23 PRIOR FILING DATE: 1998-06-24
24 PRIOR APPLICATION NUMBER: 60/090535
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49 PRIOR FILING DATE: 1998-07-01
50 PRIOR APPLICATION NUMBER: 60/091478
51 PRIOR FILING DATE: 1998-07-02
52 PRIOR APPLICATION NUMBER: 60/091544
53 PRIOR FILING DATE: 1998-07-01
54 PRIOR APPLICATION NUMBER: 60/091519
55 PRIOR FILING DATE: 1998-07-02
56 PRIOR APPLICATION NUMBER: 60/091626
57 PRIOR FILING DATE: 1998-07-02
58 PRIOR APPLICATION NUMBER: 60/091633
59 PRIOR FILING DATE: 1998-07-02
60 PRIOR APPLICATION NUMBER: 60/091978
61 PRIOR FILING DATE: 1998-07-07
62 PRIOR APPLICATION NUMBER: 60/091982
63 PRIOR FILING DATE: 1998-07-07
64 PRIOR APPLICATION NUMBER: 60/092182
65 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 449; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.9e-48;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 KGPLMCMSPNSNANCFSLKNSDIHPESFNLOWFNDSCAPPTGFKPTSDNTMASGW 60
111 KGPLMCMSPNSNANCFSLKNSDIHPESFNLOWFNDSCAPPTGFKPTSDNTMASGW 170

Qy
Db

Qy 61 RASSPHDSEENKRLIHS 80
Db 171 RASSPHDSEENKRLIHS 190

RESULT 5

US-08-793-273C-2
; Sequence 2, Application US/08793273C
; Patent No. 6482410
; GENERAL INFORMATION:
; APPLICANT: Crossin, Kathryn L.
; APPLICANT: Phillips, Greg
; APPLICANT: Prieto, Anne L.
; TITLE OF INVENTION: CYTOTACTIN DERIVATIVES THAT STIMULATE ATTACHMENT AND
; FILE REFERENCE: BEC0022S
; CURRENT APPLICATION NUMBER: US/08/793,273C
; PRIOR FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: PCT/US95/11684
; PRIOR FILING DATE: 1995-09-14
; PRIOR APPLICATION NUMBER: 08/308,359
; PRIOR FILING DATE: 1994-09-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2199
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-08-793-273C-2

Query Match 15.1%; Score 68; DB 2; Length 2199;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 12; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 22 NISDIHPESFNLOWFND 39
Db 1444 NVSDITPESFNLSWATD 1461

RESULT 6

PCT-US95-11684-2
; Sequence 2, Application PC/TUS9511684
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; TITLE OF INVENTION: CYTOTACTIN DERIVATIVES THAT STIMULATE
; TITLE OF INVENTION: ATTACHMENT AND NEURITE OUTGROWTH, AND METHODS OF MAKING
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSER: Patent Counsel
; STREET: 10666 North Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/11684
; FILING DATE: 14-SEP-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,359
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Logan, April C.
; REGISTRATION NUMBER: 33,950
; REFERENCE/DOCKET NUMBER: BEC0019P

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2199 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-11684-2

Query Match 15.1%; Score 68; DB 4; Length 2199;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 12; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 22 NISDIHPESFNLOWFFND 39
Db 1444 NVSDITPESFNLSMATD 1461

RESULT 7
US-09-796-575-2
; Sequence 2, Application US/09796575
; Patent No. 6632671
; GENERAL INFORMATION:
; APPLICANT: Geneseques, Inc.
; TITLE OF INVENTION: NANOCAPSULE ENCAPSULATION SYSTEM AND METHOD
; FILE REFERENCE: G332.12-0001
; CURRENT APPLICATION NUMBER: US/09/796,575
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/185,282
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 2200
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-575-2

Query Match 15.1%; Score 68; DB 2; Length 2200;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 12; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 22 NISDIHPESFNLOWFFND 39
Db 1444 NVSDITPESFNLSMATD 1461

RESULT 8
US-09-248-796A-26951
; Sequence 26951, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 26951
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-26951

Query Match 14.9%; Score 67; DB 2; Length 345;
Best Local Similarity 27.5%; Pred. No. 4.2;
Matches 1; Indels 0; Gaps 0;
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Matches 22; Conservative 10; Mismatches 28; Indels 20; Gaps 3;

Qy 17 EFSLKNI SDI-HPESFNLOWFFNDSCAPP-----TGFNKPTSDNTMAS 58
Db 29 KPSLNQLQDIFHEETETKISFVETSTPQPKQKAPRRKNWPSYKSIKTTFKKQKQKNTFAS 88
Qy 59 GWRASSFHPDSEENKHLIH 78
Db 89 KHRAA--HTPEEPNSYQGVH 106

RESULT 9
US-09-345-468-12
; Sequence 12, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-345-468-12

Query Match 14.9%; Score 67; DB 2; Length 631;
Best Local Similarity 24.0%; Pred. No. 9.3;
Matches 23; Conservative 16; Mismatches 35; Indels 22; Gaps 4;

Qy 3 PLMCNPSNSNANCFSLKNISDIHPESFNLOWFFNDSCAPP-----TGF-NKPT-- 51
Db 68 PLDRNNPLEPKNKARFSIPSMTEHHAGRYRCHYYSSAGNWEPSDPLELVMTGPNKPTLS 127
Qy 52 -----SNDTMASGWRASSFHFD-SEENKHL 76
Db 128 ALPSPVVVASGNNMTLRCSQSGYHHFVLMKEGHL 163

RESULT 10
US-09-414-453A-12
; Sequence 12, Application US/09414453A
; Patent No. 6383779
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/414,453A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-453A-12

Query Match 14.9%; Score 67; DB 2; Length 631;
Best Local Similarity 24.0%; Pred. No. 9.3;
Matches 23; Conservative 16; Mismatches 35; Indels 22; Gaps 4;

Qy 3 PLMCNPSNSNANCFSLKNISDIHPESFNLOWFFNDSCAPP-----TGF-NKPT-- 51
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Db 68 PLDRNLEPKKARFIPSTHAGRIYCHYSSAGWSEPSDPLBLVMTGFYKPTLS 127
Qy 52 -----SNDTMASGWRASSFFHD-SEENKRL 76
Db 128 ALPSPVVASGGMTRCGSQGYHFFVLMKGEHQ 163

RESULT 11
US-09-248-796A-14877
; Sequence 14877, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14877
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-14877

Query Match 14.8%; Score 66.5; DB 2; Length 271;
Best Local Similarity 27.9%; Pred. No. 3.5;
Matches 19; Conservative 11; Mismatches 29; Indels 9; Gaps 2;

Qy 2 GPLMCSNPSNANCEFSLKNSIDHPESFNLOWFNDSCAPPTGFKNPTSNMTMASGWR 61
Db 1 GRILPASVGDNNQNSMANIVDAKNYFQIQWYR-----PRDISKTSRLL----- 51

Qy 62 ASSFPDTS 69
Db 52 FASMHDTDS 59

RESULT 12
US-09-902-540-11280
; Sequence 11280, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11280
; LENGTH: 1627
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11280

Query Match 14.8%; Score 66.5; DB 2; Length 1627;
Best Local Similarity 28.6%; Pred. No. 37;
Matches 16; Conservative 8; Mismatches 27; Indels 5; Gaps 1;

Qy 2 GPLMCSNPSNANCEFSLKNSIDHPESFNLOWFNDSCAPPTGFKNPTSNMTMA 57
Db 61 GPCMNGPLILSHWDHDCDLGRYPYFPCRWL-----APQOHMTGVTCRDIVA 111
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RESULT 13
US-08-121-713D-60
; Sequence 60, Application US/08121713D
; Patent No. 5639856
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713D
; FILING DATE: 13-SEP-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 650 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-121-713D-60

Query Match 14.6%; Score 65.5; DB 1; Length 650;
Best Local Similarity 31.8%; Pred. No. 15;
Matches 21; Conservative 7; Mismatches 27; Indels 11; Gaps 2;

Qy 7 NSPNS---NANCEFSLKNSIDHPESFNLOWFNDSCAPPTGFKNPTSNMTMASGWRAS 63
Db 202 NTPSNIPGSVACAFALQDIADTFEQGKEQTGINSNLPVNNAKVDPD-----RPG 253

Qy 64 SFHPDS 69
Db 254 SCHNDS 259

RESULT 14
US-08-835-268-60
; Sequence 60, Application US/08835268
; Patent No. 5807826
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
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OM protein - protein search, using sw model

Run on: December 22, 2005, 02:42:57 ; Search time 240 Seconds
(without alignments)
235.176 Million cell updates/sec

Title: US-10-063-553-48_COPY_111_190

Perfect score: 449

Sequence: 1 KGPLMCPNSPNSNANCFSL.....RASSFHFDSEKNKRLIHFS 80

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	449	100.0	229	2	Q5U609 HUMAN
5	237.5	52.9	226	2	Q9CQV8 m mus muscu
6	237.5	52.9	226	2	Q9D3R0 MOUSE
7	231.5	51.6	226	2	Q9D3Q0 MOUSE
8	93	20.7	242	2	Q4KL96 XENLA
9	83.5	18.6	277	2	Q66S52 9UROC
10	83	18.5	342	2	Q9PT67 XENLA
11	82	18.3	142	2	Q695C3 PICMA
12	82	18.3	148	2	Q65095 PICMA
13	80	17.8	352	2	Q9PRJ8 XENLA
14	79	17.6	808	2	Q70W02 CIOIN
15	78.5	17.5	149	2	Q695B5 PICMA
16	78.5	17.5	149	2	Q695B6 PICMA
17	78.5	17.5	149	2	Q695B7 PICMA
18	78.5	17.5	149	2	Q695B8 PICAB
19	78.5	17.5	154	2	Q9SPX7 PICAB
20	78.5	17.5	156	2	Q65096 PICMA
21	78.5	17.5	281	2	Q65061 PICMA
22	78	17.4	832	2	Q9IBT8 PLAF7
23	77.5	17.3	151	2	Q695B3 PICMA
24	77.5	17.3	156	2	Q65097 PICMA
25	76.5	17.0	149	2	Q695B0 TSUCA
26	76.5	17.0	149	2	Q695B1 PSEMZ
27	76.5	17.0	149	2	Q695B2 PINCE
28	76.5	17.0	149	2	Q695B4 PICGL
29	76.5	17.0	154	2	Q9SPW4 PICGL
30	75	16.7	853	2	Q93245 ONCORN
31	75	16.7	989	2	Q6FP46 CANGA

32	74.5	16.6	296	2	Q722C5 LISMF
33	73.5	16.4	353	2	Q9PT68 XENLA
34	73	16.3	145	2	Q695C2 PICAB
35	73	16.3	150	2	Q9SPX8 PICAB
36	73	16.3	412	1	AATC MOUSE
37	72	16.0	854	2	Q93244 ONCMY
38	72	16.0	1443	2	Q5A450 CANAL
39	71	15.8	352	2	Q5WM45 XENTR
40	71	15.8	852	2	Q6CLB3 KLULA
41	70.5	15.7	146	2	Q695B9 PICGL
42	70.5	15.7	146	2	Q695C0 PICGL
43	70.5	15.7	146	2	Q695C1 PICAB
44	70.5	15.7	151	2	Q9SPW5 PICGL
45	70.5	15.7	151	2	Q9SPX9 PICAB
46	70.5	15.7	527	2	Q8BYW9 MOUSE
47	70	15.6	490	1	NOT3 YEAST
48	70	15.6	814	2	Q9VNP2 DROME
49	70	15.6	1011	2	Q24273 DROME
50	68.5	15.3	710	2	Q5CR22 CRYPV
51	68.5	15.3	710	2	Q5CN99 CRYHO
52	68.5	15.3	890	2	Q54YH9 DICDI
53	68	15.1	293	2	Q692Q7 SCLOS
54	68	15.1	2201	1	TENA HUMAN
55	68	15.1	2201	1	Q5T7S3 HUMAN
56	68	15.1	2233	2	Q4LE33 HUMAN
57	67.5	15.0	351	2	Q4WIU3 ASPFU
58	67.5	15.0	527	2	Q5NDL0 RAT
59	67.5	15.0	623	2	Q8JNB7 WSSV
60	67.5	15.0	623	2	Q91LN4 WSSV
61	67.5	15.0	1282	2	Q6PRR1 CANGA
62	67	14.9	296	2	Q8Y8V0 LISMO
63	67	14.9	322	2	Q52GL5 MAGGR
64	67	14.9	369	2	Q54B59 DICDI
65	67	14.9	619	2	Q62701 RAT
66	66.5	14.8	126	2	Q4I7X6 GIBZE
67	66.5	14.8	296	2	Q4YK55 PLABE
68	66.5	14.8	375	2	Q6LYB9 METWP
69	66	14.7	926	2	Q6ZUI1 HUMAN
70	66	14.7	575	2	Q62657 RAT
71	66	14.7	1131	2	Q54K42 DICDI
72	66	14.7	1217	2	Q5W9G9 HUMAN
73	66	14.7	1324	2	Q8JKQ9 9VIRU
74	66	14.7	1425	2	Q5KHV2 CRYNE
75	66	14.7	1538	2	Q5UU33 CRYNE
76	66	14.7	1538	2	Q5KHV3 CRYNE
77	65.5	14.6	413	2	Q4R511 MACFA
78	65.5	14.6	620	2	Q9LXX4 ARATH
79	65.5	14.6	760	2	Q4IDC6 GIBZE
80	65.5	14.6	850	1	SEMIA DROME
81	65.5	14.6	1043	2	Q55DW9 DICDI
82	65.5	14.6	1073	2	Q9WIT8 DROME
83	65.5	14.6	1173	2	Q6NR54 DROME
84	65.5	14.6	1278	2	Q42391 PLABE
85	65.5	14.6	2525	2	Q4Q184 LEIMA
86	65	14.5	144	2	Q9J6E7 9HIV1
87	65	14.5	193	2	Q6PI73 HUMAN
88	65	14.5	389	2	Q4PFM5 USTWA
89	65	14.5	493	2	Q65XF7 ORYSA
90	65	14.5	652	2	Q97WJ1 CLOAB
91	65	14.5	1612	2	Q5BFT6 BMENT
92	64.5	14.4	343	2	Q54EK7 DICDI
93	64.5	14.4	350	2	Q6BNJ6 DEBHA
94	64.5	14.4	387	2	P90905 CABEL
95	64.5	14.4	460	2	Q61D03 CABER
96	64.5	14.4	461	2	P91197 CABEL
97	64.5	14.4	468	2	Q52KU4 XENLA
98	64.5	14.4	475	2	Q74315 SCHPO
99	64.5	14.4	486	2	Q73CW4 BACCL
100	64.5	14.4	503	1	YEPA SCHPO
101	64.5	14.4	508	2	Q74118 9HIV2
102	64.5	14.4	577	2	Q894E2 CLOTE
103	64.5	14.4	754	2	Q8IBU4 PLAF7
104	64.5	14.4	764	2	Q97343 SUBDO

Q722C5	listeria mo
Q9pt68	xenopus lae
Q695c2	picea abies
Q9SPX8	picea abies
P05201	mus musculus
Q5a450	candida alb
Q5WM45	xenopus tro
Q6clb3	kluyveromyc
Q695B9	picea glauc
Q695C0	picea glauc
Q695C1	picea abies
Q9SPW5	picea glauc
Q9SPX9	picea abies
Q8BYW9	mus musculus
P54785	saccharomyc
Q9VNP2	drosophila
Q24273	drosophila
Q5CR22	cryptospori
Q5CN99	cryptospori
Q54YH9	dictyosteli
Q692Q7	citrus tris
P24821	homo sapien
Q5T7S3	homo sapien
Q4LE33	homo sapien
Q4WIU3	aspergillus
Q5NDL0	rattus norv
Q8JNB7	white spot
Q91LN4	white spot
Q6FRR1	candida gla
Q8Y8V0	listeria mo
Q52GL5	magnaporthe
Q54B59	dictyosteli
Q62701	rattus norv
Q4I7X6	gibberella
Q4YK55	plasmodium
Q6LYB9	methanococc
Q6ZUI1	homo sapien
Q62657	rattus norv
Q54K42	dictyosteli
Q5W9G9	homo sapien
Q8JKQ9	heliothis z
Q5KHV2	cryptococcu
Q5UU33	cryptococcu
Q4R511	macaca fasc
Q9LXX4	arabidopsis
Q4IDC6	gibberella
Q24322	drosophila
Q55DW9	dictyosteli
Q9WIT8	drosophila
Q6NR54	drosophila
Q42391	plasmodium
Q4Q184	leishmania
Q9J6E7	human immun
Q6PI73	homo sapien
Q4PFM5	ustilago ma
Q65XF7	oryza sativ
Q97WJ1	clostridium
Q5BFT6	aspergillus
Q54EK7	dictyosteli
Q6BNJ6	debaromyce
P90905	caenorhabdi
Q61D03	caenorhabdi
P91197	caenorhabdi
Q52KU4	xenopus lae
Q74315	schizosacch
Q73CW4	bacillus ce
O14470	schizosacch
Q74118	human immun
Q894E2	plasmodium
Q8IBU4	clote
Q97343	suberites d

105	64.5	14.4	1163	1	LEPR MACWU	Q9my10 macaca mula	178	62	13.8	293	2	Q692Q5_9CLOS	Q692Q5 citrus tris
106	64	14.3	228	1	IP4E2 CABEL	Q21693 caenorhabdi	179	62	13.8	293	2	Q692Q6_9CLOS	Q692Q6 citrus tris
107	64	14.3	252	1	Q6C9P9_YARLI	Q6c9e9 yarrowia li	180	62	13.8	293	2	Q692Q8_9CLOS	Q692Q8 citrus tris
108	64	14.3	798	2	Q86HW6_DICDI	Q86hw6 dictyosteli	181	62	13.8	293	2	Q692R0_9CLOS	Q692R0 citrus tris
109	64	14.3	802	2	Q5U4U6_CRYNE	Q5u4u6 cryptococcu	182	62	13.8	293	2	Q692R2_9CLOS	Q692R2 citrus tris
110	64	14.3	802	2	Q5KI96_CRYNE	Q5ki96 cryptococcu	183	62	13.8	327	2	Q5DD47_SCHJA	Q5dd47 schistosoma
111	64	14.3	819	2	Q5U4I7_CRYNE	Q5u4i7 cryptococcu	184	62	13.8	382	2	Q83E23_COXBU	Q83e23 coxtella bu
112	64	14.3	819	2	Q5KI97_CRYNE	Q5ki97 cryptococcu	185	62	13.8	498	2	Q50NM6_ENTHI	Q50nm6 entamoeba h
113	64	14.3	881	2	Q8XSI4_RALSO	Q8xsi4 ralstonia s	186	62	13.8	508	2	Q74116_9HIV2	Q74116 human immun
114	64	14.3	992	1	PHS2_DICDI	Q34114 dictyosteli	187	62	13.8	537	1	ACEA_EHNI	P28298 emericeella
115	64	14.3	993	2	Q54F21_DICDI	Q54f21 dictyosteli	188	62	13.8	592	2	Q54AE1_CANAL	Q54ae1 candida alb
116	64	14.3	1500	2	Q42080_9BETA	Q42080 human herpe	189	62	13.8	862	2	Q74113_9HIV2	Q74113 human immun
117	64	14.3	1500	2	Q77283_HV6U	Q77283 human herpe	190	62	13.8	864	2	Q6CD66_YARLI	Q6cd66 yarrowia li
118	64	14.3	3056	2	Q81639_PLAF7	Q8i639 plasmodium	191	62	13.8	868	2	Q54VT5_DICDI	Q54vt5 dictyosteli
119	64	14.3	5864	2	Q86913_DICDI	Q86913 dictyosteli	192	62	13.8	917	2	Q591T3_RAT	Q591t3 rattus norv
120	63.5	14.1	341	2	Q5ACM8_CANAL	Q5acm8 candida alb	193	62	13.8	924	2	Q9FIC2_ARATH	Q9fic2 arabidopsis
121	63.5	14.1	415	2	Q61NN9_XENLA	Q61nn9 xenopus lae	194	62	13.8	971	1	SECS_YEAST	P89102 saccharomyc
122	63.5	14.1	450	2	Q55DH3_DICDI	Q55dh3 dictyosteli	195	62	13.8	1011	2	Q7RD67_PLAYO	Q7rd67 plasmodium
123	63.5	14.1	485	2	Q81HD7_BACCR	Q81hd7 bacillus ce	196	62	13.8	1466	2	Q8BB47_9BETA	Q8bb47 human herpe
124	63.5	14.1	654	2	Q7TLW5_NPVCF	Q7tlw5 choristoneu	197	62	13.8	1604	2	Q4UNE0_RICPE	Q4une0 rickettsia
125	63.5	14.1	864	2	Q6BGY9_DEBHA	Q6bgy9 debaryomyce	198	62	13.8	1921	2	Q5X4P0_LEGPA	Q5x4p0 legionella
126	63.5	14.1	886	2	Q622L7_CAEBR	Q622l7 caenorhabdi	199	62	13.8	2179	2	Q7PDL7_PLAYO	Q7pdl7 plasmodium
127	63.5	14.1	906	2	Q93X51_PRUPE	Q93x51 prunus pers	200	62	13.8	2266	2	Q8WYP5_HUMAN	Q8wyp5 homo sapien
128	63	14.0	187	2	Q5BWA1_SCHJA	Q5bwa1 schistosoma	201	62	13.8	3115	2	Q91FX0_9CLOS	Q91fx0 citrus tris
129	63	14.0	231	2	Q8VRH7_ABRHY	Q8vrh7 aeromonas h	202	61.5	13.7	411	2	Q6NX26_XENTR	Q6nx26 xenopus tro
130	63	14.0	299	2	Q6FD33_ACIAD	Q6fd33 acinetobact	203	61.5	13.7	417	2	Q8YX26_ANASP	Q8yx26 anabaena sp
131	63	14.0	418	1	NAC9_ARATH	Q9zvh0 arabidopsis	204	61.5	13.7	422	2	Q4H078_CAMUP	Q4hq78 campylobact
132	63	14.0	467	2	Q660K0_BORGA	Q660k0 borrelia ga	205	61.5	13.7	442	2	Q5CFX3_CRYHO	Q5cfx3 cryptospori
133	63	14.0	577	2	Q9AUH9_PINTA	Q9auh9 pinus taeda	206	61.5	13.7	473	2	Q5GUG0_XANOR	Q5gu60 xanthomonas
134	63	14.0	617	2	Q4YHS1_PLABE	Q4yhs1 plasmodium	207	61.5	13.7	487	2	Q9P6E4_NEUCR	Q9p6e4 neuropept
135	63	14.0	684	1	CDC4_CANAL	P53699 candida alb	208	61.5	13.7	492	2	Q511W5_MAGGR	Q511w5 magnaporthe
136	63	14.0	737	2	Q6J3P9_SIVCZ	Q6j3p9 chimpanzee	209	61.5	13.7	493	2	Q4MMI7_BACCE	Q4mmi7 bacillus ce
137	63	14.0	742	2	Q55Z44_CRYNE	Q55z44 cryptococcu	210	61.5	13.7	512	2	Q6BH61_DEBHA	Q6bh61 debaryomyce
138	63	14.0	742	2	Q5KNJ9_CRYNE	Q5knj9 cryptococcu	211	61.5	13.7	519	2	Q50ZAO_ENTHI	Q50zao entamoeba h
139	63	14.0	768	2	Q5A9A6_CANAL	Q5a9a6 candida alb	212	61.5	13.7	544	2	Q4H3K1_CIOIN	Q4h3k1 clona intes
140	63	14.0	830	2	Q69565_9BETA	Q69565 human herpe	213	61.5	13.7	556	2	Q6DEK7_BRABE	Q6dek7 brachydanio
141	63	14.0	1080	2	Q6R7G6_SHERP	Q6r7g6 ostrleid her	214	61.5	13.7	647	2	Q99077_USTHO	Q99077 ustilago ho
142	63	14.0	1081	2	Q4P8L6_USTMA	Q4p8l6 ustilago ma	215	61.5	13.7	686	2	Q4WKV2_ASFPF	Q4wkv2 aspergillus
143	63	14.0	1165	1	CHS3_YEAST	P29465 saccharomyc	216	61.5	13.7	825	2	Q9FK21_ARATH	Q9fk21 arabidopsis
144	63	14.0	1198	2	Q5SE26_DICDI	Q5se26 dictyosteli	217	61.5	13.7	889	2	Q6ZHH7_ORYSA	Q6zhh7 oryza sativ
145	63	14.0	1295	2	Q69471_9BETA	Q69471 human herpe	218	61.5	13.7	1034	1	ULP2_YEAST	P40537 saccharomyc
146	63	14.0	1447	2	Q6FLG8_CANGA	Q6flg8 candida gla	219	61.5	13.7	1282	2	Q7Z8J6_USTMA	Q7z8j6 ustilago ma
147	63	14.0	1570	2	Q9U0H8_PLAF7	Q9u0h8 plasmodium	220	61.5	13.7	1351	2	Q4RQD6_TETNG	Q4rqd6 tetradodon n
148	63	14.0	1740	2	Q81JK9_PLAF7	Q81jk9 plasmodium	221	61.5	13.7	1413	2	Q9NBD3_CAEBL	Q9nbd3 caenorhabdi
149	63	14.0	1931	2	Q7YXK9_CRYPV	Q7yxk9 cryptospori	222	61.5	13.7	1439	2	Q5COG9_CRYPV	Q5cog9 cryptospori
150	63	14.0	2051	2	Q96682_DROME	Q96682 drosophila	223	61.5	13.7	1493	2	Q9NSD3_CAEBL	Q9nsd3 caenorhabdi
151	63	14.0	2051	2	Q9V4A7_DROME	Q9v4a7 drosophila	224	61.5	13.7	1873	2	Q83044_9CLOS	Q83044 lettuce inf
152	62.5	13.9	177	2	Q4Y2N4_PLACH	Q4y2n4 plasmodium	225	61.5	13.7	3023	2	Q4P701_USTMA	Q4p701 ustilago ma
153	62.5	13.9	180	2	Q7RK89_PLAYO	Q7rk89 plasmodium	226	61.5	13.7	3462	1	RELN_RAT	P58751 rattus norv
154	62.5	13.9	201	2	Q5AYF3_EHNI	Q5ayf3 aspergillus	227	61	13.6	192	2	Q49390_MYCGE	Q49390 mycoplasma
155	62.5	13.9	210	2	Q4IRL6_GIBZE	Q4irl6 gibberella	228	61	13.6	204	1	RPC8_HUMAN	Q9y535 homo sapien
156	62.5	13.9	296	2	Q92DM8_LISIN	Q92dm8 listeria in	229	61	13.6	204	1	RPC8_MOUSE	Q9d2c6 mus musculu
157	62.5	13.9	318	2	Q4WX16_ASFPF	Q4wx16 aspergillus	230	61	13.6	204	2	Q5M7Y8_HUMAN	Q5m7y8 homo sapien
158	62.5	13.9	368	2	Q5JZR1_BOYBN	Q5jzr1 glycine max	231	61	13.6	212	2	Q4Y2P3_PLACH	Q4y2p3 plasmodium
159	62.5	13.9	412	1	RATC_HUMAN	P17174 homo sapien	232	61	13.6	241	2	Q8AI21_9HIV1	Q8ai21 human immun
160	62.5	13.9	413	2	Q5VM80_HUMAN	Q5vm80 homo sapien	233	61	13.6	326	2	Q23659_ARABIDOP	Q23659 arabidopsis
161	62.5	13.9	561	2	Q8LM20_ORYSA	Q8lm20 oryza sativ	234	61	13.6	326	2	Q8H1N3_ARATH	Q8h1n3 arabidopsis
162	62.5	13.9	646	2	Q99071_USTHO	Q99071 ustilago ho	235	61	13.6	375	2	Q5S5S2_CRYNE	Q5s5s2 cryptococcu
163	62.5	13.9	702	2	Q7XF64_ORYSA	Q7xf64 oryza sativ	236	61	13.6	375	2	Q5KGR4_CRYNE	Q5kgk4 cryptococcu
164	62.5	13.9	702	2	Q8SB54_ORYSA	Q8sb54 oryza sativ	237	61	13.6	406	2	Q6ZC71_ORYSA	Q6zc71 oryza sativ
165	62.5	13.9	826	2	Q8SX11_DROME	Q8sx11 drosophila	238	61	13.6	412	1	AATC_RAT	P13221 rattus norv
166	62.5	13.9	826	2	Q7VHN9_DROME	Q7vhn9 drosophila	239	61	13.6	413	2	Q6P721_RAT	Q6p721 rattus norv
167	62.5	13.9	851	2	Q4Y406_PLACH	Q4y4g6 plasmodium	240	61	13.6	419	2	Q86M56_DROME	Q86m56 drosophila
168	62.5	13.9	911	2	Q7RJ02_PLAYO	Q7rj02 plasmodium	241	61	13.6	493	2	P94128_AERPU	P94128 aeromonas p
169	62.5	13.9	932	2	Q7VJK1_HELHP	Q7vjk1 helicobacte	242	61	13.6	574	2	Q8EC75_SHEON	Q8ec75 shewanella
170	62.5	13.9	1014	2	Q52F11_MAGGR	Q52f11 magnaporthe	243	61	13.6	642	2	Q75JG6_DICDI	Q75jg6 dictyosteli
171	62.5	13.9	1071	2	Q4HZT1_GIBZE	P17174 gibberella	244	61	13.6	681	2	Q552J1_DICDI	Q552j1 dictyosteli
172	62.5	13.9	1215	2	Q600C2_MYCHV	Q600c2 mycoplasma	245	61	13.6	687	2	Q8W3M2_CITUN	Q8w3m2 citrus unsh
173	62.5	13.9	1445	2	Q5CP73_CRYPV	Q5cpt3 cryptospori	246	61	13.6	715	2	Q59K73_CANAL	Q59k73 candida alb
174	62.5	13.9	1630	2	Q6PC80_MOUSE	Q6pc80 mus musculu	247	61	13.6	725	2	Q8T124_DICDI	Q8t124 dictyosteli
175	62.5	13.9	1811	2	Q36184_9VIRU	Q36184 plautia sta	248	61	13.6	729	2	Q59K69_CANAL	Q59k69 candida alb
176	62.5	13.9	2222	2	Q4RY92_TETNG	Q4ry92 tetradodon n	249	61	13.6	771	2	Q815E1_PLAF7	Q815e1 plasmodium
177	62.5	13.9	3446	2	Q86AC8_DICDI	Q86ac8 dictyosteli	250	61	13.6	788	2	Q9W4N2_DROME	Q9w4n2 drosophila

251	61	13.6	852	2	Q89607_9HIV2	Q89607 human immun	324	60	13.4	691	2	Q9NJ24_DROHE	Q9nj24 drosophila
252	61	13.6	889	2	Q6ZC72_ORYSA	Q6zc72 oryza sativ	325	60	13.4	701	2	Q9NJ23_DROHE	Q9nj23 drosophila
253	61	13.6	905	2	Q4XEP1_PLACH	Q4xep1 plasmodium	326	60	13.4	708	2	Q4RNN8_TETNG	Q4rnn8 tetraodon n
254	61	13.6	915	2	Q43042_PETUNIA	Q43042 petunia hyb	327	60	13.4	777	2	Q5R600_PONGY	Q5r600 pongo pygma
255	61	13.6	1023	2	Q5CUV4_CRYPTV	Q5cuv4 cryptospori	328	60	13.4	841	2	Q9NJY9_DROHE	Q9njy9 drosophila
256	61	13.6	1109	2	Q6BWC1_DEBHA	Q6bwcl debaryomyce	329	60	13.4	841	2	Q9NJY5_DROHE	Q9njy5 drosophila
257	61	13.6	1203	2	Q55B98_DICTY	Q55b98 dictyosteli	330	60	13.4	841	2	Q9NJZ6_DROHE	Q9njz6 drosophila
258	61	13.6	1469	2	Q4P4A6_USTWA	Q4p4a6 ustilago ma	331	60	13.4	938	2	Q7N2M7_PHOLL	Q7n2m7 photorhabdu
259	61	13.6	1550	2	Q55601_9VIRU	Q55601 garlic viru	332	60	13.4	947	2	Q4S557_TETNG	Q4s557 tetraodon n
260	61	13.6	1668	2	Q4RUS6_TETNG	Q4rus6 tetraodon n	333	60	13.4	955	2	Q54V91_DICTI	Q54v91 dictyosteli
261	61	13.6	1714	2	Q90995_CHICK	Q90995 gallus gall	334	60	13.4	1016	2	Q5ATD1_EMENI	Q5atd1 aspergillus
262	61	13.6	1808	1	TENA_CHICK	P10039 gallus gall	335	60	13.4	1148	1	AT8A2_MOUSE	P98200 mus musculu
263	61	13.6	1810	2	Q90824_CHICK	Q90824 gallus gall	336	60	13.4	1321	2	Q6A7F3_PROAC	Q6a7f3 propionibac
264	61	13.6	2019	2	Q80YX2_MOUSE	Q80yx2 mus musculu	337	60	13.4	1336	2	Q6UK63_DICTI	Q6uk63 dictyosteli
265	61	13.6	2019	2	Q64706_MOUSE	Q64706 mus musculu	338	60	13.4	1946	2	Q97291_PLAF7	Q97291 plasmodium
266	61	13.6	2110	2	Q80YX1_MOUSE	Q80yx1 mus musculu	339	60	13.4	2504	2	Q54FL8_DICTI	Q54fl8 dictyosteli
267	61	13.6	4293	2	Q08852_MOUSE	Q08852 mus musculu	340	60	13.4	3574	2	Q8IDA8_PLAF7	Q8ida8 plasmodium
268	60.5	13.5	127	2	Q18855_SHEEP	Q18855 ovis aries	341	60	13.4	4540	2	Q558G2_DICTI	Q55eg2 dictyosteli
269	60.5	13.5	135	2	Q5TSP8_ANOGA	Q5tsf8 anopheles g	342	59.5	13.3	126	2	Q7S979_NEUCR	Q7s979 neuropept
270	60.5	13.5	139	2	Q8LRP9_CRANM	Q8lrp9 crataegus m	343	59.5	13.3	187	2	Q4UKA1_RICPE	Q4uka1 rickettsia
271	60.5	13.5	241	2	Q8AI44_9HIV1	Q8ai44 human immun	344	59.5	13.3	208	2	Q60RG6_CABER	Q60rg6 caenorhabdi
272	60.5	13.5	267	2	Q84HS5_RHIET	Q84hs5 rhizobium e	345	59.5	13.3	255	2	Q68926_9HYME	Q68926 cotesia glo
273	60.5	13.5	343	2	Q7TU21_PROMP	Q7tu21 prochloroco	346	59.5	13.3	297	2	Q6H970_ANTWA	Q6h970 antirrhinum
274	60.5	13.5	382	2	Q60U30_CAEBR	Q60u30 caenorhabdi	347	59.5	13.3	321	2	Q83AR3_COXBA	Q83ar3 coxella bu
275	60.5	13.5	402	2	Q4V9H4_BRARE	Q4v9h4 brachydanio	348	59.5	13.3	368	2	Q5NVH2_PONGY	Q5nvh2 pongo pygma
276	60.5	13.5	444	2	Q97HP3_CLOAB	Q97hp3 clostridium	349	59.5	13.3	379	2	Q8BH91_MOUSE	Q8bh91 mus muscu
277	60.5	13.5	468	2	Q9XY08_BOMBO	Q9xy08 bombyx mori	350	59.5	13.3	395	2	Q69347_9VIBR	Q69347 vibrio sp.
278	60.5	13.5	502	2	Q6BKPE_DEBHA	Q6bkpe debaryomyce	351	59.5	13.3	398	2	Q66LE0_9HIV1	Q66le0 human immun
279	60.5	13.5	602	2	Q6MY96_ASPTU	Q6my96 aspergillus	352	59.5	13.3	413	2	Q5R524_PONGY	Q5r524 pongo pygma
280	60.5	13.5	602	2	Q4WS52_ASPTU	Q4ws52 aspergillus	353	59.5	13.3	413	2	Q5R691_PONGY	Q5r691 pongo pygma
281	60.5	13.5	604	2	Q51X20_MAGGR	Q51x20 magnaporth	354	59.5	13.3	420	2	Q68VY9_RICTY	Q68vy9 rickettsia
282	60.5	13.5	612	2	Q7RGB3_PLAYO	Q7rgb3 plasmodium	355	59.5	13.3	428	2	Q5CV4_CRYPTV	Q5cv4 cryptospori
283	60.5	13.5	661	1	INVB_DAUCA	P80065 daucus caro	356	59.5	13.3	460	2	Q9MAV1_ELAVG	Q9ma1 elaeis guin
284	60.5	13.5	668	2	Q6BY17_DEBHA	Q6by17 debaryomyce	357	59.5	13.3	515	2	Q4PD21_USTWA	Q4pd21 ustilago ma
285	60.5	13.5	740	2	Q5RD05_PONGY	Q5rds05 pongo pygma	358	59.5	13.3	530	2	Q4YWN6_PLABE	Q4ywn6 plasmodium
286	60.5	13.5	747	2	Q9DSJ3_9HIV2	Q9dsj3 human immun	359	59.5	13.3	555	2	Q9AUI0_PINTA	Q9au10 pinus taeda
287	60.5	13.5	764	2	Q6BUR8_DEBHA	Q6bur8 debaryomyce	360	59.5	13.3	557	2	P94522_CLOCL	P94622 clostridium
288	60.5	13.5	780	2	Q5AWVO_EMENI	Q5awvo aspergillus	361	59.5	13.3	562	2	Q51ZT1_MAGGR	Q51zt1 magnaporth
289	60.5	13.5	785	2	Q54C80_DICTI	Q54c80 dictyosteli	362	59.5	13.3	627	2	Q8BXM6_MOUSE	Q8bxm6 mus musculu
290	60.5	13.5	913	2	Q6BIQ9_DEBHA	Q6biq9 debaryomyce	363	59.5	13.3	628	2	Q8D349_WIGBR	Q8d349 wiglesswort
291	60.5	13.5	937	1	NUP98_RAT	P49793 rattus norv	364	59.5	13.3	637	2	Q86B13_DICTI	Q86b13 dictyosteli
292	60.5	13.5	941	2	Q6BZ13_DEBHA	Q6bz13 debaryomyce	365	59.5	13.3	639	2	Q4WR68_ASPTU	Q4wr68 aspergillus
293	60.5	13.5	992	1	VPS41_YEAST	P38959 saccharonyc	366	59.5	13.3	657	2	Q558M6_DICTI	Q558m6 dictyosteli
294	60.5	13.5	1042	2	Q9NAL5_CAEEL	Q9nal5 caenorhabdi	367	59.5	13.3	740	2	Q86IHL_DICTI	Q86ihl dictyosteli
295	60.5	13.5	1125	2	Q54H49_DICTI	Q54h49 dictyosteli	368	59.5	13.3	821	2	P87237_SCHPO	P87237 schizosacch
296	60.5	13.5	1168	2	Q5VH52_CIOIN	Q5vh52 ciona intes	369	59.5	13.3	832	2	Q6ZGD1_ORYSA	Q6zgd1 oryza sativ
297	60.5	13.5	1313	2	Q93UN0_HELPV	Q93un0 helicobacte	370	59.5	13.3	862	2	Q76606_9HIV2	Q76606 human immun
298	60.5	13.5	1335	2	Q4P846_USTWA	Q4p846 ustilago ma	371	59.5	13.3	862	2	Q9WLD7_9HIV2	Q9wld7 human immun
299	60.5	13.5	1471	2	Q5CKX5_CRYHO	Q5ckx5 cryptospori	372	59.5	13.3	901	2	Q6H972_ANTWA	Q6h972 antirrhinum
300	60.5	13.5	1736	2	Q95PH7_DICTI	Q95ph7 dictyosteli	373	59.5	13.3	902	2	Q4N4B5_THEPA	Q4n4b5 thelleria p
301	60.5	13.5	1736	2	Q86AT9_DICTI	Q86at9 dictyosteli	374	59.5	13.3	905	2	Q88A43_PSESM	Q88a43 pseudomonas
302	60.5	13.5	4816	2	Q8T103_BOMBO	Q8t103 bombyx mori	375	59.5	13.3	1317	2	Q7RNN19_PLAYO	Q7rnn19 plasmodium
303	60	13.4	162	2	Q91M77_CLOS	Q91m77 citrus tris	376	59.5	13.3	1330	2	Q9SXX5_9STRA	Q9sxx5 heterosigma
304	60	13.4	162	2	Q91M85_CLOS	Q91m85 citrus tris	377	59.5	13.3	1357	2	Q8IKL1_PLAF7	Q8ikl1 plasmodium
305	60	13.4	182	2	Q4YF21_PLABE	Q4yf21 plasmodium	378	59.5	13.3	1358	2	Q4RWU3_TETNG	Q4rwu3 tetraodon n
306	60	13.4	236	2	Q6GMW1_HUMAN	Q6gmw1 homo sapien	379	59.5	13.3	1361	2	Q7REY0_PLAYO	Q7rey0 plasmodium
307	60	13.4	266	2	Q18362_CAEEL	Q18362 caenorhabdi	380	59.5	13.3	1421	2	Q5CH19_CRYHO	Q5ch19 cryptospori
308	60	13.4	349	2	Q6LJ09_PROPR	Q6lj09 photobacter	381	59.5	13.3	1962	1	TNR6A_HUMAN	Tnrdv7 homo sapien
309	60	13.4	350	2	Q59WV1_CANAL	Q59wv1 candida alb	382	59.5	13.3	4261	2	Q8IFP4_PLAF7	Q8ifp4 plasmodium
310	60	13.4	350	2	Q59X06_CANAL	Q59x06 candida alb	383	59.5	13.3	7716	2	Q7UWZ8_RHOBA	Q7uwz8 rhodopirell
311	60	13.4	362	2	Q9CNG0_PASMO	Q9cng0 pasteurella	384	59	13.1	119	2	Q84NA0_9FABA	Q84na0 anthyllis h
312	60	13.4	365	2	Q4Z2P3_PLABE	Q4z2p3 plasmodium	385	59	13.1	120	2	Q7RB16_PLAYO	Q7rb16 plasmodium
313	60	13.4	372	2	Q61SF0_CAEBR	Q61sf0 caenorhabdi	386	59	13.1	145	2	Q6HNB8_BACHK	Q6hnb8 bacillus th
314	60	13.4	466	2	Q6CF22_YARROW	Q6cf22 yarrowia li	387	59	13.1	145	2	Q63F08_BACILL	Q63f08 bacillus ce
315	60	13.4	482	2	Q4ZJM7_MOUSE	Q4zjm7 mus musculu	388	59	13.1	146	1	CYB5M_HUMAN	Cy43169 homo sapien
316	60	13.4	489	2	Q5LSH1_CHLAB	Q5lsh1 chlamydomo	389	59	13.1	159	2	Q9JER3_9HIV1	Q9jer3 human immun
317	60	13.4	507	2	Q74115_9HIV2	Q74115 human immun	390	59	13.1	159	2	Q9JER6_9HIV1	Q9jer6 human immun
318	60	13.4	514	1	G6PD_BOSIN	Q7y837 bos indicus	391	59	13.1	183	2	Q46871_HUMAN	Q46871 homo sapien
319	60	13.4	518	2	Q9NJZ5_DROHE	Q9njz5 drosophila	392	59	13.1	188	2	Q9S466_HUMAN	Q9s466 homo sapien
320	60	13.4	577	2	Q17165_CAEEL	Q17165 caenorhabdi	393	59	13.1	198	2	Q8GLI3_AERHY	Q8gli3 aeromonas h
321	60	13.4	613	2	Q60VC0_CAEBR	Q60vc0 caenorhabdi	394	59	13.1	201	2	Q519E5_ENTHI	Q519e5 entamoeba h
322	60	13.4	667	2	Q7RLG1_PLAYO	Q7rlg1 plasmodium	395	59	13.1	227	2	Q5SQ91_HUMAN	Q5sq91 homo sapien
323	60	13.4	682	2	Q81115_PLAF7	Q81115 plasmodium	396	59	13.1	231	2	Q8MGQ8_HUMAN	Q8mgq8 homo sapien

397	59	13.1	231	2	Q8VL68_AERHY	Q8VL68_aeromonas h	470	58.5	13.0	177	2	Q6NI13_CORDI	Q6NI13_corynebacte
398	59	13.1	231	2	Q8VRH4_AERHY	Q8VRH4_aeromonas h	471	58.5	13.0	179	2	Q6TGIS_PYRGO	Q6TGIS_pyru commu
399	59	13.1	231	2	Q8VRH5_AERHY	Q8VRH5_aeromonas h	472	58.5	13.0	179	2	Q8IWS2_HUMAN	Q8IWS2_homo sapien
400	59	13.1	254	2	Q5DFB4_SCHJA	Q5DFB4_schistosoma	473	58.5	13.0	208	2	Q8NI31_HUMAN	Q8NI31_homo sapien
401	59	13.1	256	2	Q5SQ92_HUMAN	Q5SQ92_homo sapien	474	58.5	13.0	241	2	Q8AI13_9HIVI	Q8AI13_human immu
402	59	13.1	260	2	Q5JPI8_HUMAN	Q5JPI8_homo sapien	475	58.5	13.0	241	2	Q8AI14_9HIVI	Q8AI14_human immu
403	59	13.1	264	2	Q5SQ93_HUMAN	Q5SQ93_homo sapien	476	58.5	13.0	241	2	Q8AI18_9HIVI	Q8AI18_human immu
404	59	13.1	272	2	Q7P0X1_CHRVO	Q7P0X1_chromobacte	477	58.5	13.0	241	2	Q8AI24_9HIVI	Q8AI24_human immu
405	59	13.1	275	2	Q5SQ90_HUMAN	Q5SQ90_homo sapien	478	58.5	13.0	241	2	Q8AI27_9HIVI	Q8AI27_human immu
406	59	13.1	280	2	Q8IINK6_PLAF7	Q8IINK6_plasmodium	479	58.5	13.0	241	2	Q8AI28_9HIVI	Q8AI28_human immu
407	59	13.1	284	2	Q65499_ARATH	Q65499_arabidopseis	480	58.5	13.0	241	2	Q8AI30_9HIVI	Q8AI30_human immu
408	59	13.1	289	2	Q4L968_STAHL	Q4L968_staphylococ	481	58.5	13.0	241	2	Q8AI31_9HIVI	Q8AI31_human immu
409	59	13.1	295	1	METF_BUCBP	Q89B13_buchnera ap	482	58.5	13.0	241	2	Q8AI32_9HIVI	Q8AI32_human immu
410	59	13.1	324	2	Q4IG36_GIBZE	Q4IG36_gibberella	483	58.5	13.0	241	2	Q8AI33_9HIVI	Q8AI33_human immu
411	59	13.1	330	2	Q6GP91_XENLA	Q6GP91_xenopus lae	484	58.5	13.0	241	2	Q8AI34_9HIVI	Q8AI34_human immu
412	59	13.1	334	2	Q8RN80_AERHY	Q8RN80_aeromonas h	485	58.5	13.0	241	2	Q8AI36_9HIVI	Q8AI36_human immu
413	59	13.1	337	2	Q8RN84_AERHY	Q8RN84_aeromonas h	486	58.5	13.0	241	2	Q8AI37_9HIVI	Q8AI37_human immu
414	59	13.1	337	2	Q8RN87_AERHY	Q8RN87_aeromonas h	487	58.5	13.0	241	2	Q8AI38_9HIVI	Q8AI38_human immu
415	59	13.1	338	2	Q8RN88_AERHY	Q8RN88_aeromonas h	488	58.5	13.0	241	2	Q8AI39_9HIVI	Q8AI39_human immu
416	59	13.1	343	2	Q8RN78_AERHY	Q8RN78_aeromonas h	489	58.5	13.0	241	2	Q8AI42_9HIVI	Q8AI42_human immu
417	59	13.1	348	2	Q5LBM6_BACFN	Q5LBM6_bacteroides	490	58.5	13.0	241	2	Q8AI43_9HIVI	Q8AI43_human immu
418	59	13.1	366	2	Q8RN82_AERHY	Q8RN82_aeromonas h	491	58.5	13.0	254	2	Q4YIE7_PLACH	Q4YIE7_plasmodium
419	59	13.1	367	2	Q8RN86_AERHY	Q8RN86_aeromonas h	492	58.5	13.0	265	2	Q7S8J8_NEUCR	Q7S8J8_neurospora
420	59	13.1	369	2	Q8RN83_AERHY	Q8RN83_aeromonas h	493	58.5	13.0	272	2	Q7QH5_ANOGA	Q7QH5_anopheles g
421	59	13.1	369	2	Q8RN85_AERHY	Q8RN85_aeromonas h	494	58.5	13.0	276	1	SLBP_DROME	Q9VAN6_drosophila
422	59	13.1	371	2	Q8RJH3_AERHY	Q8RJH3_aeromonas h	495	58.5	13.0	328	1	EMB_RAT	Q88775_rattus norv
423	59	13.1	375	2	Q7RIV1_PLAYO	Q7RIV1_plasmodium	496	58.5	13.0	332	1	Q4PIN4_USTMA	Q4PIN4_ustilago ma
424	59	13.1	380	2	Q8RN77_AERHY	Q8RN77_aeromonas h	497	58.5	13.0	362	2	Q5BI20_EMENT	Q5BI20_aspergillus
425	59	13.1	382	2	Q95QW1_CABEL	Q95QW1_caenorhabdi	498	58.5	13.0	376	2	Q95UP2_STYFU	Q95UP2_stylyonchia
426	59	13.1	393	2	Q54R14_DICDI	Q54R14_dictyosteli	499	58.5	13.0	405	2	Q8BMN8_MOUSE	Q8BMN8_mus muscu
427	59	13.1	394	2	Q34835_KLULA	Q34835_kluyveromyc	500	58.5	13.0	421	2	Q9BIC9_TRISP	Q9BIC9_trichinella
428	59	13.1	396	2	Q6DN58_KLULA	Q6DN58_kluyveromyc	501	58.5	13.0	431	2	Q93227_CABEL	Q93227_caenorhabdi
429	59	13.1	409	2	Q4YQC9_PLABE	Q4YQC9_plasmodium	502	58.5	13.0	439	2	Q88928_WASNV	Q88928_watermelon
430	59	13.1	410	2	Q7ZUM8_BRARE	Q7ZUM8_brachydanio	503	58.5	13.0	452	2	Q6GMG6_ERARR	Q6GMG6_brachydanio
431	59	13.1	412	1	RATC_HORSE	Q8ZU86_equus cabal	504	58.5	13.0	526	2	Q517U8_ENTHI	Q517U8_entamoeba h
432	59	13.1	429	2	Q4QR59_XENLA	Q4QR59_xenopus lae	505	58.5	13.0	538	2	Q55JU4_CRYNE	Q55JU4_cryptococcu
433	59	13.1	431	2	Q6DCR0_XENLA	Q6DCR0_xenopus lae	506	58.5	13.0	538	2	Q5KQ97_CRYNE	Q5KQ97_cryptococcu
434	59	13.1	493	2	Q8GN63_AERHY	Q8GN63_aeromonas h	507	58.5	13.0	555	2	Q9ZQW3_POPTR	Q9ZQW3_populus tri
435	59	13.1	493	2	Q44063_AERHY	Q44063_aeromonas h	508	58.5	13.0	555	2	Q9PSC9_POPTR	Q9PSC9_populus tri
436	59	13.1	493	2	Q9S5D4_AERHY	Q9S5D4_aeromonas h	509	58.5	13.0	561	2	Q68FR5_RAT	Q68FR5_rattus norv
437	59	13.1	517	2	Q559D0_DICDI	Q559D0_dictyosteli	510	58.5	13.0	579	2	Q8T392_DUGJA	Q8T392_dugesia jap
438	59	13.1	518	2	Q9NJ21_DICDI	Q9NJ21_drosophila	511	58.5	13.0	588	2	Q4SGI2_TETNG	Q4SGI2_tetradodon n
439	59	13.1	554	2	Q9VDD5_DROME	Q9VDD5_drosophila	512	58.5	13.0	595	2	Q4V721_DROME	Q4V721_drosophila
440	59	13.1	554	2	Q9LGG0_ARATH	Q9LGG0_arabidopseis	513	58.5	13.0	610	2	Q5L922_BACFN	Q5L922_bacteroides
441	59	13.1	557	2	Q54I17_DICDI	Q54I17_dictyosteli	514	58.5	13.0	610	2	Q64Q99_BACFR	Q64Q99_bacteroides
442	59	13.1	575	2	Q4S208_TETNG	Q4S208_tetradodon n	515	58.5	13.0	615	2	Q8BXH8_MOUSE	Q8BXH8_mus muscu
443	59	13.1	605	2	Q6BK98_DEBHA	Q6BK98_debaryomyc	516	58.5	13.0	624	2	Q9V789_DROME	Q9V789_drosophila
444	59	13.1	616	2	Q7SEI7_NEUCR	Q7SEI7_neurospora	517	58.5	13.0	640	1	IGFIR_BOVIN	Q95688_bos taurus
445	59	13.1	663	2	Q51JY6_MAGGR	Q51JY6_magnaporthe	518	58.5	13.0	647	2	Q4N9M6_THBPA	Q4N9M6_theileria p
446	59	13.1	677	2	Q7JFW7_RABIT	Q7JFW7_oryctolagus	519	58.5	13.0	762	2	Q55B06_DICDI	Q55B06_dictyosteli
447	59	13.1	695	2	Q9NJ22_DROSL	Q9NJ22_drosophila	520	58.5	13.0	782	2	Q55C90_DICDI	Q55C90_dictyosteli
448	59	13.1	709	2	Q8TFN1_METAC	Q8TFN1_methanosarc	521	58.5	13.0	789	2	Q8CPX1_MOUSE	Q8CPX1_mus muscu
449	59	13.1	741	1	HOX1_HALRO	Q28468_holocynthia	522	58.5	13.0	797	2	Q8BLH1_MOUSE	Q8BLH1_mus muscu
450	59	13.1	769	2	Q86IH4_DICDI	Q86IH4_dictyosteli	523	58.5	13.0	826	2	Q75JF0_DICDI	Q75JF0_dictyosteli
451	59	13.1	819	2	Q8I435_PLAF7	Q8I435_plasmodium	524	58.5	13.0	837	2	Q552H0_DICDI	Q552H0_dictyosteli
452	59	13.1	820	2	Q6CMX7_KLULA	Q6CMX7_kluyveromyc	525	58.5	13.0	883	1	LMBL3_MOUSE	Q881b7_mus muscu
453	59	13.1	838	2	Q9TXM3_CABEL	Q9TXM3_caenorhabdi	526	58.5	13.0	885	2	Q5CGV6_CRYHO	Q5CGV6_cryptospori
454	59	13.1	840	2	Q8I5X4_PLAF7	Q8I5X4_plasmodium	527	58.5	13.0	932	2	Q7QB67_ANOGA	Q7QB67_anopheles g
455	59	13.1	841	2	Q9NJ20_DROSL	Q9NJ20_drosophila	528	58.5	13.0	961	2	Q8IC12_PLAF7	Q8IC12_plasmodium
456	59	13.1	905	2	Q75AU7_ASHGO	Q75AU7_ashbya goss	529	58.5	13.0	966	2	Q55Y62_CRYNE	Q55Y62_cryptococcu
457	59	13.1	922	2	Q54H00_DICDI	Q54H00_dictyosteli	530	58.5	13.0	996	2	Q67V89_ORYSA	Q67V89_oryza sativ
458	59	13.1	988	2	Q4P446_USTMA	Q4P446_ustilago ma	531	58.5	13.0	999	2	Q54BN8_DICDI	Q54BN8_dictyosteli
459	59	13.1	1006	2	Q74458_SCHPO	Q74458_schizosacch	532	58.5	13.0	1003	2	Q4UIV2_THEAN	Q4UIV2_theileria a
460	59	13.1	1074	2	Q503K3_BRARE	Q503K3_brachydanio	533	58.5	13.0	1014	2	Q6BT63_DEBHA	Q6BT63_debaryomyc
461	59	13.1	1095	2	Q4XZ33_PLACH	Q4XZ33_plasmodium	534	58.5	13.0	1085	2	Q4XXA1_PLACH	Q4XXA1_plasmodium
462	59	13.1	1515	2	Q95XK2_CABEL	Q95XK2_caenorhabdi	535	58.5	13.0	1256	2	Q8I575_PLAF7	Q8I575_plasmodium
463	59	13.1	1540	2	Q4XL97_PLACH	Q4XL97_plasmodium	536	58.5	13.0	1315	2	Q8JKP9_9VIRU	Q8JKP9_heliothis z
464	59	13.1	1781	2	Q5SLB9_LACRE	Q5SLB9_lactobacill	537	58.5	13.0	1549	2	Q6MIW7_BOEBA	Q6MIW7_belliovi
465	59	13.1	1818	2	Q8EVFI_MYCPE	Q8EVFI_mycoplasma	538	58.5	13.0	1615	1	LRP5_HUMAN	Q75197_homo sapien
466	59	13.1	2352	1	MOKI2_SCHPO	Q9Uu14_schizosacch	539	58.5	13.0	1615	2	Q9UBS7_HUMAN	Q9UBS7_homo sapien
467	59	13.1	2413	2	Q4S378_TETNG	Q4S378_tetradodon n	540	58.5	13.0	1748	1	FOLR_ELV	P35928_erysimum la
468	59	13.1	3001	2	Q8IL08_PLAF7	Q8IL08_plasmodium	541	58.5	13.0	1748	2	Q549L0_ELV	Q549L0_erysimum la
469	58.5	13.0	140	2	Q801D0_LATME	Q801D0_latimeria m	542	58.5	13.0	2251	2	Q5CJT6_CRYHO	Q5CJT6_cryptospori


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1425 55 12.2 650 2 Q42722_DAUCA
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1493 55 12.2 1984 2 Q552K7_DICDI
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1495 55 12.2 2463 2 Q4HWO0_GIBBEA
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1497 55 12.2 2666 2 Q4TIQ5_TETNG
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ALIGNMENTS

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DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ22800.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RA Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
RA Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
RA Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y.,
RA Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,
RA Isogai T., Sugano S.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK026453; BAB15488.1; -; mRNA.
DR Ensembl; ENSG00000168955; Homo sapiens.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR InterPro; IPR008661; L6_membrane.
DR Pfam; PF05805; L6_membrane; 1.
SQ SEQUENCE 229 AA; 25103 MW; B7505D2798B34CDF CRC64;
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Query Match 100.0%; Score 449; DB 2; Length 229;
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Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 KGPLMGNPSNSNANCEFSLKNISDHPESFNLQWFFNDSCAPPTGFKNKTSDNTMASGW 60
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Qy 61 RASSFHFDSSEKRLIHFS 80
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Db 171 RASSFHFDSSEKRLIHFS 190
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Q53R12 HUMAN
ID Q53R12 HUMAN PRELIMINARY; PRT; 229 AA.
AC Q53R12;
DT 13-SEP-2005 (T-EMBLrel. 31, Created)
DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
DE Hypothetical protein FLJ22800.
GN Name=PLJ22800;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RA Nguyen C., Harris A., Meyer R.;
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RT "The sequence of Homo sapiens BAC clone RP11-56306.";  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Waterston R.H.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RA Waterston R.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RA Wilson R.K.;  
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC097662; AAY24253.1; -, Genomic_DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 229 AA; 25075 MW; 1718E0594997A1A1 CRC64;  
  
Query Match 100.0%; Score 449; DB 2; Length 229;  
Best Local Similarity 100.0%; Pred. No. 8.6e-42;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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ID Q6UWS1_HUMAN PRELIMINARY; PRT; 229 AA.  
AC Q6UWS1;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE TCCE518.  
GN ORFNames=UNQ518;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,  
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Haldens S.,  
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,  
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
Vandlen R.L., Watanabe C., Weand D., Woods K., Xie M.-H.,  
Yanura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,  
Wood W.I., Godowski P.J., Gray A.M.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
effort to identify novel human secreted and transmembrane proteins: a  
bioinformatics assessment.";  
RL Genome Res. 13:2265-2270(2003).  
DR EMBL; AY358671; AA089034.1; -, mRNA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR InterPro; IPR008661; L6_membrane.  
DR Pfam; PF05805; L6_membrane; 1.  
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Db 111 KGPLMNCSPNSNANCEFSLKNTSDIHPESFNLOWFFNDSCAPPTGFNKPSTNDTMASGW 170  
QY 61 RASSFHFDSSEKRLIHFS 80  
Db 171 RASSFHFDSSEKRLIHFS 190  
  
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AC Q5U609;  
DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE Transmembrane 4 L six family member 20.  
GN Name=TM4SF20;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX NIH MGC Project;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC031574; AAH35754.1; -, mRNA.  
DR Ensembl; ENSG00000168955; Homo sapiens.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR InterPro; IPR008661; L6_membrane.  
DR Pfam; PF05805; L6_membrane; 1.  
KW Transmembrane.  
SQ SEQUENCE 229 AA; 25137 MW; B750504AFD7C247D CRC64;  
  
Query Match 100.0%; Score 449; DB 2; Length 229;  
Best Local Similarity 100.0%; Pred. No. 8.6e-42;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KGPLMNCSPNSNANCEFSLKNTSDIHPESFNLOWFFNDSCAPPTGFNKPSTNDTMASGW 60  
Db 111 KGPLMNCSPNSNANCEFSLKNTSDIHPESFNLOWFFNDSCAPPTGFNKPSTNDTMASGW 170  
QY 61 RASSFHFDSSEKRLIHFS 80  
Db 171 RASSFHFDSSEKRLIHFS 190  
  
RESULT 5  
Q9CQY8_MOUSE
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ID Q3CQV8; 2001 (TrEMBLrel. 17, Created)
AC 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 29, Last annotation update)
DE Mus musculus 11 days pregnant adult female ovary and uterus cDNA,
DE RIKEN full-length enriched library, clone:5033426G15 product:similar
DE to cDNA: FLJ22800 FIS, CLONE KATA2630 (Mus musculus 10 day old male
DE pancreas cDNA, RIKEN full-length enriched library, clone:1810018L02
DE product:similar to cDNA: FLJ22800 FIS, CLONE KATA2630).
GN Names=Tm48f20;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Bono H., Baldarelli R., Barah G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohteuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaudo I., Osaoto N., Saito R., Suzuki H., Yananaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schirml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.B., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Giasi C., Godzik A., Gough J.,
RA Grimond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai J., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kagnaga A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagahima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

RA Hara A., Hashizume W., Inotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki K., Shibata K., Shinagawa A., J.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohata E., Watahiki M.,
RA Oneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanakawa T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima J., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK017195; BAB30629.1; -; mRNA.
DR EMBL; AK007532; BAB25093.1; -; mRNA.
DR Ensembl; ENSMUSG00000026149; Mus musculus.
DR MGI; MGI:191351; Tm48f20.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR008661; L6 membrane.
DR Pfam; PF05805; L6 membrane; 1.
SQ SEQUENCE 226 AA; 24760 MW; 3FE6BA1C6A335EAD CRC64;
Query Match 52.9%; Score 237.5; DB 2; Length 236;
Best Local Similarity 53.8%; Pred. No. 3.3e-18;
Matches 43; Conservative 13; Mismatches 21; Indels 3; Gaps 2;
Qy 1 KGPLMGNPSNSNANCEPSLNKSIDIHPSFNLOWPFNDSCAPPTGPNKPTSDNTMASGW 60
Db 111 EGPLICNTQANSTVTCFESLNKLSKFPESFNLLWFFNGTCVSPDTPKNTINN-MVSNW 169
Qy 61 RASSFHFDSEENKRLIHFS 80
Db 170 KIP-NSNSEDRHIFHS 187
RESULT 6
Q9D3R0 MOUSE
ID Q9D3R0 MOUSE PRELIMINARY; PRT; 226 AA.
AC Q9D3R0; 2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Mus musculus 11 days pregnant adult female ovary and uterus cDNA,
 DE RIKEN full-length enriched library, clone:5033405M13 product:similar
 DE to cDNA: FLJ22800 FIS, CLONE KAJA2630.
 GN Name=Tm48f20; Synonym=1810018L02Rik;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
 RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RX Shihata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuami T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Iizawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:1757-1771(2000).

DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Mus musculus 11 days pregnant adult female ovary and uterus cDNA,
 DE RIKEN full-length enriched library, clone:5033405M13 product:similar
 DE to cDNA: FLJ22800 FIS, CLONE KAJA2630.
 GN Name=Tm48f20; Synonym=1810018L02Rik;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
 RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RX Shihata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuami T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Iizawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:1757-1771(2000).

DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Mus musculus 11 days pregnant adult female ovary and uterus cDNA,
 DE RIKEN full-length enriched library, clone:5033405M13 product:similar
 DE to cDNA: FLJ22800 FIS, CLONE KAJA2630.
 GN Name=Tm48f20; Synonym=1810018L02Rik;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
 RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RX Shihata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuami T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Iizawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:1757-1771(2000).

DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Mus musculus 11 days pregnant adult female ovary and uterus cDNA,
 DE RIKEN full-length enriched library, clone:5033405M13 product:similar
 DE to cDNA: FLJ22800 FIS, CLONE KAJA2630.
 GN Name=Tm48f20; Synonym=1810018L02Rik;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
 RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RX Shihata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuami T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Iizawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:1757-1771(2000).

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayaehizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayaehizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayaehizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami T., Tegawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayaehizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK017209; BAB30635.1; -; mRNA.
DR Ensembl; ENSMUSG00000026149; Mus musculus.
DR MGI; MGI:1913511; 1810018L02Rik.
DR MGI; MGI:1913511; Tm48f20.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR008661; L6 membrane.
DR Pfam; PF05805; L6_membrane; 1.
SQ SEQUENCE 226 AA; 24786 MW; 3FE6BA06703344B7 CRC64;

Query Match 51.6%; Score 231.5; DB 2; Length 226;
Best Local Similarity 52.5%; Pred. No. 1.5e-17;
Matches 42; Conservative 13; Mismatches 22; Indels 3; Gaps 2;

QY 1 KGPLCMSPNSNANCFSLKNSDIHPESFNLMQFFNDSCAPPTGFNKTSDNTMASGW 60

Db 111 EGPLCMTQANSTVTCFSLKNSKDFPESFNLMQFFNCGVCTPDKFNPTINN-WVINW 169
QY 61 RASSFHFDSEENKRLTHFS 80
Db 170 KIP--NSNSEDRHRIFHFS 187
RESULT 8
Q4KL96 XENLA
ID Q4KL96 XENLA PRELIMINARY; PRT; 242 AA.
AC Q4KL96;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.E., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Sapotnick M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RA Klein S., Gerhard D.S.;
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC09340; AAH99340.1; -; mRNA.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 242 AA; 25805 MW; 286B614727816168 CRC64;
Query Match 20.7%; Score 93; DB 2; Length 242;
Best Local Similarity 37.8%; Pred. No. 0.046;
Matches 17; Conservative 10; Mismatches 16; Indels 2; Gaps 1;

QY 1 KGPLCMSPNSNANCFSLKNS--DIHPESFNLMQFFNDSCAP 43
Db 125 KGPLCICGTGSELSSCDYTLANLSSNFKELQFDLWLRNTTCTP 169

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RESULT 9
Q66S52_9UROC PRELIMINARY; PRT; 277 AA.
AC Q66S52_9UROC PRELIMINARY; PRT; 277 AA.
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Chymotrypsin B-like protein.
GN ORFName=008-07;
OS Oikopleura dioica.
OC Eukaryota; Metazoa; Chordata; Urochordata; Appendicularia;
OC Oikopleuridae; Oikopleura.
OX NCBI_TaxID=34765;
RN [1]
RP NUCLEOTIDE SEQUENCE
RX PubMed=15343333; DOI=10.1038/nature02709;
RA Seo H.C., Edvardsen R.B., Mealand A.D., Bjordal M., Jensen M.P.,
Hansen A., Flaatt M., Weissenbach J., Lehrach H., Wincker P.,
Reinhardt R., Chourrout D.;
RT "Hox cluster disintegration with persistent anteroposterior order of
expression in Oikopleura dioica.";
RL Nature 431:67-71 (2004).
[2]
RN NUCLEOTIDE SEQUENCE
RX PubMed=15649342; DOI=10.1016/j.cub.2004.12.010;
RA Edvardsen R.B., Seo H.C., Jensen M.P., Mialon A., Mikhalava J.,
Bjordal M., Cartry J., Reinhardt R., Weissenbach J., Wincker P.,
Chourrout D.;
RT "Remodelling of the homeobox gene complement in the tunicate
Oikopleura dioica.";
RL Curr. Biol. 15:R12-R13 (2005).
DR EMBL; AV613856; AF47850.1; -; Genomic DNA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00202; Tryp_SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 277 AA; 30581 MW; 2BC4FEBA5AA27C8C CRC64;

Query Match 18.6%; Score 83.5; DB 2; Length 277;
Best Local Similarity 32.8%; Pred. No. 0.62;
Matches 22; Conservative 9; Mismatches 23; Indels 13; Gaps 3;

QY 2 GPLMCSNPSNANCFSLKNISDIHPESFNLOWFNDSCAP--PTGFNKPSTNDTWASG 59
DB 214 GPLVC-ARSGNMTREISGVSS-----WSQSCVCPANPTGFMKGPTRNKLKSC 262

QY 60 WRASSPH 66
DB 263 YRFSDPH 269

RESULT 10
Q9PT67_XENLA PRELIMINARY; PRT; 342 AA.
AC Q9PT67_XENLA PRELIMINARY; PRT; 342 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE XFD-12, protein.
GN XFD-12, protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]

RP NUCLEOTIDE SEQUENCE
RX MEDLINE=20025545; PubMed=10559492; DOI=10.1016/S0925-4773(99)00195-1;
RA Soelter M., Koester M., Hollemann T., Brey A., Pieler T., Knoechel W.;
RT "Characterization of a subfamily of related winged helix genes, XFD-
12/12'/12'' (XFLIP), during Xenopus embryogenesis.";
RL Mech. Dev. 89:161-165 (1999).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AJ242678; CAB44730.1; -; mRNA.
DR HSSP; O63245; 2HDC.
DR SNR; O9PT67; 96-192.
DR TRANSFAC; T04174; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR001766; TF_Fork_head.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00250; Fork head; 1.
DR PRINTS; PR00053; FORKHEAD.
DR ProDom; PD000425; TF_Fork_head; 1.
DR SMART; SM00339; FH; 1.
DR PROSITE; PS00657; FORK_HEAD_1; 1.
DR PROSITE; PS00658; FORK_HEAD_2; 1.
DR PROSITE; PS50039; FORK_HEAD_3; 1.
KW DNA-binding; Nuclear protein.
SQ SEQUENCE 342 AA; 38498 MW; 665D66F09F27F4FD CRC64;

Query Match 18.5%; Score 83; DB 2; Length 342;
Best Local Similarity 36.5%; Pred. No. 0.9;
Matches 19; Conservative 7; Mismatches 14; Indels 12; Gaps 2;

QY 7 NSPSNANCFSLKNI-----SDIHPESFNLOWFND-----SCAPPTG 46
DB 270 NHPNSHSCFSFIENIMGETKEPKHLTSFNQNMVNHLLQSSRLCLLPSG 321

RESULT 11
Q695C3_PICMA PRELIMINARY; PRT; 142 AA.
ID Q695C3_PICMA PRELIMINARY; PRT; 142 AA.
AC Q695C3_PICMA PRELIMINARY; PRT; 142 AA.
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE NAM protein (Fragment).
GN Name=Sb29;
OS Picea mariana (Black spruce).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
OX NCBI_TaxID=3335;
RN [1]
RP NUCLEOTIDE SEQUENCE
RA Bouille M., Bousquet J.;
RT "Trans-species shared polymorphisms at orthologous nuclear gene loci
among distant species in the conifer Picea (Pinaceae): implications
for the long-term maintenance of genetic diversity in trees.";
RL Am. J. Bot. 91:63-73 (2005).
DR EMBL; AY611037; AAT88035.1; -; Genomic DNA.
DR NON_TER.
FT NON_TER.
SQ SEQUENCE 142 AA; 15971 MW; 96380ADB9E498344 CRC64;

Query Match 18.3%; Score 82; DB 2; Length 142;
Best Local Similarity 29.7%; Pred. No. 0.41;
Matches 30; Conservative 14; Mismatches 27; Indels 30; Gaps 7;

QY 5 MCMSPSNANCFSLKNISD-----THP--ESFNLOW-----FPND- 39
DB 14 LCVSPMNSNI-CLQNLDFSDSTLKAQVQTAFTPIYSSINHOWTNCNSTDLMGLHNS 72

QY 40 SCAPPTGFNKPSTNDTWASGWRASSPHFDSEENKRLIHF 79
DB 73 SCSKPSFSFPISEKEVQSFRLENF---SQEQQSLFNF 110
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Q69S85_PTCGL PRELIMINARY;      PRT;   149 AA.
Q69S85;
25-OCT-2004 (TREMBlrel. 28, Created)
25-OCT-2004 (TREMBlrel. 28, Last sequence update)
25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DN  NAM protein (Fragment).
GN  Name=8b29;
OS  Picea glauca (White spruce).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
NCBI_TaxID=3330;
[1]
RN  NUCLEOTIDE SEQUENCE
RP  Bouille M., Bousquet J.;
RA  "Trans-species shared polymorphisms at orthologous nuclear gene loci
RT  among distant species in the conifer Picea (Pinaceae): implications
RT  for the long-term maintenance of genetic diversity in trees.";
RL  Am. J. Bot. 91:163-73 (2005).
DR  EMBL; AY611045; AAT88043.1; -; Genomic_DNA.
RN  NON TER 1
FT  SEQUENCE 149 AA; 16691 MW; 1EA438165F833P93 CRC64;

Query Match
Best Local Similarity 29.0%; Score 78.5; DB 2; Length 149;
Matches 31; Conservative 14; Mismatches 27; Indels 35; Gaps 8;

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Search completed: December 22, 2005, 03:01:08
Job time : 292 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 22, 2005, 03:01:15 ; Search time 96.3265 Seconds
(without alignments)
347.011 Million cell updates/sec

Perfect score: 449
Sequence: 1 KGPLMCNPSNANCFSL.....RASSFHFDSEKRLIHFS 80

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Published Applications AA.Main.*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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564	449	100.0	229	4	US-10-174-587-198
628	449	100.0	229	4	US-10-063-742-48
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1456	38.5	8.6	108	6	US-10-925-366A-194	Sequence 194, App
1457	38.5	8.6	108	6	US-10-925-366A-195	Sequence 195, App
1458	38.5	8.6	108	6	US-10-925-366A-196	Sequence 196, App
1459	38.5	8.6	108	6	US-10-925-366A-197	Sequence 197, App
1460	38.5	8.6	108	6	US-10-925-366A-198	Sequence 198, App
1461	38.5	8.6	108	6	US-10-925-366A-200	Sequence 200, App
1462	38.5	8.6	108	6	US-10-925-366A-201	Sequence 201, App
1463	38.5	8.6	108	6	US-10-925-366A-202	Sequence 202, App
1464	38.5	8.6	108	6	US-10-925-366A-205	Sequence 205, App
1465	38.5	8.6	108	6	US-10-925-366A-206	Sequence 206, App
1466	38.5	8.6	108	6	US-10-925-366A-207	Sequence 207, App
1467	38.5	8.6	108	6	US-10-925-366A-232	Sequence 232, App
1468	38.5	8.6	108	6	US-10-925-366A-237	Sequence 237, App
1469	38.5	8.6	108	6	US-10-925-366A-239	Sequence 239, App
1470	38.5	8.6	108	6	US-10-925-366A-284	Sequence 284, App
1471	38.5	8.6	108	6	US-10-925-366A-288	Sequence 288, App
1472	38.5	8.6	108	6	US-10-925-366A-290	Sequence 290, App
1473	38.5	8.6	108	6	US-10-925-366A-292	Sequence 292, App
1474	38.5	8.6	108	6	US-10-925-366A-297	Sequence 297, App
1475	38.5	8.6	108	6	US-10-665-658-2	Sequence 2, Appli
1476	38.5	8.6	108	7	US-11-173-071-16	Sequence 16, Appl
1477	38.5	8.6	108	7	US-11-127-677-33	Sequence 33, Appl
1478	38.5	8.6	108	7	US-11-127-677-75	Sequence 75, Appl
1479	38.5	8.6	109	7	US-11-127-677-29	Sequence 29, Appl
1480	38.5	8.6	109	7	US-11-127-932-16	Sequence 16, Appl
1481	38.5	8.6	109	7	US-11-127-932-17	Sequence 17, Appl
1482	38.5	8.6	109	7	US-11-127-932-20	Sequence 20, Appl
1483	38.5	8.6	111	7	US-11-077-978-1	Sequence 1, Appli
1484	38.5	8.6	114	6	US-10-925-366A-12	Sequence 12, Appl
1485	38.5	8.6	127	7	US-11-193-512-71	Sequence 71, Appl
1486	38.5	8.6	127	7	US-11-193-512-88	Sequence 88, Appl
1487	38.5	8.6	128	6	US-10-721-763-31	Sequence 31, Appl
1488	38.5	8.6	131	6	US-10-721-763-27	Sequence 27, Appl
1489	38.5	8.6	140	6	US-10-967-093-4	Sequence 4, Appli
1490	38.5	8.6	151	7	US-11-059-814-7	Sequence 7, Appli
1491	38.5	8.6	153	6	US-10-977-334-4	Sequence 4, Appli
1492	38.5	8.6	182	6	US-10-510-386-70	Sequence 70, Appl
1493	38.5	8.6	182	6	US-10-510-386-182	Sequence 182, App
1494	38.5	8.6	204	6	US-10-980-388-102	Sequence 102, App
1495	38.5	8.6	211	7	US-11-170-653-18	Sequence 18, Appl
1496	38.5	8.6	219	7	US-11-134-795-14	Sequence 14, Appl
1497	38.5	8.6	231	6	US-10-884-730-367	Sequence 367, App
1498	38.5	8.6	231	6	US-10-884-730-368	Sequence 368, App
1499	38.5	8.6	231	6	US-10-884-730-369	Sequence 369, App
1500	38.5	8.6	237	6	US-10-884-730-336	Sequence 336, App

Search completed: December 22, 2005, 03:08:51
Job time : 9.34694 secs

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GenCore version 5.1.6
OM protein - protein search, using sw model
Run on: -December 22, 2005, 02:28:47 ; Search time 228.571 Seconds
        (without alignments)
        153.783 Million cell updates/sec

Title:      US-10-063-553-48_COPY_111_190
Perfect score: 449
Sequence:   1 KGPLMCMSPNSNANCEFSL.....RASSFHFDSENKRLIHFS 80
Scoring table:
BLOSUM62

Searched:  2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                Maximum Match 100%
                Listing first 1500 summaries

Database :  A_Geneseq_21.*
            1: Geneseqp1980s.*
            2: Geneseqp1990s.*
            3: Geneseqp2000s.*
            4: Geneseqp2001s.*
            5: Geneseqp2002s.*
            6: Geneseqp2003as.*
            7: Geneseqp2003bs.*
            8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

No.  Score  Match Length DB  ID  Description
RESULT 1
ID  AAY66703 standard; protein; 229 AA.
DE  Membrane-bound protein PRO994.
PN  W09963088-A2.
PD  09-DEC-1999.
PA  (GETH ) GENENTECH INC.
    Query Match 100.0%; Score 449; DB 3; Length 229;
    Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 2
ID  AAU29122 standard; protein; 229 AA.
DE  Human PRO polypeptide sequence #99.
PN  W0200168848-A2.
PD  20-SEP-2001.
PA  (GETH ) GENENTECH INC.
    Query Match 100.0%; Score 449; DB 4; Length 229;
    Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 3
ID  AAB87549 standard; protein; 229 AA.
DE  Human PRO994.
PN  W0200116318-A2.
PD  08-MAR-2001.
PA  (GETH ) GENENTECH INC.
    Query Match 100.0%; Score 449; DB 4; Length 229;
    Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 4
ID  AAB65226 standard; protein; 229 AA.
DE  Human PRO994 (UNQ518) protein sequence SEQ ID NO:258.
PN  W0200073454-A1.
PD  07-DEC-2000.
PA  (GETH ) GENENTECH INC.
    Query Match 100.0%; Score 449; DB 4; Length 229;
    Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 5
ID  ASG95874 standard; protein; 229 AA.
DE  Human secreted/transmembrane protein PRO994.
PN  US200219130-A1.
PD  29-AUG-2002.
PA  (GETH ) GENENTECH INC.
    Query Match 100.0%; Score 449; DB 5; Length 229;
    Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 6
ID  ABU58498 standard; protein; 229 AA.
DE  Novel human secreted and transmembrane protein PRO994.
PN  US2003036147-A1.

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DE  Human PRO polypeptide #99.
PN  US2003027272-A1.
PD  06-FEB-2003.
    Query Match 100.0%; Score 449; DB 6; Length 229;
    Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 7
ID  ABU88046 standard; protein; 229 AA.
DE  Novel human secreted and transmembrane protein PRO994.
PN  US2003032127-A1.
PD  13-FEB-2003.
    Query Match 100.0%; Score 449; DB 6; Length 229;
    Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 8
ID  ABU84361 standard; protein; 229 AA.
DE  Human secreted/transmembrane protein (PRO) #99.
PN  US2003032112-A1.
PD  13-FEB-2003.
    Query Match 100.0%; Score 449; DB 6; Length 229;
    Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 9
ID  ABR66235 standard; protein; 229 AA.
DE  Human secreted polypeptide PRO994, SEQ ID NO:198.
PN  US2003027278-A1.
PD  06-FEB-2003.
    Query Match 100.0%; Score 449; DB 6; Length 229;
    Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 10
ID  ABR65625 standard; protein; 229 AA.
DE  Human secreted polypeptide PRO994, SEQ ID NO:198.
PN  US2003036159-A1.
PD  20-FEB-2003.
    Query Match 100.0%; Score 449; DB 6; Length 229;
    Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 11
ID  ABU99565 standard; protein; 229 AA.
DE  Human secreted/transmembrane protein (PRO) #99.
PN  US2003040070-A1.
PD  27-FEB-2003.
    Query Match 100.0%; Score 449; DB 6; Length 229;
    Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 12
ID  ABU58041 standard; protein; 229 AA.
DE  Human PRO polypeptide #73.
PN  US2003027163-A1.
PD  06-FEB-2003.
    Query Match 100.0%; Score 449; DB 6; Length 229;
    Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 13
ID  ABU59119 standard; protein; 229 AA.
DE  Novel human secreted or transmembrane protein PRO994.
PN  US2002132252-A1.
PD  19-SEP-2002.
PA  (GETH ) GENENTECH INC.
    Query Match 100.0%; Score 449; DB 6; Length 229;
    Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 14
ID  ABU82631 standard; protein; 229 AA.
DE  Human secreted/transmembrane protein PRO994.
PN  US2003032023-A1.
PD  13-FEB-2003.
    Query Match 100.0%; Score 449; DB 6; Length 229;
    Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 15
ID  ABU82804 standard; protein; 229 AA.
DE  Human PRO polypeptide #99.
PN  US2003032113-A1.
PD  13-FEB-2003.
    Query Match 100.0%; Score 449; DB 6; Length 229;
    Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 16
ID  ABU89925 standard; protein; 229 AA.
DE  Novel human secreted and transmembrane protein PRO994.
PN  US2003036147-A1.

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PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 17
ID ABR68174 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 18
ID ABU60550 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, #103.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 19
ID ABU96227 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 20
ID ABU92658 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 21
ID ABO08735 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 22
ID ABO02787 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 23
ID ABR74941 standard; polypeptide PRO994, SEQ ID NO:198.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 24
ID ABR94703 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 25
ID ABU13932 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 26
ID ABU85676 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036140-A1.
PD 20-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 27
ID ABU98836 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 28
ID ABU98051 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 29
ID ABU91757 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 30
ID ABU89450 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 31
ID ABU86291 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 32
ID ABU67504 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 33
ID ABU80532 standard; protein; 229 AA.
DE Human PRO protein #99.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 34
ID ABU72517 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 35
ID ABU90899 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 36
ID ABO33958 standard; protein; 229 AA.

DE Human secreted/transmembrane protein PRO994.
PN US2003009013-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 37
ID ABR99450 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 38
ID ABR98840 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 39
ID ABO16363 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 40
ID ABR92263 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 41
ID ABO18904 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 42
ID ABR79325 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 43
ID ABU71975 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 44
ID ABUS061 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 45
ID ABO00200 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 46
ID ABO11532 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040060-A1.

DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 47
ID ABO02177 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 48
ID ABUS8751 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 49
ID ABUS3446 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 50
ID ABO06247 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 51
ID ABR59283 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 52
ID ABO09345 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 53
ID ABO19209 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 54
ID ABO11227 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 55
ID ABR66845 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 56
ID ABO16058 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040060-A1.

PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 57
ID ABO13764 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 58
ID ABU71529 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 59
ID ABU65667 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, SEQ ID NO:198.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 60
ID ABO07515 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 61
ID ABO03702 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 62
ID ABR67150 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 63
ID ABO15753 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 64
ID ABU56034 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, PRO994.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 65
ID ABU72310 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 66
ID ABU65362 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032102-A1.

PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 67
ID ABU95307 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 68
ID ABU71210 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 69
ID ABO07820 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 70
ID ABR70061 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 71
ID ABR69394 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 72
ID ABO01535 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 73
ID ABU81337 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 74
ID ABR60134 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 75
ID ABU90983 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 76
ID ABR67869 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027269-A1.

PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 77
ID ABR65257 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 78
ID ABR68479 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 79
ID ABR71891 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 80
ID ABR64952 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 81
ID ABR68784 standard; protein; 229 AA.
DE Human secreted polypeptide #99.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 82
ID ABR9061 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 83
ID ABR83141 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 84
ID ABR94997 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 85
ID ABR90545 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 86
ID ABR84056 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 87
ID ABR93707 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 88
ID ABR25963 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 89
ID ABR64952 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 90
ID ABR27304 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO994.
PN US200309012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 91
ID ABR68784 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 92
ID ABR06600 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 93
ID ABR99145 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 94
ID ABR57029 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 95
ID ABR85981 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 96
ID ABR2268 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;

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Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 97
ID ABR66540 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027281-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
Pred. No. 2.8e-43;
RESULT 98
ID ABR90958 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
Pred. No. 2.8e-43;
RESULT 99
ID ABO08125 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
Pred. No. 2.8e-43;
RESULT 100
ID ABU92499 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
Pred. No. 2.8e-43;
RESULT 101
ID ABU81836 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
Pred. No. 2.8e-43;
RESULT 102
ID ABU66000 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
Pred. No. 2.8e-43;
RESULT 103
ID ABU81169 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
Pred. No. 2.8e-43;
RESULT 104
ID ABR59829 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
Pred. No. 2.8e-43;
RESULT 105
ID ABU94017 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
Pred. No. 2.8e-43;
RESULT 106
ID ABU98870 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
Pred. No. 2.8e-43;
RESULT 107
ID ABR66540 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
Pred. No. 2.8e-43;
RESULT 108
ID ABR90958 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
Pred. No. 2.8e-43;
RESULT 109
ID ABO53284 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
Pred. No. 2.8e-43;
RESULT 110
ID ABU58972 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, #103.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
Pred. No. 2.8e-43;
RESULT 111
ID ABU94385 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
Pred. No. 2.8e-43;
RESULT 112
ID ABU79267 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
Pred. No. 2.8e-43;
RESULT 113
ID ABU86596 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
Pred. No. 2.8e-43;
RESULT 114
ID ABU86901 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
Pred. No. 2.8e-43;
RESULT 115
ID ABU94690 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
Pred. No. 2.8e-43;
RESULT 116
ID ABO04617 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
Pred. No. 2.8e-43;
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RESULT 117
ID ABR70366 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 118
ID ABR70366 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032187-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 119
ID ABR70366 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032301-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 120
ID ABR65930 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036165-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 121
ID ABR64647 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 122
ID ABR59415 standard; protein; 229 AA.
DE Novel human secreted or transmembrane protein PRO812.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 123
ID ABR79572 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 124
ID ABR92963 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 125
ID ABR95922 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 126
ID ABR91142 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 127
ID ABR90235 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 128
ID ABR09650 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 129
ID ABR01922 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 130
ID ABR70976 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 131
ID ABR98286 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 132
ID ABR87584 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032293-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 133
ID ABR91452 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 134
ID ABR92991 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 135
ID ABR84666 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 136
ID ABR69756 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 137
ID ABR80133 standard; protein; 229 AA.
DE Human PRO protein #99.

PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 138
ID ABU82498 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 139
ID ABU92181 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 140
ID ABU93402 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 141
ID ABO09955 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 142
ID ABO09040 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 143
ID ABU96462 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 144
ID ABU10887 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 145
ID ABU10608 standard; protein; 229 AA.
DE Human secreted/transmembrane protein #99.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 146
ID ABU81639 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 147

ID ABU72132 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 148
ID ABU95617 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 149
ID ABU96826 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 150
ID ABR70671 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 151
ID ABO05022 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US200308352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 152
ID ABO08430 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 153
ID ABU88578 standard; protein; 229 AA.
DE Human secreted and transmembrane polypeptide PRO994.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 154
ID ABO34092 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 155
ID ABO05637 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 156
ID ABR74026 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;

RESULT 157
ID ABR95618 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 158
ID ABR80915 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 159
ID ABR81220 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 160
ID ABR88518 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 161
ID ABR88518 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 162
ID ABM77339 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 163
ID ABO28823 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 164
ID ABO31568 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 165
ID ABM07985 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 166
ID ABO40465 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 167
ID ABO35890 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 168
ID ABO44029 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 169
ID ADA77950 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 170
ID ABM24824 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 171
ID ABO30392 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 172
ID ABR90348 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 173
ID ABM17262 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 174
ID ABR95008 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 175
ID ABR95313 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

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Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 176
ID ADB17105 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US200305459-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 177
ID ABO21551 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 178
ID ABR97815 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 179
ID ABR87603 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 180
ID ABM77644 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 181
ID ABM27874 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 182
ID ABM03661 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 183
ID ABM03661 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 184
ID ABM35112 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 185
ID ABM26349 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 186
ID ABO48131 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 187
ID ABR92873 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 188
ID ABO24634 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 189
ID ADA37769 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 190
ID ABM11645 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 191
ID ABM02746 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 192
ID ABM16042 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 193
ID ABO27603 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 194
ID ABO27603 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 194
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ID ABM29094 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 195
ID ABM07070 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 196
ID ABM21164 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 197
ID ABM09510 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 198
ID ABO41380 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 199
ID ABO36195 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 200
ID ABO43724 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 201
ID ABM76424 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 202
ID ABM76120 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 203
ID ABM25739 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 204
ID ABM26044 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 205
ID ADA21455 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO994.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 206
ID ABO03397 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 207
ID ABO02482 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 208
ID ABO44262 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO 994.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 209
ID ABR90653 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036130-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 210
ID ABR73721 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 211
ID ABO16973 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 212
ID ABR94398 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 213
ID ABR75905 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.

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PN US2003044929-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 214
ID ABR71281 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 215
ID ABR93178 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 216
ID ABR93483 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 217
ID ADA10242 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, PRO994.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 218
ID ABR87908 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 219
ID ABO27908 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 220
ID ABO30043 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 221
ID ABO33252 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 222
ID ABR04940 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 223
ID ABR08900 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 224
ID ABO36500 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 225
ID ABO35585 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 226
ID ABO39550 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 227
ID ABR10425 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 228
ID ABR11950 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 229
ID ABO52096 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 230
ID ABO52401 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
RESULT 231
ID ADA19910 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 6; Length 229;
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Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 232
ID ABO23719 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 233
ID ADB17293 standard; protein; 229 AA.
DE Human transmembrane PRO polypeptide (SeqID 48).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 234
ID ADA17786 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 235
ID ABR97205 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 236
ID ABR6993 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 237
ID ABM11035 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 238
ID ABM28179 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 239
ID ABO32178 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 240
ID ABM15305 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 241
ID ABM06460 standard; protein; 229 AA.

DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 242
ID ABM04271 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 243
ID ABM22384 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 244
ID ABM07680 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 245
ID ABO40770 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 246
ID ABM35417 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 247
ID ABM33180 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 248
ID ABO52706 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 249
ID ABO50266 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 250
ID ABU99260 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040055-A1.

PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 251
ID ABO04312 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 252
ID ABO05942 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 253
ID ABM18482 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 254
ID ADA27894 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 255
ID ABR97510 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 256
ID ABR80610 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 257
ID ABM01221 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 258
ID ABR8823 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 259
ID ABM13475 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 260
ID ABM20859 standard; protein; 229 AA.

DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 261
ID ABO41990 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 262
ID ABO42600 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 263
ID ABM10120 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 264
ID ABO38635 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 265
ID ABM32875 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 266
ID ABM22689 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 267
ID ABM74900 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 268
ID ADA79742 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 269
ID ABR96290 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;

Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 270
ID ABO2441 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 271
ID ABR86383 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 272
ID ABR86688 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 273
ID ABM16652 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 274
ID ABM29704 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 275
ID ABO29128 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 276
ID ABM23909 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 277
ID ABM23299 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 278
ID ABM22079 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;

RESULT 279
ID ABO37720 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 280
ID ABM28484 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 281
ID ABM28789 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 282
ID ABM66433 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 283
ID ABM75815 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 284
ID ABM34095 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 285
ID ABM34400 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 286
ID ABO20331 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 287
ID ABO21246 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 288
ID ABO22161 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054477-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 289
ID ADA20082 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US200305222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 290
ID ABO34190 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO 994.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 291
ID ABR96595 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 292
ID ADA94474 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 293
ID ABR85773 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 294
ID ABR99755 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 295
ID AEM00306 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 296
ID AEM00611 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 297
ID ABO29738 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 298
ID ABR23026 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003054461-A1.
PD 20-MAR-2003.

ID ABR23604 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 299
ID ABR29399 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 300
ID ABO38330 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 301
ID ABO45630 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 302
ID ABR20554 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 303
ID ADA81469 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 304
ID ABO16668 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 305
ID ABO18294 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 306
ID ABO22721 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 307
ID ABO23026 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003054461-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 308
ID ABR92568 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 309
ID ABR81525 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 310
ID ABR77949 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 311
ID ABR89738 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 312
ID ABR26654 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 313
ID ABR13780 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 314
ID ABO28518 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 315
ID ABO30348 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 316
ID ABR07375 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 317
ID ABO03966 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 318
ID ABO37110 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 319
ID ABO41685 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 320
ID ABO35280 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 321
ID ABR25129 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 322
ID ABO47521 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 323
ID ABO47826 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 324
ID ABO48436 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 325
ID ABO51486 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 326
ID ABO51791 standard; protein; 229 AA.

DE Human PRO polypeptide #99.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 327
ID ABO50571 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 328
ID ABR79695 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 329
ID ABM16957 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 330
ID ABO17989 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 331
ID ABO20941 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 332
ID ABR96900 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 333
ID ADA38699 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 334
ID ABM12255 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 335
ID ABM16347 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
DE Human PRO polypeptide #99.

Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 336
ID ABM24214 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 337
ID ABM14695 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 338
ID ABM04576 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 339
ID ABM06765 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 340
ID ABM09205 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 341
ID ABO39245 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 342
ID ABM75510 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 343
ID ABM25434 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 344
ID ABM19944 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 345
ID ABO46850 standard; protein; 229 AA.
DE Human PRO polypeptide #99.

PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 346
ID ABO47155 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 347
ID ADA83267 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 348
ID ABR71586 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 349
ID ABR72196 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 350
ID ABR98535 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 351
ID ABO06905 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 352
ID ABR84858 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 353
ID ABR73416 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 354
ID ABR76510 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 355
ID ABR73111 standard; protein; 229 AA.

DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 356
ID ABM18177 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 357
ID ABO20636 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 358
ID ABO25379 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 359
ID ABO25684 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 360
ID ABR94093 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 361
ID ADA92820 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 362
ID ABR80000 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 363
ID ABM11340 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 364
ID ABO32947 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;

DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068739-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 384
ID ABO3356 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 385
ID ABO39855 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 386
ID ABO49961 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 387
ID ABO50876 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 388
ID ABO5332 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 389
ID ABR74636 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 390
ID ABR77115 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 391
ID ABR17872 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 392
ID ABR95923 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 393
ID ABO21856 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 394
ID ABO20026 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 395
ID ABO24329 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 396
ID ABR86078 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 397
ID ABR10730 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 398
ID ABR76729 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 399
ID ABR89433 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 400
ID ABR12560 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 401
ID ABO5850 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 402
ID ABO34975 standard; protein; 229 AA.
DE Human PRO polypeptide #99.

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PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 403
ID ABR03051 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 404
ID ABR19029 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 405
ID ABR19334 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 406
ID ABO46545 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 407
ID ABO49046 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 408
ID ABR63089 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 409
ID ABR89128 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 410
ID ABR72501 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 411
ID ABR74331 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 412
ID ABO18599 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 413
ID ABR80305 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 414
ID ABR01526 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 415
ID ABR02136 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 416
ID ABR87298 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 417
ID ABR12865 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 418
ID ABR30619 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 419
ID ABR24519 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 420
ID ABO29433 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 421
ID ABR74331 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
```

ID ABO31263 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 422
ID ABO14390 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 423
ID ABO09815 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 424
ID ABO38940 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 425
ID ABO34705 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 426
ID ABO51181 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 427
ID ABO04007 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 428
ID ABO10477 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 429
ID ABO53178 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 430
ID ABO77720 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 431
ID ABR78930 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 432
ID ABO24024 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 433
ID ABR93788 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 434
ID ABO01831 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 435
ID ABR78254 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 436
ID ABR90043 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 437
ID ADA22381 standard; protein; 229 AA.
DE Human secreted/transmembrane polypeptide PRO994.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 438
ID ABR27569 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 439
ID ABO13170 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 440
ID ABO31873 standard; protein; 229 AA.

DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068731-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 441
ID ABM14085 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 442
ID ABM08290 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068754-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 443
ID ABM74595 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096351-A1.
PD 22-MAY-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 444
ID ABM33790 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096358-A1.
PD 22-MAY-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 445
ID ABM33790 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096358-A1.
PD 22-MAY-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 446
ID ABM20249 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104556-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 447
ID ABO48741 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049756-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 448
ID ABO22548 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 449
ID ABR72806 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 450
ID ABO15448 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036121-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 451
ID ABR85163 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 452
ID ABO15143 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 453
ID ABO17278 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 454
ID ABM17567 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 455
ID ADA06547 standard; protein; 229 AA.
DE Human secreted/transmembrane PRO polypeptide #73.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 456
ID ADA39240 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 457
ID ABR85468 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049746-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 458
ID ABM77034 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054464-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 459
ID ABO28213 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064459-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 460
ID ABO28213 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064459-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;

Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 460
ID ABM22994 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 461
ID ABM30314 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 462
ID ABM21774 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 463
ID ABM21469 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 464
ID ABM15000 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 465
ID ABO41075 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 466
ID ABO36805 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 467
ID ABO37415 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 468
ID ABM75205 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 469
ID ABM33485 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 470
ID ABO46240 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 471
ID ADA82633 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 472
ID ADB85621 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 473
ID ADB96266 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 474
ID ABM31939 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 475
ID ABM31229 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 476
ID ADB85941 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 477
ID ABM32144 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 478
ID ABM32449 standard; protein; 229 AA.

DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
PD 03-APR-2003.
ID ADB68300 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
PD 27-MAR-2003.
ID ADB68107 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
PD 10-APR-2003.
ID ADB90924 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
PD 01-MAY-2003.
ID ADB90924 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003068771-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
PD 06-FEB-2003.
ID ADC57738 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
PD 06-MAR-2003.
ID ADC55102 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
PD 13-MAR-2003.
ID ADC11969 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
PD 27-MAR-2003.
ID ADC07004 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
PD 03-APR-2003.
ID ADC56391 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
PD 03-APR-2003.
ID ADC17183 standard; protein; 229 AA.
DE Mammalian PRO polypeptide (SeqID 48).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
PD 10-APR-2003.
ID ADC07446 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003068647-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
PD 10-APR-2003.
ID ADC11436 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003069403-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
PD 17-APR-2003.
ID ADC14881 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
PD 24-JUL-2003.
ID ADC52376 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
PD 01-MAY-2003.
ID ADC14558 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
PD 01-MAY-2003.
ID ADD08090 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003068623-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
PD 01-MAY-2003.
ID ADC81915 standard; protein; 229 AA.
DE Human PRO polypeptide #73.
PN US2003083461-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
PD 19-DEC-2002.

PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 449; DB 7; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.8e-43;
 RESULT 498
 ID ADC82448 standard; protein; 229 AA.
 DE Human PRO polypeptide #73.
 PN US2003059833-A1.
 PD 27-MAR-2003.
 Query Match 100.0%; Score 449; DB 7; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.8e-43;
 RESULT 499
 ID ADD05671 standard; protein; 229 AA.
 DE Human secreted/transmembrane protein (PRO) #99.
 PN US2003087376-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 449; DB 7; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.8e-43;
 RESULT 500
 ID ADD08628 standard; protein; 229 AA.
 DE Novel human secreted and transmembrane protein PRO994.
 PN US2003073090-A1.
 PD 17-APR-2003.
 Query Match 100.0%; Score 449; DB 7; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.8e-43;
 RESULT 501
 ID ADD06877 standard; protein; 229 AA.
 DE Novel human secreted and transmembrane protein PRO994.
 PN US2002193300-A1.
 PD 19-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 449; DB 7; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.8e-43;
 RESULT 502
 ID ADC83124 standard; protein; 229 AA.
 DE Human PRO polypeptide #73.
 PN US2003059783-A1.
 PD 27-MAR-2003.
 Query Match 100.0%; Score 449; DB 7; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.8e-43;
 RESULT 503
 ID ADD55231 standard; protein; 229 AA.
 DE Human PRO polypeptide #73.
 PN US2003077593-A1.
 PD 24-APR-2003.
 Query Match 100.0%; Score 449; DB 7; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.8e-43;
 RESULT 504
 ID ADD36052 standard; protein; 229 AA.
 DE Novel human secreted and transmembrane protein PRO994.
 PN US2003105298-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 449; DB 7; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.8e-43;
 RESULT 505
 ID ADD56189 standard; protein; 229 AA.
 DE Human PRO polypeptide #73.
 PN US2003077594-A1.
 PD 24-APR-2003.
 Query Match 100.0%; Score 449; DB 7; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.8e-43;
 RESULT 506
 ID ADD54627 standard; protein; 229 AA.
 DE Human PRO polypeptide #73.
 PN US2002132253-A1.
 PD 19-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 449; DB 7; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.8e-43;
 RESULT 507
 ID ADE26781 standard; protein; 229 AA.
 DE Novel human secreted and transmembrane protein PRO994.

PN US2003087304-A1.
 PD 08-MAY-2003.
 Query Match 100.0%; Score 449; DB 7; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.8e-43;
 RESULT 508
 ID ADE26248 standard; protein; 229 AA.
 DE Novel human secreted and transmembrane protein PRO994.
 PN US2003087305-A1.
 PD 08-MAY-2003.
 Query Match 100.0%; Score 449; DB 7; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.8e-43;
 RESULT 509
 ID ADF67185 standard; protein; 229 AA.
 DE Human PRO994 amino acid sequence SEQ ID NO:258.
 PN US2002198148-A1.
 PD 26-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 449; DB 7; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.8e-43;
 RESULT 510
 ID ADG01053 standard; protein; 229 AA.
 DE Novel human secreted and transmembrane protein PRO994.
 PN US2003078387-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 449; DB 7; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.8e-43;
 RESULT 511
 ID ADG08606 standard; protein; 229 AA.
 DE Novel human secreted and transmembrane protein PRO994.
 PN US2003180793-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 449; DB 7; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.8e-43;
 RESULT 512
 ID ADG03666 standard; protein; 229 AA.
 DE Novel human secreted and transmembrane protein PRO994.
 PN US2003207397-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 449; DB 7; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.8e-43;
 RESULT 513
 ID ADG01373 standard; protein; 229 AA.
 DE Novel human secreted and transmembrane protein PRO994.
 PN US2003207399-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 449; DB 7; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.8e-43;
 RESULT 514
 ID ADF95548 standard; protein; 229 AA.
 DE Novel human secreted and transmembrane protein PRO994.
 PN US2003207398-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 449; DB 7; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.8e-43;
 RESULT 515
 ID ADF95227 standard; protein; 229 AA.
 DE Novel human secreted and transmembrane protein PRO994.
 PN US2003180795-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 449; DB 7; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.8e-43;
 RESULT 516
 ID ADG12363 standard; protein; 229 AA.
 DE Novel human secreted and transmembrane protein PRO994.
 PN US2003207392-A1.
 PD 06-NOV-2003.
 Query Match 100.0%; Score 449; DB 7; Length 229;

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Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 517
ID ADH24080 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 518
ID ADH34106 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 519
ID ADH29939 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 520
ID ADH23910 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 521
ID ADH09023 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 522
ID ADH85314 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 523
ID ADH24590 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 524
ID ADH37446 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 525
ID ADH02035 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 526
ID ADH37616 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 527
ID ADH85654 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 528
ID ADH24250 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 529
ID ADH38544 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 530
ID ADH36665 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 531
ID ADH29473 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 532
ID ADH27589 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 533
ID ADH37786 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 534
ID ADH37963 standard; protein; 229 AA.
DE Human secreted and transmembrane protein PRO994.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 535
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ID ADH57383 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 536
ID ADH53525 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 537
ID ADH53695 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 538
ID ADH52031 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 539
ID ADH49886 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 540
ID ADI25396 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 541
ID ADH90189 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 542
ID ADI25566 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 543
ID ADH97740 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
ID ADI35439 standard; protein; 229 AA.

DE Human PRO polypeptide #73.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 545
ID ADI03588 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 546
ID ADI11945 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 547
ID ADH90019 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 548
ID ADH99931 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 549
ID ADH98420 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 550
ID ADI11095 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 551
ID ADI11605 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 552
ID ADH98250 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 553
ID ADH98590 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181708-A1.
PD 25-SEP-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 554
ID ADH98080 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 555
ID ADI05068 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 556
ID ADI03418 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 557
ID ADI04813 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 558
ID ADH78267 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 559
ID ADI19611 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 560
ID ADH90359 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 561
ID ADI03078 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 562
ID ADH79227 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 563
ID ADH97910 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 564
ID ADI01295 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 565
ID ADI01990 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 566
ID ADI03248 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 567
ID ADI11435 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 568
ID ADI02337 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 569
ID ADI11775 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 570
ID ADI05412 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 571
ID ADH79484 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
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Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 572
ID ADI19441 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 573
ID ADI05242 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 574
ID ADH79654 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 575
ID ADI01480 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 576
ID ADI01650 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 577
ID ADI01820 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 578
ID ADH79824 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 579
ID ADI04642 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 580
ID ADI02778 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 581
ID ADH78097 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 582
ID ADI25736 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 583
ID ADI25906 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 584
ID ADK65418 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 585
ID ADH98760 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 586
ID ADH80001 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 587
ID ADL32804 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 588
ID ADM30338 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 589
ID ADL93732 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 590
ID ADL93732 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;

ID A8M85217 standard; protein; 229 AA.
DE Human protein sequence hCP1734062.
PN W02003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 100.0%; Score 449; DB 7; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 591
ID AUC52186 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 592
ID ADE74335 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 593
ID ADE74947 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 594
ID ADF35384 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 595
ID ADG11634 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 596
ID ADF96160 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 597
ID ADG04431 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 598
ID ADG00591 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 599
ID ADH06618 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 600
ID ADH06448 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 601
ID ADG68869 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 602
ID ADH27759 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 603
ID ADH25100 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 604
ID ADH37372 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 605
ID ADG82847 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 606
ID ADH02375 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 607
ID ADH07982 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 608
ID ADG69379 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;

Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 609
ID ADH39200 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 610
ID ADH26128 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 611
ID ADG83940 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 612
ID ADH19504 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 613
ID ADG85484 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 614
ID ADH06278 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 615
ID ADH30108 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 616
ID ADH24420 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 617
ID ADH33097 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 618
ID ADG69549 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 619
ID ADH07812 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 620
ID ADG85824 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 621
ID ADH39370 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 622
ID ADH33562 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 623
ID ADH33902 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 624
ID ADH01112 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 625
ID ADG69719 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 626
ID ADH20997 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 627
ID ADH02205 standard; protein; 229 AA.

DE Human PRO polypeptide #24.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 628
ID ADG69209 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 629
ID ADG85994 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 630
ID ADH24930 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 631
ID ADH39547 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 632
ID ADH20037 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 633
ID ADH02545 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 634
ID ADG69039 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 635
ID ADH07642 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
ID ADG86164 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.

PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 637
ID ADH24760 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 638
ID ADH25808 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 639
ID ADH38374 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 640
ID ADH57213 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 641
ID ADH52201 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 642
ID ADH49567 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 643
ID ADH90529 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 644
ID ADH11265 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
ID ADH98930 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003190698-A1.

PA 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 646
ID AD102160 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 647
ID ADH90699 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 648
ID ADJ54836 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 649
ID ADJ98574 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 650
ID ADJ98744 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 651
ID ADH78903 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 652
ID ADJ99137 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 653
ID ADJ99307 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 654
ID ADJ98925 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 655
ID ADH79073 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 656
ID ADK00933 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 657
ID ADK14454 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 658
ID ADJ64607 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 659
ID ADM31503 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 660
ID ADM36550 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 661
ID ADM40355 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 662
ID ADM80903 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 449; DB 8; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.8e-43;
RESULT 663
ID ADN37963 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 449; DB 8; Length 229;
RESULT 664
ID ADR14507 standard; protein; 229 AA.
DE Human NF-kappaB pathway-associated protein SeqID508.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match
Best Local Similarity 100.0%; Score 449; DB 8; Length 229;
RESULT 665
ID ADY77743 standard; protein; 229 AA.
DE Neoplastic disease detection protein PRO994.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (SATO)/ EATON D L.
PA (FILV)/ FILVAROFF E.
PA (GERR)/ GERRITSEN M E.
PA (GODD)/ GODDARD A.
PA (GODO)/ GODOWSKI P J.
PA (GRIM)/ GRIMALDI J C.
PA (GURN)/ GURNEY A L.
PA (WATA)/ WATANABE C K.
PA (WOOD)/ WOOD W I.
Query Match
Best Local Similarity 100.0%; Score 449; DB 9; Length 229;
RESULT 666
ID AZA38511 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, #141.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 449; DB 9; Length 229;
RESULT 667
ID ABM85216 standard; protein; 230 AA.
DE Mouse protein sequence MCP5099.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match
Best Local Similarity 52.9%; Score 237.5; DB 7; Length 230;
RESULT 668
ID ADT66602 standard; protein; 413 AA.
DE Murine aspartate aminotransferase protein.
PN WO2004070383-A2.
PD 19-AUG-2004.
PA (CHEF) GRUENENTHAL GMBH.
Query Match
Best Local Similarity 16.3%; Score 73; DB 8; Length 413;
RESULT 669
ID ADP90866 standard; protein; 527 AA.
DE Mouse extracellular matrix protein #6.
PN JP2004180541-A.
PD 02-JUL-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA (RIKA) RIKAGAKU KENKYUSHO.
PA (DANA-) DANAFOMU KK.
Query Match
Best Local Similarity 15.7%; Score 70.5; DB 8; Length 527;
RESULT 670
ID AAB61263 standard; protein; 631 AA.
DE Human monocyte inhibitory receptor precursor.
PN WO200100810-A1.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 15.6%; Score 70; DB 4; Length 631;
RESULT 671
ID ABB71337 standard; protein; 1079 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40803.
PN WO200171042-A2.
PD 27-SEP-2001.

PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 15.6%; Score 70; DB 4; Length 1079;
RESULT 672
ID AG84914 standard; protein; 610 AA.
DE Shrimp white spot Bacilliform virus (WSBV) protein 5.
PN WO200138351-A2.
PD 31-MAY-2001.
PA (PENY-) PE CORP NY.
PA (THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI C A.
PA (SINO-) SINOGENOMAX CO LTD.
Query Match
Best Local Similarity 15.5%; Score 69.5; DB 4; Length 610;
RESULT 673
ID ABB98338 standard; protein; 292 AA.
DE Human anti-tenascin C monoclonal antibody SEQ ID NO 2.
PN JP2002234900-A.
PD 23-AUG-2002.
PA (MIED-) MIE DAIGAKUCHO.
Query Match
Best Local Similarity 15.1%; Score 68; DB 6; Length 292;
RESULT 674
ID ADF04284 standard; protein; 292 AA.
DE Human tenascin C fibronectin III-like domain BCD domain polypeptide.
PN JP2004138489-A.
PD 13-MAY-2004.
PA (MENE-) MENEKI SEIBUTSU KENKYUSHO KK.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Query Match
Best Local Similarity 15.1%; Score 68; DB 8; Length 292;
RESULT 675
ID ADM18489 standard; protein; 362 AA.
DE Pinus radiata transcription factor protein NAC family Seq 2279.
PN WO2005001050-A2.
PD 06-JAN-2005.
PA (ARBO-) ARBORGEN LLC.
Query Match
Best Local Similarity 15.1%; Score 68; DB 9; Length 362;
RESULT 676
ID ADN05803 standard; protein; 2000 AA.
DE Antiproliferative protein sequence #1065.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 15.1%; Score 68; DB 8; Length 2000;
RESULT 677
ID ABO01379 standard; protein; 2108 AA.
DE Human protein NOV35b.
PN WO2003023008-A2.
PD 20-MAR-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 15.1%; Score 68; DB 6; Length 2108;
RESULT 678
ID ADN96130 standard; protein; 2108 AA.
DE Human NOVX polypeptide #92.
PN US2004067490-A1.
PD 08-APR-2004.
PA (ZHON)/ ZHONG M.
PA (LILL)/ LI L.
PA (GORM)/ GORMAN L.
PA (SPYT)/ SPYTEK K A.
PA (KEKU)/ KEKUDA R.
PA (TAUP)/ TAUPIER R J.
PA (ANDE)/ ANDERSON D W.
PA (VERN)/ VERNET C A M.
PA (CATT)/ CATTERTON E.
PA (MILL)/ MILLER C E.
PA (SHEN)/ SHENOY S G.
PA (PATI)/ PATTURAJAN M.
PA (PENA)/ PENNA C E A.
PA (TCHE)/ TCHERNEV V T.

PA (PADI/) PADIGARU M.
PA (GUSE/) GUSEV V Y.
PA (MALY/) MALYANKAR U M.
PA (BURG/) BURGESS C E.
PA (GERL/) GERLACH V.
PA (CASM/) CASMAN S J.
PA (RIEG/) RIEGER D K.
PA (GROS/) GROSSE W M.
PA (SMIT/) SMITHSON G.
PA (PEYM/) PEYMAN J A.
PA (STAR/) STARLING G.
PA (ROTH/) ROTHENBERG M E.
PA (LARO/) LAROCHELLE W J.
PA (SHIM/) SHIMKETS R A.
PA (CRAB/) CRABTREE J.
PA (RAST/) RASTELLI L.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (EDIN/) EDINGER S R.
PA (MILL/) MILLET I.
PA (MACD/) MACDOUGALL J R.
PA (ELLE/) ELLERMAN K.
PA (CHAP/) CHAPOVAL A.
Query Match 15.1%; Score 68; DB 8; Length 2108;
Best Local Similarity 66.7%; Pred. No. 4.4e+02;
RESULT 679
ID AAO30847 standard; protein; 2110 AA.
DE Human cell adhesion and extracellular matrix protein (CADECM)-37.
PN WO2003047526-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 15.1%; Score 68; DB 7; Length 2110;
Best Local Similarity 66.7%; Pred. No. 4.4e+02;
RESULT 680
ID ADM80773 standard; protein; 2110 AA.
DE Human CADECM-2 protein SEQ ID NO:2.
PN WO2004013396-A2.
PD 19-FEB-2004.
PA (INCY-) INCYTE CORP.
Query Match 15.1%; Score 68; DB 8; Length 2110;
Best Local Similarity 66.7%; Pred. No. 4.4e+02;
RESULT 681
ID ABM83292 standard; protein; 2116 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3541.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 15.1%; Score 68; DB 8; Length 2116;
Best Local Similarity 66.7%; Pred. No. 4.4e+02;
RESULT 682
ID ABM83291 standard; protein; 2122 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3540.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 15.1%; Score 68; DB 8; Length 2122;
Best Local Similarity 66.7%; Pred. No. 4.4e+02;
RESULT 683
ID ABG70361 standard; protein; 2167 AA.
DE Novel human thrombopoietin variant protein, NV-20.
PN US2002068342-A1.
PD 06-JUN-2002.
PA (KHOS/) KHOSRAVI R.
PA (BERN/) BERNSTEIN J.
Query Match 15.1%; Score 68; DB 5; Length 2167;
Best Local Similarity 66.7%; Pred. No. 4.5e+02;
RESULT 684
ID AAR94562 standard; protein; 2199 AA.
DE Human cytotoxin.
PN WO9608513-A1.
PD 21-MAR-1996.
PA (SCRI) SCRIPPS RES INST.
Query Match 15.1%; Score 68; DB 2; Length 2199;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 685
ID ABO01378 standard; protein; 2199 AA.
DE Human protein NOV35a.
PN WO2003023008-A2.
PD 20-MAR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.1%; Score 68; DB 6; Length 2199;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 686
ID ADN96128 standard; protein; 2199 AA.
DE Human NOVX polypeptide #91.
PN US2004067490-A1.
PD 08-APR-2004.
PA (ZHON/) ZHONG M.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (SPYT/) SPYTEK K A.
PA (KEKU/) KEKUDA R.
PA (TAUP/) TAUPIER R J.
PA (ANDE/) ANDERSON D W.
PA (VERN/) VERNET C A M.
PA (CATT/) CATTERTON E.
PA (MILL/) MILLER C E.
PA (SHEN/) SHENOY S G.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENNA C E A.
PA (TCHE/) TCHERNEV V T.
PA (PADI/) PADIGARU M.
PA (GUSE/) GUSEV V Y.
PA (MALY/) MALYANKAR U M.
PA (BURG/) BURGESS C E.
PA (GERL/) GERLACH V.
PA (CASM/) CASMAN S J.
PA (RIEG/) RIEGER D K.
PA (GROS/) GROSSE W M.
PA (SMIT/) SMITHSON G.
PA (PEYM/) PEYMAN J A.
PA (STAR/) STARLING G.
PA (ROTH/) ROTHENBERG M E.
PA (LARO/) LAROCHELLE W J.
PA (SHIM/) SHIMKETS R A.
PA (CRAB/) CRABTREE J.
PA (RAST/) RASTELLI L.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (EDIN/) EDINGER S R.
PA (MILL/) MILLET I.
PA (MACD/) MACDOUGALL J R.
PA (ELLE/) ELLERMAN K.
PA (CHAP/) CHAPOVAL A.
Query Match 15.1%; Score 68; DB 8; Length 2199;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 687
ID AAB36935 standard; protein; 2201 AA.
DE Human tenascin-C.
PN WO2000066628-A1.
PD 09-NOV-2000.
PA (DYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
Query Match 15.1%; Score 68; DB 4; Length 2201;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 688
ID ABP97745 standard; protein; 2201 AA.
DE Amino acid sequence of human HXB polypeptide.
PN WO2003010205-A1.
PD 06-FEB-2003.
PA (UYDU-) UNIV DUKE MEDICAL CENT.
Query Match 15.1%; Score 68; DB 6; Length 2201;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 689
ID ABM78955 standard; protein; 2201 AA.
DE Breast cancer specific marker under-expressed in breast cancer.
PN WO2003073911-A2.

PD 12-SEP-2003.
PA (GBOU) UNIV GEORGETOWN.
Query Match 15.1%; Score 68; DB 7; Length 2201;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 690
ID ADD69400 standard; protein; 2201 AA.
DE Human tenascin protein - SEQ ID 136.
PN WO2003048185-A2.
PD 12-JUN-2003.
PA (GENV-) GENVEC INC.
Query Match 15.1%; Score 68; DB 7; Length 2201;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 691
ID ADD47935 standard; protein; 2201 AA.
DE Human Protein XP_005348, SEQ ID NO 13631.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 15.1%; Score 68; DB 7; Length 2201;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 692
ID ADE62224 standard; protein; 2201 AA.
DE Human Protein P24821, SEQ ID NO 8153.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 15.1%; Score 68; DB 7; Length 2201;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 693
ID ADO17766 standard; protein; 2201 AA.
DE Differentially expressed protein Lul, SEQ ID 1.
PN WO2004015390-A2.
PD 19-FEB-2004.
PA (APPL-) APPLERA CORP.
Query Match 15.1%; Score 68; DB 8; Length 2201;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 694
ID ADO19756 standard; protein; 2201 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2575.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 15.1%; Score 68; DB 8; Length 2201;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 695
ID ADU06359 standard; protein; 2201 AA.
DE Novel bronchial cancer-associated human protein SeqID583.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VBLEZ E.
Query Match 15.1%; Score 68; DB 8; Length 2201;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 696
ID ADV02008 standard; protein; 2201 AA.
DE Tumor-associated antigenic target polypeptide TAT450.
PN WO2004112829-A2.
PD 29-DEC-2004.
PA (GFTH) GENENTECH INC.
Query Match 15.1%; Score 68; DB 9; Length 2201;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 697
ID ADW88533 standard; peptide; 2201 AA.
DE Human tenascin-C.
PN WO2005009366-A2.
PD 03-FEB-2005.
PA (CORR) CORNELL RES FOUND INC.
Query Match 15.1%; Score 68; DB 9; Length 2201;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 698
ID ADW83294 standard; protein; 2207 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3543.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 15.1%; Score 68; DB 8; Length 2207;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 699
ID AWM83293 standard; protein; 2207 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3542.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 15.1%; Score 68; DB 8; Length 2207;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 700
ID AWM83295 standard; protein; 2207 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3544.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 15.1%; Score 68; DB 8; Length 2207;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
RESULT 701
ID ABE49395 standard; protein; 296 AA.
DE Listeria monocytogenes protein #2099.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 14.9%; Score 67; DB 5; Length 296;
Best Local Similarity 28.4%; Pred. No. 48;
RESULT 702
ID ABR41213 standard; protein; 337 AA.
DE Human DITHP receptor.
PN WO200297031-A2.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 14.9%; Score 67; DB 6; Length 337;
Best Local Similarity 24.0%; Pred. No. 57;
RESULT 703
ID ABE10579 standard; protein; 500 AA.
DE Human macrophage-expressed protein #4.
PN WO200164839-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 14.9%; Score 67; DB 4; Length 500;
Best Local Similarity 24.0%; Pred. No. 93;
RESULT 704
ID ABG10535 standard; protein; 500 AA.
DE Novel human diagnostic protein #10526.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 14.9%; Score 67; DB 4; Length 500;
Best Local Similarity 24.0%; Pred. No. 93;
RESULT 705
ID ADE62222 standard; protein; 619 AA.
DE Rat Protein AAA50761, SEQ ID NO 8151.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 14.9%; Score 67; DB 7; Length 619;
Best Local Similarity 40.0%; Pred. No. 1.2e+02;
RESULT 706
ID ABUL1229 standard; protein; 631 AA.
DE Human monocyte inhibitory receptor precursor protein.
PN WO200280968-A1.
PD 17-OCT-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 14.9%; Score 67; DB 6; Length 631;
Best Local Similarity 24.0%; Pred. No. 1.2e+02;
RESULT 707

ID ABU12086 standard; protein; 632 AA.
DE Human NOV27a CG93884-01 protein SEQ ID 92.
PN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 14.9%; Score 67; DB 6; Length 632;
Best Local Similarity 24.0%; Pred. No. 1.3e+02;
RESULT 708
ID ABG01737 standard; protein; 161 AA.
DE Novel human diagnostic protein #1728.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 14.8%; Score 66.5; DB 4; Length 161;
Best Local Similarity 29.5%; Pred. No. 26;
RESULT 709
ID ABR82240 standard; protein; 677 AA.
DE Human nucleic acid-associated protein (NAAP)-Id 2848827CD1.
PN WO2003052048-A2.
PD 26-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 14.8%; Score 66.5; DB 6; Length 677;
Best Local Similarity 31.6%; Pred. No. 1.6e+02;
RESULT 710
ID AQQ66763 standard; protein; 926 AA.
DE Novel human protein sequence #1736.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 14.8%; Score 66.5; DB 8; Length 926;
Best Local Similarity 31.6%; Pred. No. 2.3e+02;
RESULT 711
ID ABM92081 standard; protein; 1627 AA.
DE M. xanthus protein sequence, seq id 11280.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS-) MONSANTO TECHNOLOGY LLC.
Query Match 14.8%; Score 66.5; DB 9; Length 1627;
Best Local Similarity 28.6%; Pred. No. 4.7e+02;
RESULT 712
ID ADU82617 standard; protein; 1725 AA.
DE Human MDTT polypeptide (ID 7526175CD1).
PN WO2004093930-A2.
PD 18-NOV-2004.
PA (INCY-) INCYTE CORP.
Query Match 14.8%; Score 66.5; DB 8; Length 1725;
Best Local Similarity 31.6%; Pred. No. 5.1e+02;
RESULT 713
ID ADT77471 standard; protein; 2046 AA.
DE Human nucleic acid-associated protein 7526176CD1.
PN WO2004087875-A2.
PD 14-OCT-2004.
PA (INCY-) INCYTE CORP.
Query Match 14.8%; Score 66.5; DB 8; Length 2046;
Best Local Similarity 31.6%; Pred. No. 6.3e+02;
RESULT 714
ID ADD47933 standard; protein; 575 AA.
DE Rat Protein AAA56909, SEQ ID NO 13629.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 14.7%; Score 66; DB 7; Length 575;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
RESULT 715
ID ADP09773 standard; protein; 1217 AA.
DE JNK3 human KIAA0569 protein.
PN WO2003086462-A1.
PD 23-OCT-2003.
PA (CELE-) CELESTAR LEXICO SCI INC.
PA (DAUC) DAIICHI PHARM CO LTD.
Query Match 14.7%; Score 66; DB 7; Length 1217;
Best Local Similarity 27.5%; Pred. No. 3.7e+02;

RESULT 716
ID AEG12658 standard; protein; 1219 AA.
DE Novel human diagnostic protein #12649.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 14.7%; Score 66; DB 4; Length 1219;
Best Local Similarity 27.5%; Pred. No. 3.7e+02;
RESULT 717
ID AAM78969 standard; protein; 1279 AA.
DE Human protein SEQ ID NO 1631.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 14.7%; Score 66; DB 4; Length 1279;
Best Local Similarity 27.5%; Pred. No. 4e+02;
RESULT 718
ID AAM79953 standard; protein; 1301 AA.
DE Human protein SEQ ID NO 3599.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 14.7%; Score 66; DB 4; Length 1301;
Best Local Similarity 27.5%; Pred. No. 4e+02;
RESULT 719
ID AAR71382 standard; protein; 650 AA.
DE Drosophila semaphorin I protein.
PN WO9507706-A1.
PD 23-MAR-1995.
PA (REGC) UNIV CALIFORNIA.
Query Match 14.6%; Score 65.5; DB 2; Length 650;
Best Local Similarity 31.8%; Pred. No. 1.9e+02;
RESULT 720
ID ABB64331 standard; protein; 771 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 19785.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 14.6%; Score 65.5; DB 4; Length 771;
Best Local Similarity 31.8%; Pred. No. 2.4e+02;
RESULT 721
ID ABB68283 standard; protein; 905 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 31641.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 14.6%; Score 65.5; DB 4; Length 905;
Best Local Similarity 27.3%; Pred. No. 2.9e+02;
RESULT 722
ID ABM84660 standard; protein; 452 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4909.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 14.5%; Score 65; DB 8; Length 452;
Best Local Similarity 24.0%; Pred. No. 1.4e+02;
RESULT 723
ID ABM84659 standard; protein; 481 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4908.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 14.5%; Score 65; DB 8; Length 481;
Best Local Similarity 24.0%; Pred. No. 1.5e+02;
RESULT 724
ID ADN99607 standard; protein; 512 AA.
DE Novel human protein sequence #423.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 14.5%; Score 65; DB 8; Length 512;
Best Local Similarity 24.0%; Pred. No. 1.6e+02;
RESULT 725

ID AAM20306 standard; protein; 79 AA.
DE Peptide #6740 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 03-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.4%; Score 64.5; DB 4; Length 79;
Best Local Similarity 32.8%; Pred. No. 18;
RESULT 726
ID ABB40757 standard; peptide; 79 AA.
DE Peptide #8263 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.4%; Score 64.5; DB 4; Length 79;
Best Local Similarity 32.8%; Pred. No. 18;
RESULT 727
ID AAM34523 standard; protein; 79 AA.
DE Peptide #8560 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.4%; Score 64.5; DB 4; Length 79;
Best Local Similarity 32.8%; Pred. No. 18;
RESULT 728
ID ABB24972 standard; protein; 79 AA.
DE Protein #5971 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.4%; Score 64.5; DB 4; Length 79;
Best Local Similarity 32.8%; Pred. No. 18;
RESULT 729
ID AAM74409 standard; protein; 79 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 34715.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.4%; Score 64.5; DB 4; Length 79;
Best Local Similarity 32.8%; Pred. No. 18;
RESULT 730
ID AAM61617 standard; protein; 79 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 33722.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.4%; Score 64.5; DB 4; Length 79;
Best Local Similarity 32.8%; Pred. No. 18;
RESULT 731
ID ABG56204 standard; peptide; 79 AA.
DE Human liver peptide, SEQ ID NO 34852.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.4%; Score 64.5; DB 4; Length 79;
Best Local Similarity 32.8%; Pred. No. 18;
RESULT 732
ID ABG44311 standard; peptide; 79 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 33976.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 14.4%; Score 64.5; DB 5; Length 79;
Best Local Similarity 32.8%; Pred. No. 18;
RESULT 733
ID ADN22431 standard; protein; 461 AA.
DE Bacterial polypeptide #5084.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.

Query Match 14.4%; Score 64.5; DB 8; Length 461;
Best Local Similarity 26.5%; Pred. No. 1.6e+02;
RESULT 734
ID ADI45315 standard; protein; 1185 AA.
DE Rice isoprenoid biosynthesis-associated protein #123.
PN US2004010815-A1.
PD 15-JAN-2004.
PA (LANG/) LANGE B M.
PA (GHAS/) GHASSEMIAN M.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZE BROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICHKE D.
PA (ZHUT/) ZHU T.
Query Match 14.4%; Score 64.5; DB 8; Length 1185;
Best Local Similarity 27.8%; Pred. No. 5.4e+02;
RESULT 735
ID ADN24041 standard; protein; 228 AA.
DE Bacterial polypeptide #6694.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 14.3%; Score 64; DB 8; Length 228;
Best Local Similarity 31.9%; Pred. No. 77;
RESULT 736
ID ABM87753 standard; protein; 959 AA.
DE Rice abiotic stress responsive polypeptide SEQ ID NO:5999.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 14.3%; Score 64; DB 7; Length 959;
Best Local Similarity 26.6%; Pred. No. 4.7e+02;
RESULT 737
ID ADR43499 standard; protein; 3056 AA.
DE CSA-binding malarial variant surface antigen.
PN WO2004067559-A1.
PD 12-AUG-2004.
PA (UYKO-) UNIV KOENHAVNS.
Query Match 14.3%; Score 64; DB 8; Length 3056;
Best Local Similarity 29.7%; Pred. No. 2e+03;
RESULT 738
ID AAB11524 standard; protein; 166 AA.
DE SEN virus protein fragment SEQ ID NO: 70.
PN WO200028039-A2.
PD 18-MAY-2000.
PA (DIAS-) DIASORIN SRL.
Query Match 14.1%; Score 63.5; DB 3; Length 166;
Best Local Similarity 24.2%; Pred. No. 59;
RESULT 739
ID ABE27727 standard; protein; 155 AA.
DE Humanized 2H7 antibody light chain sequence.
PN WO2005060999-A2.
PD 07-JUL-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 155;
Best Local Similarity 29.9%; Pred. No. 62;
RESULT 740
ID ADS33303 standard; protein; 213 AA.
DE Anti-CD20 humanised antibody hu2H7v16, light chain.
PN US2004202658-A1.
PD 14-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 8; Length 213;
Best Local Similarity 29.9%; Pred. No. 92;

RESULT 741
ID ADW03409 standard; protein; 213 AA.
DE Humanized anti-CD20 antibody (hu2H7.v16) light chain - SEQ ID 15.
PN WO2005000351-A2.
PD 06-JAN-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 213;
Best Local Similarity 29.9%; Pred. No. 92;
RESULT 742
ID AEB17637 standard; peptide; 213 AA.
DE Light chain peptide sequence of intact humanized 2H7 antibody.
PN WO2005061542-A2.
PD 07-JUL-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 213;
Best Local Similarity 29.9%; Pred. No. 92;
RESULT 743
ID ADP79583 standard; protein; 232 AA.
DE 2H7 v16 L chain amino acid sequence SEQ ID NO:21.
PN WO2004056312-A2.
PD 08-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 8; Length 232;
Best Local Similarity 29.9%; Pred. No. 1e+02;
RESULT 744
ID ADW03398 standard; protein; 232 AA.
DE Human anti-CD20 antibody (hu2H7.v16) light chain - SEQ ID 3.
PN WO2005000351-A2.
PD 06-JAN-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 232;
Best Local Similarity 29.9%; Pred. No. 1e+02;
RESULT 745
ID ADW21318 standard; protein; 232 AA.
DE Mouse anti-CD20 antibody 2H7 humanized clone v16, light chain.
PN WO2005005462-A2.
PD 20-JAN-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 232;
Best Local Similarity 29.9%; Pred. No. 1e+02;
RESULT 746
ID ADX00804 standard; protein; 232 AA.
DE Humanized 2H7 v16 antibody light chain variable region, SEQ ID 3.
PN US2005032130-A1.
PD 10-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 232;
Best Local Similarity 29.9%; Pred. No. 1e+02;
RESULT 747
ID ADY62624 standard; protein; 232 AA.
DE Humanized 2H7 antibody light chain.
PN US2005053602-A1.
PD 10-MAR-2005.
PA (GETH) GENENTECH INC.
Query Match 14.0%; Score 63; DB 9; Length 232;
Best Local Similarity 29.9%; Pred. No. 1e+02;
RESULT 748
ID ADD30256 standard; protein; 418 AA.
DE Plant yield-related protein from clone G1360.
PN WO2003013227-A2.
PD 20-FEB-2003.
PA (MENDEL) MENDEL BIOTECHNOLOGY INC.
Query Match 14.0%; Score 63; DB 7; Length 418;
Best Local Similarity 27.3%; Pred. No. 2.2e+02;
RESULT 749
ID ADI44129 standard; protein; 418 AA.
DE Plant transcription factor related polypeptide #1653.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER) SHERMAN B K.
PA (RIEC) RIECHMANN J L.
PA (JIANG) JIANG C.
PA (HEAR) HEARD J E.

PA (HAAK) HAAKE V.
PA (CREE) CREELMAN R A.
PA (RATC) RATCLIFFE O.
PA (ADAM) ADAM L J.
PA (REUB) REUBER T L.
PA (KEDD) KEDDIE J.
PA (BROU) BROUN P E.
PA (FILG) FILGRIM M L.
PA (DUBE) DUBELL A N.
PA (FINE) PINEDA O.
PA (YUGG) YU G.
Query Match 14.0%; Score 63; DB 8; Length 418;
Best Local Similarity 27.3%; Pred. No. 2.2e+02;
RESULT 750
ID ABB66230 standard; protein; 816 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 25482.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 14.0%; Score 63; DB 4; Length 816;
Best Local Similarity 28.2%; Pred. No. 5e+02;
RESULT 751
ID ADS42707 standard; protein; 925 AA.
DE Bacterial polypeptide #21137.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK) HINKLE G J.
PA (SLAT) SLATER S C.
PA (CHEN) CHEN X.
PA (GOLD) GOLDMAN B S.
Query Match 14.0%; Score 63; DB 8; Length 925;
Best Local Similarity 29.8%; Pred. No. 5.9e+02;
RESULT 752
ID ADN18779 standard; protein; 1165 AA.
DE Bacterial polypeptide #1432.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK) HINKLE G J.
PA (SLAT) SLATER S C.
PA (CHEN) CHEN X.
PA (GOLD) GOLDMAN B S.
Query Match 14.0%; Score 63; DB 8; Length 1165;
Best Local Similarity 28.1%; Pred. No. 7.8e+02;
RESULT 753
ID AAB11504 standard; protein; 379 AA.
DE SEN virus protein fragment SEQ ID NO: 21.
PN WO200028039-A2.
PD 18-MAY-2000.
PA (DIAS) DIASORIN SRL.
Query Match 13.9%; Score 62.5; DB 3; Length 379;
Best Local Similarity 25.6%; Pred. No. 2.2e+02;
RESULT 754
ID ADW08912 standard; protein; 412 AA.
DE Human protein which is up-regulated in HCV-infected tissue - SEQ ID 149.
PN EP1493750-A2.
PD 05-JAN-2005.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 13.9%; Score 62.5; DB 9; Length 412;
Best Local Similarity 24.0%; Pred. No. 2.4e+02;
RESULT 755
ID ADJ68623 standard; protein; 413 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID429.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO) MITOKOR.
PA (BUCK) BUCK INST AGE RES.
Query Match 13.9%; Score 62.5; DB 7; Length 413;
Best Local Similarity 24.0%; Pred. No. 2.4e+02;
RESULT 756
ID ADO55165 standard; protein; 413 AA.
DE Protein #67 with increased gene expression in renal cell carcinoma.

PN WO2004032842-A2.
PD 22-APR-2004.
PA (VAND-) VAN ANDEL INST.
Query Match 13.9%; Score 62.5; DB 8; Length 413;
Best Local Similarity 24.0%; Pred. No. 2.4e+02;
RESULT 757
ID AD019653 standard; protein; 413 AA.
DE Human PRO polypeptide #291.
PN WO2004043361-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 13.9%; Score 62.5; DB 8; Length 413;
Best Local Similarity 24.0%; Pred. No. 2.4e+02;
RESULT 758
ID ABM81188 standard; protein; 413 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO61502, SEQ:3067.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 13.9%; Score 62.5; DB 8; Length 413;
Best Local Similarity 24.0%; Pred. No. 2.4e+02;
RESULT 759
ID ADP54767 standard; protein; 413 AA.
DE Human PRO protein sequence SEQ ID NO:743.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 13.9%; Score 62.5; DB 8; Length 413;
Best Local Similarity 24.0%; Pred. No. 2.4e+02;
RESULT 760
ID ADP24138 standard; protein; 413 AA.
DE PRO polypeptide SEQ ID NO:1316.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 13.9%; Score 62.5; DB 8; Length 413;
Best Local Similarity 24.0%; Pred. No. 2.4e+02;
RESULT 761
ID ADT65598 standard; protein; 413 AA.
DE Human aspartate aminotransferase protein.
PN WO2004070383-A2.
PD 19-AUG-2004.
PA (CHEF) GRUENENTHAL GMBH.
Query Match 13.9%; Score 62.5; DB 8; Length 413;
Best Local Similarity 24.0%; Pred. No. 2.4e+02;
RESULT 762
ID ADY16030 standard; protein; 413 AA.
DE PRO polypeptide SEQ ID NO 1836.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 13.9%; Score 62.5; DB 9; Length 413;
Best Local Similarity 24.0%; Pred. No. 2.4e+02;
RESULT 763
ID ADY23183 standard; protein; 443 AA.
DE Plant full length insert polypeptide seqid 70967.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 13.9%; Score 62.5; DB 8; Length 443;
Best Local Similarity 24.6%; Pred. No. 2.6e+02;
RESULT 764
ID AAB11509 standard; protein; 679 AA.
DE SEN virus protein fragment SEQ ID NO: 36.
PN WO200028039-A2.
PD 18-MAY-2000.
PA (DIAS-) DIASORIN SRL.
Query Match 13.9%; Score 62.5; DB 3; Length 679;
Best Local Similarity 24.6%; Pred. No. 2.6e+02;
RESULT 765
ID ADH7440 standard; protein; 711 AA.
DE Enterococcus faecalis polypeptide #1920.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 13.9%; Score 62.5; DB 7; Length 711;
Best Local Similarity 31.2%; Pred. No. 4.8e+02;
RESULT 766
ID AAB14710 standard; protein; 734 AA.
DE Mouse beta4 dominant negative protein.
PN WO200230465-A2.
PD 18-APR-2002.
PA (UYRP) UNIV ROCHESTER.
Query Match 13.9%; Score 62.5; DB 5; Length 734;
Best Local Similarity 30.3%; Pred. No. 5e+02;
RESULT 767
ID ADJ32529 standard; protein; 734 AA.
DE Mouse beta4 dominant negative protein.
PN US2003224993-A1.
PD 04-DEC-2003.
PA (LAND/) LAND H.
PA (DELE/) DELEU L.
Query Match 13.9%; Score 62.5; DB 8; Length 734;
Best Local Similarity 30.3%; Pred. No. 5e+02;
RESULT 768
ID ABB64648 standard; protein; 826 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 20736.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 13.9%; Score 62.5; DB 4; Length 826;
Best Local Similarity 28.1%; Pred. No. 5.8e+02;
RESULT 769
ID AAE14709 standard; protein; 1466 AA.
DE Mouse beta4 integrin.
PN WO200230465-A2.
PD 18-APR-2002.
PA (UYRP) UNIV ROCHESTER.
Query Match 13.9%; Score 62.5; DB 5; Length 1466;
Best Local Similarity 30.3%; Pred. No. 1.2e+03;
RESULT 770
ID ADJ32527 standard; protein; 1466 AA.
DE Mouse integrin beta4 subunit protein.
PN US2003224993-A1.
PD 04-DEC-2003.
PA (LAND/) LAND H.
PA (DELE/) DELEU L.
Query Match 13.9%; Score 62.5; DB 8; Length 1466;
Best Local Similarity 30.3%; Pred. No. 1.2e+03;
RESULT 771
ID ABO69591 standard; protein; 290 AA.
DE Pseudomonas aeruginosa polypeptide #1766.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.8%; Score 62; DB 7; Length 290;
Best Local Similarity 24.6%; Pred. No. 1.8e+02;
RESULT 772
ID ABO77973 standard; protein; 372 AA.
DE Pseudomonas aeruginosa polypeptide #10148.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.8%; Score 62; DB 7; Length 372;
Best Local Similarity 23.9%; Pred. No. 2.4e+02;
RESULT 773
ID AAG70883 standard; protein; 592 AA.
DE C albicans apoptosis associated protein #63.
PN WO200102550-A2.
PD 11-JAN-2001.

PA (JANC) JANSSEN PHARM NV.
Query Match 13.8%; Score 62; DB 4; Length 592;
Best Local Similarity 27.3%; Pred. No. 4.4e+02;
RESULT 774
ID ADX95117 standard; protein; 823 AA.
DE Plant full length insert polypeptide seqid 57781.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ)/ LIU J.
PA (ZHOU)/ ZHOU Y.
PA (KOVA)/ KOVALIC D K.
PA (SCRE)/ SCREEN S E.
PA (TABA)/ TABASKA J E.
PA (CAOY)/ CAO Y.
Query Match 13.8%; Score 62; DB 8; Length 823;
Best Local Similarity 28.6%; Pred. No. 6.6e+02;
RESULT 775
ID ADN18993 standard; protein; 891 AA.
DE Bacterial polypeptide #1646.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY)/ CAO Y.
PA (HINK)/ HINKLE G J.
PA (SLAT)/ SLATER S C.
PA (CHEW)/ CHEN X.
PA (GOLD)/ GOLDMAN B S.
Query Match 13.8%; Score 62; DB 8; Length 891;
Best Local Similarity 27.1%; Pred. No. 7.3e+02;
RESULT 776
ID ABR53813 standard; protein; 971 AA.
DE Protein sequence #SEQ ID 2491.
PN EPI258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 13.8%; Score 62; DB 6; Length 971;
Best Local Similarity 27.1%; Pred. No. 8.1e+02;
RESULT 777
ID ADK65020 standard; protein; 971 AA.
DE Disease treating protein complex-derived protein #1506.
PN EPI338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 13.8%; Score 62; DB 7; Length 971;
Best Local Similarity 27.1%; Pred. No. 8.1e+02;
RESULT 778
ID AAB84882 standard; protein; 1530 AA.
DE Human protein, SEQ ID 6.
PN W0200127270-A1.
PD 19-APR-2001.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Query Match 13.8%; Score 62; DB 4; Length 1530;
Best Local Similarity 28.2%; Pred. No. 1.4e+03;
RESULT 779
ID AEB41562 standard; protein; 1921 AA.
DE L. pneumophila protein SEQ ID NO 5894.
PN W02005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 13.8%; Score 62; DB 9; Length 1921;
Best Local Similarity 25.6%; Pred. No. 1.9e+03;
RESULT 780
ID AEB38280 standard; protein; 1956 AA.
DE L. pneumophila protein SEQ ID NO 2612.
PN W02005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 13.8%; Score 62; DB 9; Length 1956;
Best Local Similarity 25.6%; Pred. No. 1.9e+03;
RESULT 781
ID AAB84885 standard; protein; 2266 AA.
DE Human protein, SEQ ID 14.
PN W0200127270-A1.
PD 19-APR-2001.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Query Match 13.8%; Score 62; DB 4; Length 2266;
Best Local Similarity 28.2%; Pred. No. 2.4e+03;
RESULT 782
ID ADX06502 standard; protein; 2266 AA.
DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 1067.
PN W02005012875-A2.
PD 10-FEB-2005.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 13.8%; Score 62; DB 9; Length 2266;
Best Local Similarity 28.2%; Pred. No. 2.4e+03;
RESULT 783
ID ASG22400 standard; protein; 102 AA.
DE Novel human diagnostic protein #22391.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.7%; Score 61.5; DB 4; Length 102;
Best Local Similarity 27.3%; Pred. No. 54;
RESULT 784
ID ADM05710 standard; protein; 122 AA.
DE Human protein of the invention SEQ ID NO:4395.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 13.7%; Score 61.5; DB 7; Length 122;
Best Local Similarity 25.6%; Pred. No. 68;
RESULT 785
ID ADO05882 standard; peptide; 130 AA.
DE C. jacchus M3-24 MOG-specific Ig kappa light chain Fab fragment.
PN W02004034031-A2.
PD 22-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 13.7%; Score 61.5; DB 8; Length 130;
Best Local Similarity 30.3%; Pred. No. 74;
RESULT 786
ID ADC85015 standard; protein; 269 AA.
DE HLA DQB1 protein.
PN W0200283947-A1.
PD 24-OCT-2002.
PA (OGOS/) OGOSHI K.
Query Match 13.7%; Score 61.5; DB 7; Length 269;
Best Local Similarity 21.9%; Pred. No. 1.8e+02;
RESULT 787
ID ADC85018 standard; protein; 269 AA.
DE HLA DQB1 protein.
PN W0200283947-A1.
PD 24-OCT-2002.
PA (OGOS/) OGOSHI K.
Query Match 13.7%; Score 61.5; DB 7; Length 269;
Best Local Similarity 21.9%; Pred. No. 1.8e+02;
RESULT 788
ID ADC85012 standard; protein; 269 AA.
DE HLA DQB1 protein.
PN W0200283947-A1.
PD 24-OCT-2002.
PA (OGOS/) OGOSHI K.
Query Match 13.7%; Score 61.5; DB 7; Length 269;
Best Local Similarity 21.9%; Pred. No. 1.8e+02;
RESULT 789
ID ADY24666 standard; protein; 616 AA.
DE Plant full length insert polypeptide seqid 72450.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ)/ LIU J.
PA (ZHOU)/ ZHOU Y.
PA (KOVA)/ KOVALIC D K.

PA (SCRE//) SCREEN S E. 13.7%; Score 61.5; DB 8; Length 616;
PA (CAOV//) CAO Y. 25.0%; Pred. No. 5.2e+02;
Query Match
Best Local Similarity 25.0%; Pred. No. 5.2e+02;
RESULT 790
ID ADM18493 standard; protein; 1024 AA.
DE Pinus radiata transcription factor protein SBP family Seq 2283.
PN W02005001050-A2.
PD 06-JAN-2005.
PA (ARBO-) ARBORGEN LLC.
Query Match
Best Local Similarity 27.1%; Score 61.5; DB 9; Length 1024;
RESULT 791
ID ADM17829 standard; protein; 1024 AA.
DE Pinus radiata transcription factor protein SBP family Seq 1606.
PN W02005001050-A2.
PD 06-JAN-2005.
PA (ARBO-) ARBORGEN LLC.
Query Match
Best Local Similarity 27.1%; Score 61.5; DB 9; Length 1024;
RESULT 792
ID ADS943681 standard; protein; 1034 AA.
DE Bacterial polypeptide #22111.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOV//) CAO Y.
PA (HINK//) HINKLE G J.
PA (SLAT//) SLATER S C.
PA (CHEN//) CHEN X.
PA (GOLD//) GOLDMAN B S.
Query Match
Best Local Similarity 28.8%; Score 61.5; DB 8; Length 1034;
RESULT 793
ID ADS05365 standard; protein; 45 AA.
DE Staphylococcus epidermis polypeptide seqid 4660.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC//) DOUCETTE-STAMM L.
PA (BUSH//) BUSH D.
Query Match
Best Local Similarity 42.9%; Score 61; DB 8; Length 45;
RESULT 794
ID AAB56760 standard; protein; 187 AA.
DE Human prostate cancer antigen protein sequence SEQ ID NO:1338.
PN W0200055174-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE//) ROSEN C A.
Query Match
Best Local Similarity 26.2%; Score 61; DB 3; Length 187;
RESULT 795
ID ADZ59470 standard; protein; 283 AA.
DE L19 antibody protein with N-terminal linker & C-terminal tagged peptide.
PN W02005037312-A2.
PD 28-APR-2005.
PA (SCHD-) SCHERING AG.
Query Match
Best Local Similarity 27.5%; Score 61; DB 9; Length 283;
RESULT 796
ID AAR20807 standard; protein; 311 AA.
DE Human CDw32 antigen.
PN W09201049-A.
PD 23-JAN-1992.
PA (GEHO-) GEN HOSPITAL CORP.
Query Match
Best Local Similarity 40.6%; Score 61; DB 2; Length 311;
RESULT 797
ID AAM48902 standard; protein; 365 AA.
DE Amino transferase related human protein.
PN W0200192490-A2.
PD 06-DEC-2001.
PA (APPL-) APPLERA CORP.

Query Match
Best Local Similarity 13.6%; Score 61; DB 5; Length 365;
RESULT 798
ID ADB85178 standard; protein; 413 AA.
DE Rat aspartate aminotransferase SEQ ID NO:59.
PN EPI284297-A2.
PD 19-FEB-2003.
PA (WARN-) WARNER LAMBERT CO.
Query Match
Best Local Similarity 25.0%; Score 61; DB 7; Length 413;
RESULT 799
ID ADT66600 standard; protein; 413 AA.
DE Rat aspartate aminotransferase protein.
PN W02004070383-A2.
PD 19-AUG-2004.
PA (CHEF-) GRUENENTHAL GMBH.
Query Match
Best Local Similarity 25.0%; Score 61; DB 8; Length 413;
RESULT 800
ID AAU15075 standard; protein; 715 AA.
DE Protein encoded by C. albicans essential gene CAYJL090C (DPB11).
PN W0200160975-A2.
PD 23-AUG-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 35.9%; Score 61; DB 4; Length 715;
RESULT 801
ID ABP73165 standard; protein; 715 AA.
DE Candida albicans essential protein SEQ ID NO 7002.
PN W0200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 35.9%; Score 61; DB 5; Length 715;
RESULT 802
ID ABB62311 standard; protein; 788 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 13725.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match
Best Local Similarity 26.6%; Score 61; DB 4; Length 788;
RESULT 803
ID AAR94563 standard; protein; 1810 AA.
DE Chicken cytotactin.
PN W09608513-A1.
PD 21-MAR-1996.
PA (SCRI-) SCRIPPS RES INST.
Query Match
Best Local Similarity 46.2%; Score 61; DB 2; Length 1810;
RESULT 804
ID ADS85087 standard; protein; 2019 AA.
DE Mouse atopic dermatitis-related protein sequence SeqID89.
PN W02004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUNTENDO.
Query Match
Best Local Similarity 55.6%; Score 61; DB 8; Length 2019;
RESULT 805
ID ADY24980 standard; protein; 436 AA.
DE Plant full length insert polypeptide seqid 72764.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ//) LIU J.
PA (ZHOU//) ZHOU Y.
PA (KOVA//) KOVALIC D K.
PA (SCRE//) SCREEN S E.
PA (TABA//) TABASKA J E.
PA (CAOV//) CAO Y.
Query Match
Best Local Similarity 26.0%; Score 60.5; DB 8; Length 436;
RESULT 806

ID ABU24178 standard; protein; 444 AA.
DE Protein encoded by Prokaryotic essential gene #9705.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (BLIT-) ELITRA PHARM INC.
Query Match 13.5%; Score 60.5; DB 6; Length 444;
Best Local Similarity 29.3%; Pred. No. 4.5e+02;
RESULT 807
ID AG92810 standard; protein; 588 AA.
DE Protein encoded by fungal peptide synthetase gene cluster ORF16.
PN WO200242444-A2.
PD 30-MAY-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PA (CORR) CORNELL RES FOUND INC.
PA (YODE/) YODER O.
PA (TURG/) TURGEON B G.
PA (LUSS/) LU S.
Query Match 13.5%; Score 60.5; DB 5; Length 588;
Best Local Similarity 25.0%; Pred. No. 6.4e+02;
RESULT 808
ID AAU96804 standard; protein; 890 AA.
DE Human immunodeficiency virus type 2 derived polypeptide #4.
PN US2002051967-A1.
PD 02-MAY-2002.
PA (INSP) INST PASTEUR.
Query Match 13.5%; Score 60.5; DB 5; Length 890;
Best Local Similarity 22.9%; Pred. No. 1.1e+03;
RESULT 809
ID ADO00996 standard; protein; 937 AA.
DE Mouse homologue of Fruit fly AD-related protein CG10198.
PN US2004067535-A1.
PD 08-APR-2004.
PA (LIFE-) LIFE SCI DEV CORP.
Query Match 13.5%; Score 60.5; DB 8; Length 937;
Best Local Similarity 30.7%; Pred. No. 1.2e+03;
RESULT 810
ID ADO07917 standard; protein; 937 AA.
DE Rat polypeptide.
PN US2004071700-A1.
PD 15-APR-2004.
PA (LIFE-) LIFE SCI DEV CORP.
Query Match 13.5%; Score 60.5; DB 8; Length 937;
Best Local Similarity 30.7%; Pred. No. 1.2e+03;
RESULT 811
ID ABR53184 standard; protein; 992 AA.
DE Protein sequence #SEQ ID 1233.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 13.5%; Score 60.5; DB 6; Length 992;
Best Local Similarity 19.8%; Pred. No. 1.2e+03;
RESULT 812
ID ADK63220 standard; protein; 992 AA.
DE Disease treating protein complex-derived protein #736.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 13.5%; Score 60.5; DB 7; Length 992;
Best Local Similarity 19.8%; Pred. No. 1.2e+03;
RESULT 813
ID ADI27180 standard; protein; 1611 AA.
DE Human LRP binding family protein #11.
PN WO2003106657-A2.
PD 24-DEC-2003.
PA (STOW-) STOWERS INST MEDICAL RES.
Query Match 13.5%; Score 60.5; DB 8; Length 1611;
Best Local Similarity 28.1%; Pred. No. 2.3e+03;
RESULT 814
ID ABP31105 standard; protein; 116 AA.
DE Human ORF78 protein; SEQ ID NO:156.
PN WO200190366-A2.
PD 29-NOV-2001.
PA (CURA-) CURAGEN CORP.

Query Match 13.4%; Score 60; DB 5; Length 116;
Best Local Similarity 26.5%; Pred. No. 95;
RESULT 815
ID AAO03609 standard; protein; 141 AA.
DE Human polypeptide SEQ ID NO 17501.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.4%; Score 60; DB 4; Length 141;
Best Local Similarity 24.2%; Pred. No. 1.2e+02;
RESULT 816
ID AAE35326 standard; protein; 213 AA.
DE Humanised murine antibody BIWA4 light chain protein.
PN EP1258255-A1.
PD 20-NOV-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Query Match 13.4%; Score 60; DB 6; Length 213;
Best Local Similarity 29.9%; Pred. No. 2e+02;
RESULT 817
ID AAE34878 standard; protein; 213 AA.
DE BIWA4/8 antibody light chain mature protein.
PN WO200294879-A1.
PD 28-NOV-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Query Match 13.4%; Score 60; DB 6; Length 213;
Best Local Similarity 29.9%; Pred. No. 2e+02;
RESULT 818
ID AAE34877 standard; protein; 213 AA.
DE BIWA4 antibody light chain mature protein.
PN WO200294879-A1.
PD 28-NOV-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Query Match 13.4%; Score 60; DB 6; Length 213;
Best Local Similarity 29.9%; Pred. No. 2e+02;
RESULT 819
ID ADL15441 standard; protein; 213 AA.
DE Humanised murine antibody BIWA4 light chain protein.
PN EP1391213-A1.
PD 25-FEB-2004.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Query Match 13.4%; Score 60; DB 8; Length 213;
Best Local Similarity 29.9%; Pred. No. 2e+02;
RESULT 820
ID ADL15445 standard; protein; 213 AA.
DE Humanised murine antibody BIWA8 light chain protein.
PN EP1391213-A1.
PD 25-FEB-2004.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Query Match 13.4%; Score 60; DB 8; Length 213;
Best Local Similarity 29.9%; Pred. No. 2e+02;
RESULT 821
ID ADO00849 standard; protein; 213 AA.
DE Humanised murine antibody BIWA 4 light chain protein SEQ ID NO:4.
PN EP1417974-A1.
PD 12-MAY-2004.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Query Match 13.4%; Score 60; DB 8; Length 213;
Best Local Similarity 29.9%; Pred. No. 2e+02;
RESULT 822
ID ADO00853 standard; protein; 213 AA.
DE Humanised murine antibody BIWA 8 light chain protein SEQ ID NO:8.
PN EP1417974-A1.
PD 12-MAY-2004.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Query Match 13.4%; Score 60; DB 8; Length 213;
Best Local Similarity 29.9%; Pred. No. 2e+02;
RESULT 823
ID AEB29787 standard; protein; 213 AA.
DE Humanized anti-CD44 antibody light chain A.
PN WO2005065717-A2.
PD 21-JUL-2005.

PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 PA (BOEH) BOEHRINGER INGELHEIM PHARMA GMBH & CO KG.
 Query Match 13.4%; Score 60; DB 9; Length 213;
 Best Local Similarity 29.9%; Pred. No. 2e+02;
 RESULT 824
 ID ABB29791 standard; protein; 213 AA.
 DE Humanized anti-CD44 antibody light chain B.
 PN W02005065717-A2.
 PD 21-JUL-2005.
 PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 PA (BOEH) BOEHRINGER INGELHEIM PHARMA GMBH & CO KG.
 Query Match 13.4%; Score 60; DB 9; Length 213;
 Best Local Similarity 29.9%; Pred. No. 2e+02;
 RESULT 825
 ID ABB29782 standard; protein; 213 AA.
 DE Humanized anti-CD44 antibody light chain B.
 PN W02005065709-A2.
 PD 21-JUL-2005.
 PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 PA (BOEH) BOEHRINGER INGELHEIM PHARMA GMBH & CO KG.
 Query Match 13.4%; Score 60; DB 9; Length 213;
 Best Local Similarity 29.9%; Pred. No. 2e+02;
 RESULT 826
 ID ABB29778 standard; protein; 213 AA.
 DE Humanized anti-CD44 antibody light chain A.
 PN W02005065709-A2.
 PD 21-JUL-2005.
 PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 PA (BOEH) BOEHRINGER INGELHEIM PHARMA GMBH & CO KG.
 Query Match 13.4%; Score 60; DB 9; Length 213;
 Best Local Similarity 29.9%; Pred. No. 2e+02;
 RESULT 827
 ID ADY70960 standard; protein; 214 AA.
 DE Human monoclonal antibody CRJA light chain.
 PN W02005023849-A2.
 PD 17-MAR-2005.
 PA (CRUC-) CRUCCELL HOLLAND BV.
 Query Match 13.4%; Score 60; DB 9; Length 214;
 Best Local Similarity 28.4%; Pred. No. 2.1e+02;
 RESULT 828
 ID ABR01492 standard; protein; 215 AA.
 DE Human anti-TIMP-1 antibody light chain #33.
 PN W0200286085-A2.
 PD 31-OCT-2002.
 PA (FARB) BAYER CORP.
 PA (MORP-) MORPHOSYS AG.
 Query Match 13.4%; Score 60; DB 6; Length 215;
 Best Local Similarity 29.9%; Pred. No. 2.1e+02;
 RESULT 829
 ID AAQ14066 standard; protein; 234 AA.
 DE Light chain protein of the monoclonal antibody from clone JA.
 PN W0200188132-A2.
 PD 22-NOV-2001.
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 Query Match 13.4%; Score 60; DB 5; Length 234;
 Best Local Similarity 28.4%; Pred. No. 2.3e+02;
 RESULT 830
 ID ABU08018 standard; protein; 234 AA.
 DE Human monoclonal rabies virus antibody light chain, clone JH, protein.
 PN W02003016501-A2.
 PD 27-FEB-2003.
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 Query Match 13.4%; Score 60; DB 6; Length 234;
 Best Local Similarity 28.4%; Pred. No. 2.3e+02;
 RESULT 831
 ID ADP65776 standard; protein; 234 AA.
 DE Human monoclonal rabies virus antibody light chain.
 PN U82003157112-A1.
 PD 21-AUG-2003.
 PA (HOOP/) HOOPER D C.
 PA (DIET/) DIETZSCHOLD B.
 Query Match 13.4%; Score 60; DB 7; Length 234;
 Best Local Similarity 28.4%; Pred. No. 2.3e+02;
 RESULT 832
 ID ADJ92516 standard; protein; 234 AA.
 DE Human SOJA monoclonal antibody light chain protein.
 PN US2004013672-A1.
 PD 22-JAN-2004.
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 Query Match 13.4%; Score 60; DB 8; Length 234;
 Best Local Similarity 28.4%; Pred. No. 2.3e+02;
 RESULT 833
 ID AAB82912 standard; protein; 241 AA.
 DE Human immune response protein HIRPI.
 PN W0200168696-A1.
 PD 20-SEP-2001.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 13.4%; Score 60; DB 4; Length 241;
 Best Local Similarity 28.4%; Pred. No. 2.4e+02;
 RESULT 834
 ID ADV86419 standard; protein; 482 AA.
 DE Novel C1g domain-containing protein #40.
 PN US2004248156-A1.
 PD 09-DEC-2004.
 PA (HUTI/) HU T.
 PA (TANG/) TANG Y T.
 PA (GHOS/) GHOSH M J.
 PA (WANG/) WANG J.
 PA (WANG/) WANG Z.
 PA (ZHAO/) ZHAO Q.
 PA (XUCC/) XU C.
 PA (MULE/) MULERO J.
 Query Match 13.4%; Score 60; DB 9; Length 482;
 Best Local Similarity 29.3%; Pred. No. 5.7e+02;
 RESULT 835
 ID ABM68541 standard; protein; 920 AA.
 DE Photorehabitus luminescens protein sequence #1638.
 PN W0200294867-A2.
 PD 28-NOV-2002.
 PA (INSP) INST PASTEUR.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 Query Match 13.4%; Score 60; DB 6; Length 920;
 Best Local Similarity 29.8%; Pred. No. 1.3e+03;
 RESULT 836
 ID AAU30825 standard; protein; 962 AA.
 DE Novel human secreted protein #1316.
 PN W0200179449-A2.
 PD 25-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 13.4%; Score 60; DB 4; Length 962;
 Best Local Similarity 24.6%; Pred. No. 1.4e+03;
 RESULT 837
 ID AAU48592 standard; protein; 1341 AA.
 DE Propionibacterium acnes immunogenic protein #9488.
 PN W0200181581-A2.
 PD 01-NOV-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 13.4%; Score 60; DB 4; Length 1341;
 Best Local Similarity 26.5%; Pred. No. 2.1e+03;
 RESULT 838
 ID ABM45111 standard; protein; 1341 AA.
 DE Propionibacterium acnes predicted ORF-encoded polypeptide #9787.
 PN W02003033515-A1.
 PD 24-APR-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 13.4%; Score 60; DB 6; Length 1341;
 Best Local Similarity 26.5%; Pred. No. 2.1e+03;
 RESULT 839
 ID ADL70800 standard; protein; 213 AA.
 DE Anti-TNFalpha antibody VL region, SEQ ID 73.
 PN W02004020588-A2.
 PD 11-MAR-2004.
 PA (BIOR-) BIOREXIS PHARM CORP.
 Query Match 13.3%; Score 59.5; DB 8; Length 213;
 Best Local Similarity 28.8%; Pred. No. 2.3e+02;
 RESULT 840

ID ABM84937 standard; protein; 225 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5186.
PN W02004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 13.3%; Score 59.5; DB 8; Length 225;
Best Local Similarity 32.1%; Pred. No. 2.5e+02;
RESULT 841
ID ABP63108 standard; protein; 384 AA.
DE FLO11 gene expression regulator At27.
PN W0200257456-A2.
PD 25-JUL-2002.
PA (MICR-) MICROBIA.
Query Match 13.3%; Score 59.5; DB 5; Length 384;
Best Local Similarity 57.1%; Pred. No. 4.9e+02;
RESULT 842
ID ABM85836 standard; protein; 393 AA.
DE Mouse protein sequence MCP13663.
PN W02003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 13.3%; Score 59.5; DB 7; Length 393;
Best Local Similarity 27.7%; Pred. No. 5.1e+02;
RESULT 843
ID ABA42218 standard; protein; 436 AA.
DE Human ORFX ORF1982 polypeptide sequence SEQ ID NO:3964.
PN W0200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 13.3%; Score 59.5; DB 3; Length 436;
Best Local Similarity 28.4%; Pred. No. 5.8e+02;
RESULT 844
ID ABA20121 standard; protein; 650 AA.
DE Novel human polypeptide SEQ ID NO 815.
PN W02005049806-A2.
PD 02-JUN-2005.
PA (NUVE-) NUVELO INC.
Query Match 13.3%; Score 59.5; DB 9; Length 650;
Best Local Similarity 28.4%; Pred. No. 9.5e+02;
RESULT 845
ID ADZ84991 standard; protein; 668 AA.
DE Partial PHOS interacting protein, mA044679 (668).
PN U2005100966-A1.
PD 12-MAY-2005.
PA (SAKA/) SAKAMOTO T.
PA (TAKE/) TAKEDA S.
Query Match 13.3%; Score 59.5; DB 9; Length 668;
Best Local Similarity 28.4%; Pred. No. 9.9e+02;
RESULT 846
ID ABA20120 standard; protein; 725 AA.
DE Novel human polypeptide SEQ ID NO 814.
PN W02005049806-A2.
PD 02-JUN-2005.
PA (NUVE-) NUVELO INC.
Query Match 13.3%; Score 59.5; DB 9; Length 725;
Best Local Similarity 28.4%; Pred. No. 1.1e+03;
RESULT 847
ID ADS44222 standard; protein; 821 AA.
DE Bacterial polypeptide #22652.
PN U2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 13.3%; Score 59.5; DB 8; Length 821;
Best Local Similarity 28.9%; Pred. No. 1.3e+03;
RESULT 848
ID ARG79353 standard; protein; 884 AA.
DE Human GPCR15 protein.
PN W0200264793-A2.
PD 22-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 13.3%; Score 59.5; DB 5; Length 884;
Best Local Similarity 30.0%; Pred. No. 1.4e+03;
RESULT 849
ID AAM40399 standard; protein; 1150 AA.
DE Human polypeptide SEQ ID NO 3544.
PN W0200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.3%; Score 59.5; DB 4; Length 1150;
Best Local Similarity 28.4%; Pred. No. 2e+03;
RESULT 850
ID ADE59446 standard; protein; 1152 AA.
DE Human Protein XP_047123, SEQ ID NO 5341.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 13.3%; Score 59.5; DB 7; Length 1152;
Best Local Similarity 28.4%; Pred. No. 2e+03;
RESULT 851
ID AAY81947 standard; protein; 1330 AA.
DE Heterosigma akashiwo Na+-ATPase protein.
PN JP2000050874-A.
PD 22-FEB-2000.
PA (NORQ) NORINSUISANSHO KOKUSAI NORIN SUISANGYO.
Query Match 13.3%; Score 59.5; DB 3; Length 1330;
Best Local Similarity 25.9%; Pred. No. 2.3e+03;
RESULT 852
ID AEA20119 standard; protein; 1709 AA.
DE Novel human polypeptide SEQ ID NO 813.
PN W02005049806-A2.
PD 02-JUN-2005.
PA (NUVE-) NUVELO INC.
Query Match 13.3%; Score 59.5; DB 9; Length 1709;
Best Local Similarity 28.4%; Pred. No. 3.2e+03;
RESULT 853
ID ABU00419 standard; protein; 105 AA.
DE Human novel polypeptide #512.
PN W0200274961-A1.
PD 26-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 13.1%; Score 59; DB 6; Length 105;
Best Local Similarity 26.8%; Pred. No. 1.1e+02;
RESULT 854
ID ADD14077 standard; protein; 146 AA.
DE Human src biomarker polypeptide SEQ ID NO:266.
PN W02003062395-A2.
PD 31-JUL-2003.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 13.1%; Score 59; DB 7; Length 146;
Best Local Similarity 34.2%; Pred. No. 1.7e+02;
RESULT 855
ID ADD44869 standard; protein; 146 AA.
DE Human Protein O43169, SEQ ID NO 10300.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 13.1%; Score 59; DB 7; Length 146;
Best Local Similarity 34.2%; Pred. No. 1.7e+02;
RESULT 856
ID ADD47797 standard; protein; 146 AA.
DE Human Protein O43169, SEQ ID NO 13493.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 13.1%; Score 59; DB 7; Length 146;
Best Local Similarity 34.2%; Pred. No. 1.7e+02;
RESULT 857
ID ADD48851 standard; protein; 146 AA.
DE Human Protein O43169, SEQ ID NO 14562.

PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 13.1%; Score 59; DB 7; Length 146;
Best Local Similarity 34.2%; Pred. No. 1.7e+02;
RESULT 858
ID ADJ69511 standard; protein; 146 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1317.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 13.1%; Score 59; DB 7; Length 146;
Best Local Similarity 34.2%; Pred. No. 1.7e+02;
RESULT 859
ID ABM81767 standard; protein; 146 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO82609, SEQ:4554.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 59; DB 8; Length 146;
Best Local Similarity 34.2%; Pred. No. 1.7e+02;
RESULT 860
ID ADY14610 standard; protein; 146 AA.
DE PRO polypeptide SEQ ID NO 416.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 59; DB 9; Length 146;
Best Local Similarity 34.2%; Pred. No. 1.7e+02;
RESULT 861
ID AAB32861 standard; protein; 153 AA.
DE Rucalypstus grandis transcription factor protein sequence #319.
PN WO200053724-A2.
PD 14-SEP-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 13.1%; Score 59; DB 3; Length 153;
Best Local Similarity 31.9%; Pred. No. 1.8e+02;
RESULT 862
ID AAW74475 standard; protein; 155 AA.
DE Amino acid sequence of human Cytochrome B5.
PN WO9836071-A1.
PD 20-AUG-1998.
PA (INCY-) INCYTE PHARM INC.
Query Match 13.1%; Score 59; DB 2; Length 155;
Best Local Similarity 34.2%; Pred. No. 1.8e+02;
RESULT 863
ID AAG73876 standard; protein; 155 AA.
DE Human colon cancer antigen protein SEQ ID NO:4640.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.1%; Score 59; DB 4; Length 155;
Best Local Similarity 34.2%; Pred. No. 1.8e+02;
RESULT 864
ID ABP41469 standard; protein; 155 AA.
DE Human ovarian antigen HPDOC39, SEQ ID NO:2601.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.1%; Score 59; DB 5; Length 155;
Best Local Similarity 34.2%; Pred. No. 1.8e+02;
RESULT 865
ID ABR41609 standard; protein; 155 AA.
DE Human DITRP electron transfer-associated protein.
PN WO200297031-A2.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 13.1%; Score 59; DB 6; Length 155;
Best Local Similarity 34.2%; Pred. No. 1.8e+02;
RESULT 866

ID AAB43457 standard; protein; 169 AA.
DE Human cancer associated protein sequence SEQ ID NO:902.
PN WO200053350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.1%; Score 59; DB 3; Length 169;
Best Local Similarity 34.2%; Pred. No. 2e+02;
RESULT 867
ID AAV08599 standard; protein; 214 AA.
DE Anti-human TNF-alpha monoclonal antibody L-chain protein.
PN JF1127855-A.
PD 18-MAY-1999.
PA (NIHA) JAPAN ENERGY CORP.
Query Match 13.1%; Score 59; DB 2; Length 214;
Best Local Similarity 28.4%; Pred. No. 2.7e+02;
RESULT 868
ID ADU70799 standard; protein; 214 AA.
DE Anti-TNFalpha antibody VL region, SEQ ID 72.
PN WO2004020588-A2.
PD 11-MAR-2004.
PA (BIOR-) BIOREXIS PHARM CORP.
Query Match 13.1%; Score 59; DB 8; Length 214;
Best Local Similarity 28.4%; Pred. No. 2.7e+02;
RESULT 869
ID AAB75036 standard; protein; 224 AA.
DE TRO005 HuMab kappa chain protein sequence 1CC8K.
PN WO200125492-A1.
PD 12-APR-2001.
PA (BIOS-) BIOSITE DIAGNOSTICS INC.
PA (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
Query Match 13.1%; Score 59; DB 4; Length 224;
Best Local Similarity 28.4%; Pred. No. 2.8e+02;
RESULT 870
ID AAB75038 standard; protein; 224 AA.
DE TRO005 HuMab kappa chain protein sequence 1CB8K.
PN WO200125492-A1.
PD 12-APR-2001.
PA (BIOS-) BIOSITE DIAGNOSTICS INC.
PA (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
Query Match 13.1%; Score 59; DB 4; Length 224;
Best Local Similarity 28.4%; Pred. No. 2.8e+02;
RESULT 871
ID AAB75034 standard; protein; 224 AA.
DE TRO005 HuMab kappa chain protein sequence 1CC2K.
PN WO200125492-A1.
PD 12-APR-2001.
PA (BIOS-) BIOSITE DIAGNOSTICS INC.
PA (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
Query Match 13.1%; Score 59; DB 4; Length 224;
Best Local Similarity 28.4%; Pred. No. 2.8e+02;
RESULT 872
ID AAB75037 standard; protein; 224 AA.
DE TRO005 HuMab kappa chain protein sequence 1CD7K.
PN WO200125492-A1.
PD 12-APR-2001.
PA (BIOS-) BIOSITE DIAGNOSTICS INC.
PA (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
Query Match 13.1%; Score 59; DB 4; Length 224;
Best Local Similarity 28.4%; Pred. No. 2.8e+02;
RESULT 873
ID AAB75039 standard; protein; 224 AA.
DE TRO005 HuMab kappa chain protein sequence 1CC6K.
PN WO200125492-A1.
PD 12-APR-2001.
PA (BIOS-) BIOSITE DIAGNOSTICS INC.
PA (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
Query Match 13.1%; Score 59; DB 4; Length 224;
Best Local Similarity 28.4%; Pred. No. 2.8e+02;
RESULT 874
ID ADN04732 standard; protein; 227 AA.
DE Anticorporatic protein sequence #547.
PN WO2004028479-A2.
PD 08-APR-2004.

PA (GETH) GENENTECH INC.
 Query Match 13.1%; Score 59; DB 8; Length 227;
 Best Local Similarity 33.3%; Pred. No. 2.9e+02;
 RESULT 875
 ID ADW18317 standard; protein; 246 AA.
 DE Eucalyptus grandis transcription factor protein MYB family seq 2104.
 PN W02005001050-A2.
 PD 06-JAN-2005.
 PA (ARBO-) ARBOGEN LLC.
 Query Match 13.1%; Score 59; DB 9; Length 246;
 Best Local Similarity 31.9%; Pred. No. 3.2e+02;
 RESULT 876
 ID ABB59849 standard; protein; 600 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 6339.
 PN W0200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 13.1%; Score 59; DB 4; Length 600;
 Best Local Similarity 21.9%; Pred. No. 9.8e+02;
 RESULT 877
 ID ABO78248 standard; protein; 641 AA.
 DE Pseudomonas aeruginosa polypeptide #10423.
 PN U56551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 13.1%; Score 59; DB 7; Length 641;
 Best Local Similarity 31.6%; Pred. No. 1.1e+03;
 RESULT 878
 ID AAU74519 standard; protein; 1781 AA.
 DE Lactobacillus reuteri glucosyltransferase A (gtfa) polypeptide.
 PN W0200190372-A1.
 PD 29-NOV-2001.
 PA (NEDE) NEDERLANDSE ORG TOEGEPAST.
 Query Match 13.1%; Score 59; DB 5; Length 1781;
 Best Local Similarity 23.7%; Pred. No. 3.9e+03;
 RESULT 879
 ID ASG14083 standard; protein; 104 AA.
 DE Novel human diagnostic protein #14074.
 PN W0200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 13.0%; Score 58.5; DB 4; Length 104;
 Best Local Similarity 30.0%; Pred. No. 1.2e+02;
 RESULT 880
 ID ADP74724 standard; protein; 137 AA.
 DE Human porimin protein SEQ ID NO: 6.
 PN W02004047762-A2.
 PD 10-JUN-2004.
 PA (CHIR) CHIRON CORP.
 Query Match 13.0%; Score 58.5; DB 8; Length 137;
 Best Local Similarity 28.0%; Pred. No. 1.8e+02;
 RESULT 881
 ID AAB11523 standard; protein; 166 AA.
 DE SEN virus protein fragment SEQ ID NO: 69.
 PN W0200028039-A2.
 PD 18-MAY-2000.
 PA (DIAS-) DIASORIN SRL.
 Query Match 13.0%; Score 58.5; DB 3; Length 166;
 Best Local Similarity 24.4%; Pred. No. 2.2e+02;
 RESULT 882
 ID AAU14973 standard; protein; 177 AA.
 DE Novel bone marrow polypeptide #179.
 PN W0200155442-A2.
 PD 02-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 13.0%; Score 58.5; DB 4; Length 177;
 Best Local Similarity 28.0%; Pred. No. 2.4e+02;
 RESULT 883
 ID AAG68168 standard; protein; 207 AA.
 DE Zmax1 signaling pathway analysis bait protein.
 PN W020017327-A1.
 PD 18-OCT-2001.
 PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match 13.0%; Score 58.5; DB 4; Length 207;
 Best Local Similarity 26.2%; Pred. No. 2.9e+02;
 RESULT 884
 ID ABR41135 standard; protein; 207 AA.
 DE LRP5 related yeast two hybrid protein.
 PN W0200292764-A2.
 PD 21-NOV-2002.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 PA (AMHP) WYETH.
 Query Match 13.0%; Score 58.5; DB 6; Length 207;
 Best Local Similarity 26.2%; Pred. No. 2.9e+02;
 RESULT 885
 ID ADB98802 standard; protein; 207 AA.
 DE LRP5-related protein #9.
 PN W0200292000-A2.
 PD 21-NOV-2002.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 PA (AMHP) WYETH.
 Query Match 13.0%; Score 58.5; DB 7; Length 207;
 Best Local Similarity 26.2%; Pred. No. 2.9e+02;
 RESULT 886
 ID AAY66761 standard; protein; 208 AA.
 DE Membrane-bound protein PRO1271.
 PN W09963088-A2.
 PD 09-DEC-1999.
 PA (GETH) GENENTECH INC.
 Query Match 13.0%; Score 58.5; DB 3; Length 208;
 Best Local Similarity 28.0%; Pred. No. 3e+02;
 RESULT 887
 ID AAY94908 standard; protein; 208 AA.
 DE Human secreted protein clone c152_2 protein sequence SEQ ID NO:22.
 PN W0200009552-A1.
 PD 24-FEB-2000.
 PA (GEMY) GENETICS INST INC.
 Query Match 13.0%; Score 58.5; DB 3; Length 208;
 Best Local Similarity 28.0%; Pred. No. 3e+02;
 RESULT 888
 ID AAE06585 standard; protein; 208 AA.
 DE Human protein having hydrophobic domain, HP10753.
 PN W0200149728-A2.
 PD 12-JUL-2001.
 PA (PROT-) PROTEGENE INC.
 PA (SAGA) SAGAMI CHEM RES CENT.
 Query Match 13.0%; Score 58.5; DB 4; Length 208;
 Best Local Similarity 28.0%; Pred. No. 3e+02;
 RESULT 889
 ID AAU12426 standard; protein; 208 AA.
 DE Human PRO1271 polypeptide sequence.
 PN W0200140466-A2.
 PD 07-JUN-2001.
 PA (GETH) GENENTECH INC.
 Query Match 13.0%; Score 58.5; DB 4; Length 208;
 Best Local Similarity 28.0%; Pred. No. 3e+02;
 RESULT 890
 ID AAU14891 standard; protein; 208 AA.
 DE Novel bone marrow polypeptide #97.
 PN W0200155442-A2.
 PD 02-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 13.0%; Score 58.5; DB 4; Length 208;
 Best Local Similarity 28.0%; Pred. No. 3e+02;
 RESULT 891
 ID AAB01725 standard; protein; 208 AA.
 DE Human gene 12 encoded secreted protein HNTAC64, SEQ ID NO:137.
 PN W0200134767-A2.
 PD 17-MAY-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 13.0%; Score 58.5; DB 4; Length 208;
 Best Local Similarity 28.0%; Pred. No. 3e+02;
 RESULT 892
 ID AAE01683 standard; protein; 208 AA.
 DE Human gene 12 encoded secreted protein HNTAC64, SEQ ID NO:95.
 PN W0200134767-A2.

PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 893
ID AAB01724 standard; protein; 208 AA.
DE Human gene 12 encoded secreted protein HNTAC64, SEQ ID NO:136.
PN WO200134767-A2.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 894
ID AAB01723 standard; protein; 208 AA.
DE Human gene 12 encoded secreted protein HNTAC64, SEQ ID NO:135.
PN WO200134767-A2.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 895
ID AAB03766 standard; protein; 208 AA.
DE Human gene 3 encoded secreted protein HNTAC64, SEQ ID NO:136.
PN WO200132837-A1.
PD 10-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 896
ID AAB88375 standard; protein; 208 AA.
DE Human membrane or secretory protein clone PSEC0111.
PN EP1067182-A2.
PD 10-JAN-2001.
PA (HELI-) HELIX RES INST.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 897
ID AAG81329 standard; protein; 208 AA.
DE Human AFP protein sequence SEQ ID NO:176.
PN WO200129221-A2.
PD 26-APR-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 898
ID AAB50924 standard; protein; 208 AA.
DE Human PRO1271 protein.
PN WO200073452-A2.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 899
ID AAB65284 standard; protein; 208 AA.
DE Human PRO1271 (UNQ641) protein sequence SEQ ID NO:416.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 4; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 900
ID ABG63986 standard; protein; 208 AA.
DE Human albumin fusion protein #661.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 5; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 901
ID ABG63987 standard; protein; 208 AA.
DE Human albumin fusion protein #662.
PN WO200177137-A1.
PD 18-OCT-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 5; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 902
ID ABG63985 standard; protein; 208 AA.
DE Human albumin fusion protein #660.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 5; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 903
ID ABG65496 standard; protein; 208 AA.
DE Human albumin fusion protein #2171.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 5; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 904
ID ABG63988 standard; protein; 208 AA.
DE Human albumin fusion protein #663.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 5; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 905
ID ABUS8099 standard; protein; 208 AA.
DE Human PRO polypeptide #131.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 906
ID ABUS9177 standard; protein; 208 AA.
DE Novel human secreted or transmembrane protein PRO1271.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 907
ID ABUS2689 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 908
ID AB017870 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 909
ID ABUS60608 standard; protein; 208 AA.
DE Human secreted/transmembrane protein, #167.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 910
ID ABUI3990 standard; protein; 208 AA.
DE Human PRO1271 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;

RESULT 911
ID ASU81124 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 912
ID ASU72575 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 913
ID ASU66824 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 914
ID ASU59905 standard; protein; 208 AA.
DE Novel secreted and transmembrane protein PRO1271.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 915
ID ASU59324 standard; protein; 208 AA.
DE Human secreted/transmembrane protein, #167.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 916
ID ABO26021 standard; protein; 208 AA.
DE Human PRO1271 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 917
ID ABO25095 standard; protein; 208 AA.
DE Human secreted/transmembrane protein (PRO) #255.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 918
ID ASU59030 standard; protein; 208 AA.
DE Human secreted/transmembrane protein, #167.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 919
ID ASU92408 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 920
ID ASU59473 standard; protein; 208 AA.
DE Novel human secreted or transmembrane protein PRO1375.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 921
ID ASU67100 standard; protein; 208 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 510.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 922
ID ASU92339 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 923
ID ASU10945 standard; protein; 208 AA.
DE Human PRO polypeptide #131.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 924
ID ASU81697 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 925
ID ASU88636 standard; protein; 208 AA.
DE Human secreted and transmembrane polypeptide PRO1271.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 926
ID ABO34150 standard; protein; 208 AA.
DE Human PRO1271 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 927
ID ADA46029 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US200302328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 928
ID ADA76460 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 929
ID ADA19110 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;

Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 930
ID ADA61733 standard; protein; 208 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 931
ID ADB19518 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 932
ID ADB28059 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 933
ID ADA86538 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 934
ID ADB16102 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 935
ID ADA37927 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US200308297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 936
ID ADA47888 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 937
ID ADA21613 standard; protein; 208 AA.
DE Human secreted/transmembrane polypeptide PRO1271.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 938
ID ADA10400 standard; protein; 208 AA.
DE Human secreted/transmembrane protein, PRO1271.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 939
ID ADA67683 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082694-A1.
PD 01-MAY-2003.

DE Human PRO polypeptide #255.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 940
ID ADB30690 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 941
ID ADA85986 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 942
ID ADA17944 standard; protein; 208 AA.
DE Human PRO1271 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 943
ID ADA97198 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 944
ID ADA79502 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 945
ID ADA87641 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 946
ID ADB16943 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 947
ID ADA28052 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 948
ID ADA91935 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082694-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 949
ID ADB14998 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 950
ID ADB18959 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 951
ID ADA94174 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 952
ID ADB20070 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 953
ID ADB13382 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 954
ID ABO43403 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 955
ID ADA94632 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 956
ID ADA74636 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 957
ID ADB24869 standard; protein; 208 AA.
DE Human PRO polypeptide SEQ ID NO 510.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 958
ID ADA82393 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 959
ID ADA75356 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 960
ID ADA85434 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 961
ID ADA84882 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 962
ID ADB30138 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 963
ID ADA80666 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 964
ID ADA75908 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 965
ID ADA38857 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003059780-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 966
ID ADA47133 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 967

ID ADB25429 standard; protein; 208 AA.
DE Human PRO polypeptide SEQ ID NO 510.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 968
ID ADA93605 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 969
ID ADB26955 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 970
ID ADB31242 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 971
ID ADA92978 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 972
ID ADA61170 standard; protein; 208 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 973
ID ADB24317 standard; protein; 208 AA.
DE Human PRO polypeptide SEQ ID NO 510.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 974
ID ADA96646 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 975
ID ADA81218 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 976
ID ADA96094 standard; protein; 208 AA.
DE Human PRO polypeptide #255.

PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 977
ID ADB26403 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 978
ID ADB21888 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 6; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 979
ID ADA77667 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 980
ID ADB18407 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 981
ID ADA87090 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 982
ID ADA88193 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 983
ID ADA6581 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 984
ID ADB28611 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 985
ID ADB29163 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082706-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 986
ID ABO53236 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 987
ID ADA77115 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 988
ID ADA22539 standard; protein; 208 AA.
DE Human secreted/transmembrane polypeptide PRO1271.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 989
ID ADA88745 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 990
ID ADA97750 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 991
ID ADB27507 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 992
ID ADB22440 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 993
ID ABO22606 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 994
ID ADA06705 standard; protein; 208 AA.
DE Human secreted/transmembrane PRO polypeptide #131.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 995
ID ADA39398 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.

PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 996
ID ADA67131 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 997
ID ADB22992 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 998
ID ADB23765 standard; protein; 208 AA.
DE Human PRO polypeptide SEQ ID NO 510.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 999
ID ADA92487 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1000
ID ADB15550 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1001
ID ADB38802 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1002
ID ADB96424 standard; protein; 208 AA.
DE Human PRO polypeptide #131.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1003
ID ADB38250 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1004
ID ADB66722 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1005
ID ADB9802 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1006
ID ADB90534 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1007
ID ADB39635 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1008
ID ADB47258 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1009
ID ADB86865 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1010
ID ADB77470 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1011
ID ADB34627 standard; protein; 208 AA.
DE Human PRO polypeptide SEQ ID NO 510.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1012
ID ADB35731 standard; protein; 208 AA.
DE Human PRO polypeptide SEQ ID NO 510.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1013
ID ADB34075 standard; protein; 208 AA.
DE Human PRO polypeptide SEQ ID NO 510.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1014
ID ADB35179 standard; protein; 208 AA.
DE Human PRO polypeptide SEQ ID NO 510.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1015
ID ADB36283 standard; protein; 208 AA.
DE Human PRO polypeptide SEQ ID NO 510.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1016
ID ADB46678 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1017
ID ADC57896 standard; protein; 208 AA.
DE Human PRO polypeptide #131.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1018
ID ADC55260 standard; protein; 208 AA.
DE Human PRO polypeptide #131.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1019
ID ADC12127 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1020
ID ADC56549 standard; protein; 208 AA.
DE Human PRO polypeptide #131.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1021
ID ADC07604 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1022
ID ADC11594 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1023
ID ADC50551 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.

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Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1024
ID ADC72098 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1025
ID ADC60077 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1026
ID ADC53084 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein Seq ID510.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1027
ID ADC57438 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein Seq ID510.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1028
ID ADC60629 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1029
ID ADC51104 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1030
ID ADC65631 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1031
ID ADC54729 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein Seq ID510.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1032
ID ADC53690 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein Seq ID510.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1033
ID ADC59213 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein Seq ID510.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1034
ID ADC56091 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein Seq ID510.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1035
ID ADC58661 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein Seq ID510.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1036
ID ADC14716 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1037
ID ADD08248 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003068623-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1038
ID ADD03335 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1039
ID ADC90327 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1040
ID ADC82073 standard; protein; 208 AA.
DE Human PRO polypeptide #131.
PN US2003083461-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1041
ID ADC69746 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 13.0%; Score 58.5; DB 7; Length 208;
RESULT 1042
ID ADC48635 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
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PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1043
ID ADD10164 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1044
ID ADD07715 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1045
ID ADD04739 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1046
ID ADC82606 standard; protein; 208 AA.
DE Human PRO polypeptide #131.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1047
ID ADC80695 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1048
ID ADD11202 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1049
ID ADC48083 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1050
ID ADD08786 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1051
ID ADC80143 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1052
ID ADD07035 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1053
ID ADD09612 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1054
ID ADC83282 standard; protein; 208 AA.
DE Human PRO polypeptide #131.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1055
ID ADD41325 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1056
ID ADD52464 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1057
ID ADD53204 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1058
ID ADD53756 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1059
ID ADD55389 standard; protein; 208 AA.
DE Human PRO polypeptide #131.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1060
ID ADD56347 standard; protein; 208 AA.
DE Human PRO polypeptide #131.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1061
ID ADD51912 standard; protein; 208 AA.
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DE Human PRO polypeptide #255.
PD US2003194779-A1.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1062
ID ADD02711 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PD US2003203431-A1.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1063
ID ADD02145 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PD US2003203430-A1.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1064
ID ADD54327 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PD US2003203432-A1.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1065
ID ADD54785 standard; protein; 208 AA.
DE Human PRO polypeptide #131.
PD US2002132253-A1.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1066
ID ADD92644 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PD US2003195030-A1.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1067
ID ADD91540 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PD US2003195055-A1.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1068
ID ADE04154 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PD US2003195057-A1.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1069
ID ADE26939 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PD US2003087304-A1.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1070
ID ADE32451 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PD US2003194765-A1.

PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1071
ID ADE22383 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PD US2003195056-A1.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1072
ID ADD79607 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PD US2003203428-A1.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1073
ID ADE42143 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PD US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1074
ID ADE17960 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PD US2003195023-A1.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1075
ID ADD92092 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PD US2003195053-A1.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1076
ID ADE33555 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PD US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1077
ID ADE34107 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PD US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1078
ID ADD80159 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PD US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1079
ID ADD93196 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PD US2003194768-A1.
PD 16-OCT-2003.
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PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1080
ID ADE19616 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1081
ID ADE19064 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1082
ID ADE43260 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1083
ID ADD96049 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1084
ID ADE22935 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1085
ID ADD79053 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1086
ID ADE26406 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087305-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1087
ID ADE33003 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1088
ID ADE42895 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1089
ID ADD80711 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1090
ID ADD89739 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1091
ID ADE41023 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1092
ID ADE04822 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1093
ID ADF60236 standard; protein; 208 AA.
DE Human contig polypeptide sequence SEQ ID NO:2603.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1094
ID ADE92951 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1095
ID ADF67343 standard; protein; 208 AA.
DE Human PRO1271 amino acid sequence SEQ ID NO:416.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1096
ID ADG21660 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1097
ID ADG23301 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1098
ID ADE42895 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;

RESULT 1098
ID ADF97636 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1099
ID ADG80700 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1100
ID ADG80148 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1101
ID ADH55440 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1102
ID ADH55992 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1103
ID ADI35597 standard; protein; 208 AA.
DE Human PRO polypeptide #131.
PN US2003050457-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1104
ID ADI64211 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1105
ID ADI65160 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1106
ID ADI63659 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1107
ID ADH82073 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003100087-A1.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1108
ID ADI00090 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003049682-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1109
ID ADH81521 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1110
ID ADM82690 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1111
ID ADN16089 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1112
ID ADN16718 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1113
ID ADN15537 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1114
ID ADN14985 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 7; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1115
ID ADC81247 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1116
ID ADD76695 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003100087-A1.

Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1135
ID ADE91847 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1136
ID ADG11792 standard; protein; 208 AA.
DE Human PRO1271 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1137
ID ADG02426 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1138
ID ADG22212 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1139
ID ADG20282 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1140
ID ADF98188 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1141
ID ADG24405 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1142
ID ADF98759 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1143
ID ADG03590 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1144
ID ADF99311 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1145
ID ADG16896 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1146
ID ADG05355 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1147
ID ADG19622 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1148
ID ADG13459 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1149
ID ADG08516 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1150
ID ADG15686 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1151
ID ADF97084 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1152
ID ADG06269 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1153
ID ADG06269 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;

ID ADG23853 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1154
ID ADG04142 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1155
ID ADG25043 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1156
ID ADG07340 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1157
ID ADG07892 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1158
ID ADG55387 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1159
ID ADG61051 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1160
ID ADG62155 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1161
ID ADG82356 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1162
ID ADG57595 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1163
ID ADG57043 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1164
ID ADG55939 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1165
ID ADG58699 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1166
ID ADG71065 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1167
ID ADG58147 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1168
ID ADG53731 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1169
ID ADG71617 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1170
ID ADG81804 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1171
ID ADH19662 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003228656-A1.

PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1172
ID ADH30766 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1173
ID ADH12133 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1174
ID ADG52555 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1175
ID ADG54283 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1176
ID ADG81252 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1177
ID ADG56491 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1178
ID ADH12757 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1179
ID ADH21155 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1180
ID ADG61603 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1181
ID ADH20195 standard; protein; 208 AA.
DE Human secreted/transmembrane protein PRO1271.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1182
ID ADH28690 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1183
ID ADG54835 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1184
ID ADG59875 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1185
ID ADI81299 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1186
ID ADG10042 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1187
ID ADI15513 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1188
ID ADG09390 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1189
ID ADI14845 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1190
ID ADG61603 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1190
ID ADI18440 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1191
ID ADJ63721 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1192
ID ADL77250 standard; protein; 208 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 732.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE//) ROSEN C A.
PA (HASE//) HASELTINE W A.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1193
ID ADL77251 standard; protein; 208 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 733.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE//) ROSEN C A.
PA (HASE//) HASELTINE W A.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1194
ID ADL77253 standard; protein; 208 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 735.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE//) ROSEN C A.
PA (HASE//) HASELTINE W A.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1195
ID ADL77252 standard; protein; 208 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 734.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE//) ROSEN C A.
PA (HASE//) HASELTINE W A.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1196
ID ADL78763 standard; protein; 208 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 2245.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE//) ROSEN C A.
PA (HASE//) HASELTINE W A.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1197
ID ADJ77616 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1198
ID ADJ65738 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2004214269-A1.

PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1199
ID ADM27874 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1200
ID ADM42598 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1201
ID ADM28460 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1202
ID ADP07778 standard; protein; 208 AA.
DE Human secreted protein, seq id 261.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1203
ID ADP74722 standard; protein; 208 AA.
DE Human porimin protein SEQ ID NO: 4.
PN WO2004047762-A2.
PD 10-JUN-2004.
PA (CHIR) CHIRON CORP.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1204
ID ADI95942 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1205
ID ADI96494 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1206
ID ADS32446 standard; protein; 208 AA.
DE Novel human secreted and transmembrane protein PRO1271.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 13.0%; Score 58.5; DB 8; Length 208;
Best Local Similarity 28.0%; Pred. No. 3e+02;
RESULT 1207
ID ADT03430 standard; protein; 208 AA.
DE Human PRO polypeptide #255.
PN US2004214269-A1.

PA (GETH) GENENTECH INC. 28-OCT-2004.
 Query Match 13.0%; Score 58.5; DB 8; Length 208;
 Best Local Similarity 28.0%; Pred. No. 3e+02;
 RESULT 1208
 ID ADY63115 standard; protein; 208 AA.
 DE Human clone PSEC0111 protein, SEQ ID 118.
 PN EP1514933-A1.
 PD 16-MAR-2005.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 13.0%; Score 58.5; DB 9; Length 208;
 Best Local Similarity 28.0%; Pred. No. 3e+02;
 RESULT 1209
 ID ADZ03481 standard; protein; 208 AA.
 DE Human secreted/transmembrane PRO1271 protein.
 PN US2005074837-A1.
 PD 07-APR-2005.
 PA (GETH) GENENTECH INC.
 Query Match 13.0%; Score 58.5; DB 9; Length 208;
 Best Local Similarity 28.0%; Pred. No. 3e+02;
 RESULT 1210
 ID AEA38633 standard; protein; 208 AA.
 DE Human secreted/transmembrane protein, #199.
 PN US2005112725-A1.
 PD 26-MAY-2005.
 PA (GETH) GENENTECH INC.
 Query Match 13.0%; Score 58.5; DB 9; Length 208;
 Best Local Similarity 28.0%; Pred. No. 3e+02;
 RESULT 1211
 ID AEB14227 standard; protein; 208 AA.
 DE Cancer cell diagnosis method-related human protein - SEQ ID 510.
 PN US2005153396-A1.
 PD 14-JUL-2005.
 PA (BAKE/) BAKER K P.
 PA (BERE/) BERESINI M.
 PA (DEFO/) DEFORGE L.
 PA (DESN/) DESNOYERS L.
 PA (FILV/) FILVAROFF E.
 PA (GAOW/) GAO W.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (SHER/) SHERWOOD S.
 PA (SMIT/) SMITH V.
 PA (STEW/) STEWART T A.
 PA (TUMA/) TUMAS D.
 PA (WATA/) WATANABE C K.
 PA (WOOD/) WOOD W I.
 PA (ZHAN/) ZHANG Z.
 Query Match 13.0%; Score 58.5; DB 9; Length 208;
 Best Local Similarity 28.0%; Pred. No. 3e+02;
 RESULT 1212
 ID AEW84936 standard; protein; 225 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:5185.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 13.0%; Score 58.5; DB 8; Length 225;
 Best Local Similarity 30.4%; Pred. No. 3.3e+02;
 RESULT 1213
 ID AWM84934 standard; protein; 225 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:5183.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 13.0%; Score 58.5; DB 8; Length 225;
 Best Local Similarity 30.4%; Pred. No. 3.3e+02;
 RESULT 1214
 ID ADI17268 standard; protein; 230 AA.
 DE Polypeptide homologous to a human NOVX domain SeqID 804.
 PN WO200268649-A2.
 PD 06-SEP-2002.

PA (CURA-) CURAGEN CORP. 13.0%; Score 58.5; DB 5; Length 230;
 Query Match 24.6%; Pred. No. 3.4e+02;
 RESULT 1215
 ID ADI17276 standard; protein; 230 AA.
 DE Polypeptide homologous to a human NOVX domain SeqID 812.
 PN WO200268649-A2.
 PD 06-SEP-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 13.0%; Score 58.5; DB 5; Length 230;
 Best Local Similarity 24.6%; Pred. No. 3.4e+02;
 RESULT 1216
 ID ADJ83075 standard; protein; 230 AA.
 DE Tyrosin-like serine protease protein - SEQ ID 66.
 PN US2003170630-A1.
 PD 11-SEP-2003.
 PA (ALSO/) ALSOBROOK J P.
 PA (TCHE/) TCHERNEV V T.
 PA (LIUX/) LIU X.
 PA (SPYT/) SPYTEK K A.
 PA (ZERH/) ZERHUSEN B D.
 PA (PATT/) PATTURAJAN M.
 PA (LEPL/) LEPLEY D M.
 PA (BURG/) BURGESS C E.
 PA (SHIM/) SHINKETS R A.
 PA (GROS/) GROSSE W M.
 PA (SZEK/) SZEKERES E S.
 PA (VERN/) VERNET C A M.
 PA (LILL/) LI L.
 PA (CASM/) CASMAN S J.
 PA (BOLD/) BOLDOG P L.
 PA (GORM/) GORMAN L.
 PA (GANG/) GANGOLLI B A.
 PA (FERN/) FERNANDES E R.
 PA (RIEG/) RIEGER D K.
 PA (EDIN/) EDINGER S R.
 PA (GUNT/) GUNTHER E.
 PA (MILL/) MILLET I.
 PA (SCIO/) SCIORE P.
 PA (ELLE/) ELLERMAN K.
 PA (MACD/) MACDOUGALL J R.
 PA (SMIT/) SMITHSON G.
 Query Match 13.0%; Score 58.5; DB 7; Length 230;
 Best Local Similarity 24.6%; Pred. No. 3.4e+02;
 RESULT 1217
 ID ABB69469 standard; protein; 276 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 35199.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 13.0%; Score 58.5; DB 4; Length 276;
 Best Local Similarity 26.1%; Pred. No. 4.2e+02;
 RESULT 1218
 ID ADW17748 standard; protein; 288 AA.
 DE Pinus radiata transcription factor protein MYB family Seq 1522.
 PN WO2005001050-A2.
 PD 06-JAN-2005.
 PA (ARBO-) ARBORGEN LLC.
 Query Match 13.0%; Score 58.5; DB 9; Length 288;
 Best Local Similarity 25.3%; Pred. No. 4.5e+02;
 RESULT 1219
 ID ADM03974 standard; protein; 302 AA.
 DE Human protein of the invention SEQ ID NO:2659.
 PN EP1347046-A1.
 PD 24-SEP-2003.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 13.0%; Score 58.5; DB 7; Length 302;
 Best Local Similarity 29.4%; Pred. No. 4.7e+02;
 RESULT 1220
 ID ADE55614 standard; protein; 328 AA.
 DE Rat Protein CAA08796, SEQ ID NO 1433.
 PN WO2003016475-A2.
 PD 27-FEB-2003.

PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 13.0%; Score 58.5; DB 7; Length 328;
Best Local Similarity 30.5%; Pred. No. 5.3e+02;
RESULT 1221
ID ADE55610 standard; protein; 328 AA.
DE Rat Protein CAA08796, SEQ ID NO 1429.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 13.0%; Score 58.5; DB 7; Length 328;
Best Local Similarity 30.5%; Pred. No. 5.3e+02;
RESULT 1222
ID AAG47665 standard; protein; 330 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 60101.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 13.0%; Score 58.5; DB 3; Length 330;
Best Local Similarity 36.0%; Pred. No. 5.3e+02;
RESULT 1223
ID ABB63026 standard; protein; 357 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 15870.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 13.0%; Score 58.5; DB 4; Length 357;
Best Local Similarity 29.3%; Pred. No. 5.8e+02;
RESULT 1224
ID ADR20443 standard; protein; 374 AA.
DE Trichinella spiralis serine protease protein fragment 1.
PN JP2004229599-A.
PD 19-AUG-2004.
PA (GIFU-) UNIV GIFU.
Query Match 13.0%; Score 58.5; DB 8; Length 374;
Best Local Similarity 25.0%; Pred. No. 6.2e+02;
RESULT 1225
ID ADR20442 standard; protein; 421 AA.
DE Full length Trichinella spiralis serine protease protein.
PN JP2004229599-A.
PD 19-AUG-2004.
PA (GIFU-) UNIV GIFU.
Query Match 13.0%; Score 58.5; DB 8; Length 421;
Best Local Similarity 25.0%; Pred. No. 7.2e+02;
RESULT 1226
ID ADM17284 standard; protein; 494 AA.
DE Eucalyptus grandis transcription factor protein GRAS family Seq 1035.
PN WO2005001050-A2.
PD 06-JAN-2005.
PA (ARBO-) ARBORGEN LLC.
Query Match 13.0%; Score 58.5; DB 9; Length 494;
Best Local Similarity 25.0%; Pred. No. 8.8e+02;
RESULT 1227
ID ABM88793 standard; protein; 1161 AA.
DE Rice abiotic stress responsive polypeptide SEQ ID NO:7039.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 13.0%; Score 58.5; DB 7; Length 1161;
Best Local Similarity 27.7%; Pred. No. 2.6e+03;
RESULT 1228
ID AAW83310 standard; protein; 1451 AA.
DE LRP5 protein from isoform 2 (also isoform 4,5,6).
PN WO9846743-A1.
PD 22-OCT-1998.
PA (WELL) WELLCOME TRUST LTD.
PA (MERI) MERCK & CO INC.
Query Match 13.0%; Score 58.5; DB 2; Length 1451;
Best Local Similarity 26.2%; Pred. No. 3.4e+03;
RESULT 1229
ID ADC68833 standard; protein; 1494 AA.
DE Human GPCR protein SEQ ID NO:1286.
PN EPI270724-A2.

PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 13.0%; Score 58.5; DB 7; Length 1494;
Best Local Similarity 26.2%; Pred. No. 3.5e+03;
RESULT 1230
ID AAW83308 standard; protein; 1591 AA.
DE Mature LRP5 protein.
PN WO9846743-A1.
PD 22-OCT-1998.
PA (WELL) WELLCOME TRUST LTD.
PA (MERI) MERCK & CO INC.
Query Match 13.0%; Score 58.5; DB 2; Length 1591;
Best Local Similarity 26.2%; Pred. No. 3.8e+03;
RESULT 1231
ID AAW83309 standard; protein; 1615 AA.
DE LRP5 protein from the longest open reading frame.
PN WO9846743-A1.
PD 22-OCT-1998.
PA (WELL) WELLCOME TRUST LTD.
PA (MERI) MERCK & CO INC.
Query Match 13.0%; Score 58.5; DB 2; Length 1615;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1232
ID AAG68169 standard; protein; 1615 AA.
DE Human Zmax1 protein SEQ ID NO:3.
PN WO200177327-A1.
PD 18-OCT-2001.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.0%; Score 58.5; DB 4; Length 1615;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1233
ID AAG68170 standard; protein; 1615 AA.
DE Human HEM protein SEQ ID NO:4.
PN WO200177327-A1.
PD 18-OCT-2001.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.0%; Score 58.5; DB 4; Length 1615;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1234
ID AAE21740 standard; protein; 1615 AA.
DE Human BSMR protein mutant, R494Q.
PN WO200216553-A2.
PD 28-FEB-2002.
PA (AVET) AVENTIS PHARMA SA.
PA (HARD) HARVARD COLLEGE.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 13.0%; Score 58.5; DB 5; Length 1615;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1235
ID AAE21741 standard; protein; 1615 AA.
DE Human BSMR protein mutant, A1330L.
PN WO200216553-A2.
PD 28-FEB-2002.
PA (AVET) AVENTIS PHARMA SA.
PA (HARD) HARVARD COLLEGE.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 13.0%; Score 58.5; DB 5; Length 1615;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1236
ID AAE21730 standard; protein; 1615 AA.
DE Human bone strength and mineralisation regulatory protein (BSMR).
PN WO200216553-A2.
PD 28-FEB-2002.
PA (AVET) AVENTIS PHARMA SA.
PA (HARD) HARVARD COLLEGE.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 13.0%; Score 58.5; DB 5; Length 1615;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1237
ID AAU80879 standard; protein; 1615 AA.
DE Human Zmax1 polypeptide.
PN WO200192891-A2.

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PD 06-DEC-2001.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP ) WYETH.
  Query Match      13.0%; Score 58.5; DB 5; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1238
ID AAU08080 standard; protein; 1615 AA.
DE Human high bone mass (HBM) polypeptide.
PN WO200192891-A2.
PD 06-DEC-2001.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
  Query Match      13.0%; Score 58.5; DB 5; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1239
ID ABR41093 standard; protein; 1615 AA.
DE Human wild-type LRP5.
PN WO200292764-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP ) WYETH.
  Query Match      13.0%; Score 58.5; DB 6; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1240
ID ABR41094 standard; protein; 1615 AA.
DE Human LRP5 allelic variant HBM.
PN WO200292764-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP ) WYETH.
  Query Match      13.0%; Score 58.5; DB 6; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1241
ID ABR41131 standard; protein; 1615 AA.
DE Human LRP5 protein.
PN WO200292764-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP ) WYETH.
  Query Match      13.0%; Score 58.5; DB 6; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1242
ID ADB98058 standard; protein; 1615 AA.
DE Human LRP5.
PN WO200292000-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP ) WYETH.
  Query Match      13.0%; Score 58.5; DB 7; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1243
ID ADB98798 standard; protein; 1615 AA.
DE Human Zmax1 (LRP5).
PN WO200292000-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP ) WYETH.
  Query Match      13.0%; Score 58.5; DB 7; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1244
ID ADB98059 standard; protein; 1615 AA.
DE LRP5 mutein.
PN WO200292000-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP ) WYETH.
  Query Match      13.0%; Score 58.5; DB 7; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1245
ID ADE82428 standard; protein; 1615 AA.
DE Human HBM gene.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP ) WYETH.
  Query Match      13.0%; Score 58.5; DB 7; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1246
ID ADE82427 standard; protein; 1615 AA.
DE Human Zmax1 gene.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP ) WYETH.
  Query Match      13.0%; Score 58.5; DB 7; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1247
ID ADI27181 standard; protein; 1615 AA.
DE Human LRP binding family protein #12.
PN WO2003106657-A2.
PD 24-DEC-2003.
PA (STOW-) STOWERS INST MEDICAL RES.
  Query Match      13.0%; Score 58.5; DB 8; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1248
ID ADQ20524 standard; protein; 1615 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3344.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
  Query Match      13.0%; Score 58.5; DB 8; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1249
ID ADR17561 standard; protein; 1615 AA.
DE Human high bone mass gene, HBM allele, protein #2.
PN US6780609-B1.
PD 24-AUG-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
  Query Match      13.0%; Score 58.5; DB 8; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1250
ID ADR16921 standard; protein; 1615 AA.
DE Human high bone mass gene, wild type allele Zmax1, protein #1.
PN US6780609-B1.
PD 24-AUG-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
  Query Match      13.0%; Score 58.5; DB 8; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1251
ID ADR17560 standard; protein; 1615 AA.
DE Human high bone mass gene, wild type allele Zmax1, protein #2.
PN US6780609-B1.
PD 24-AUG-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
  Query Match      13.0%; Score 58.5; DB 8; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1252
ID ADR16922 standard; protein; 1615 AA.
DE Human high bone mass gene, HBM allele, protein #1.
PN US6780609-B1.
PD 24-AUG-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
  Query Match      13.0%; Score 58.5; DB 8; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1253
ID ABO84659 standard; protein; 1615 AA.
DE Human cancer-associated protein HP20-001.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRIS DISCOVERY INC.
  Query Match      13.0%; Score 58.5; DB 8; Length 1615;
  Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1254
ID ADR47572 standard; protein; 1615 AA.
DE Human high bone mass gene, wild type allele Zmax1, protein #1.
PN US2004176582-A1.

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PD 09-SEP-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON.
Query Match 13.0%; Score 58.5; DB 8; Length 1615;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1255
ID ADR48212 standard; protein; 1615 AA.
DE Human high bone mass gene, HBM allele, protein #2.
PN US2004175582-A1.
PD 09-SEP-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON.
Query Match 13.0%; Score 58.5; DB 8; Length 1615;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1256
ID ADR47573 standard; protein; 1615 AA.
DE Human high bone mass gene, HBM allele, protein #1.
PN US2004175582-A1.
PD 09-SEP-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON.
Query Match 13.0%; Score 58.5; DB 8; Length 1615;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1257
ID ADR48211 standard; protein; 1615 AA.
DE Human high bone mass gene, wild type allele Zmax1, protein #2.
PN US2004175582-A1.
PD 09-SEP-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON.
Query Match 13.0%; Score 58.5; DB 8; Length 1615;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1258
ID ADR73482 standard; protein; 1615 AA.
DE Human low density lipoprotein receptor-related protein 5, LRP5, protein.
PN WO2004076682-A2.
PD 10-SEP-2004.
PA (SUUR-) SURROMED INC.
Query Match 13.0%; Score 58.5; DB 8; Length 1615;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1259
ID ADV97195 standard; protein; 1615 AA.
DE Human low density lipoprotein receptor-related protein 5 (LRP5), SEQ:50.
PN US2005003390-A1.
PD 06-JAN-2005.
PA (AXEN/) AXENOVICH S A.
PA (STUL/) STULL R.
PA (GELM/) GELMAN M.
PA (CHUI/) CHUI K.
PA (NGDD/) NG D.
Query Match 13.0%; Score 58.5; DB 9; Length 1615;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1260
ID ABE69940 standard; protein; 1615 AA.
DE Human High Bone Mass gene, wild type allele Zmax1 protein.
PN US2005142617-A1.
PD 30-JUN-2005.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
Query Match 13.0%; Score 58.5; DB 9; Length 1615;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1261
ID ABE69301 standard; protein; 1615 AA.
DE Human High Bone Mass gene, wild type allele Zmax1 protein, SEQ ID 3.
PN US2005142617-A1.
PD 30-JUN-2005.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
Query Match 13.0%; Score 58.5; DB 9; Length 1615;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1262
ID ABE69302 standard; protein; 1615 AA.
DE Human High Bone Mass gene, mutant allele HBM protein, SEQ ID 4.

PN US2005142617-A1.
PD 30-JUN-2005.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
Query Match 13.0%; Score 58.5; DB 9; Length 1615;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1263
ID ABE65665 standard; protein; 1627 AA.
DE Human protein sequence hCP1690976.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 13.0%; Score 58.5; DB 7; Length 1627;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1264
ID ABO84660 standard; protein; 1627 AA.
DE Human cancer-associated protein HP20-001.2.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 13.0%; Score 58.5; DB 8; Length 1627;
Best Local Similarity 26.2%; Pred. No. 3.9e+03;
RESULT 1265
ID AAW83311 standard; protein; 1639 AA.
DE LRP5 isoform 3 protein.
PN WO9846743-A1.
PD 22-OCT-1998.
PA (WELL) WELLCOME TRUST LTD.
PA (MERI) MERCK & CO INC.
Query Match 13.0%; Score 58.5; DB 2; Length 1639;
Best Local Similarity 26.2%; Pred. No. 4e+03;
RESULT 1266
ID ABR41133 standard; protein; 1665 AA.
DE Human LRP5 protein.
PN WO200292764-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 13.0%; Score 58.5; DB 6; Length 1665;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1267
ID ADB98800 standard; protein; 1665 AA.
DE Human Zmax1 (LRP5).
PN WO200292000-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 13.0%; Score 58.5; DB 7; Length 1665;
Best Local Similarity 26.2%; Pred. No. 4.1e+03;
RESULT 1268
ID ABG77164 standard; protein; 236 AA.
DE Germline protein sequence of anti-IGF-1R antibody AJ30/JK1.
PN WO200253596-A2.
PD 11-JUL-2002.
PA (PFIZ) PFIZER INC.
PA (ABGE-) ABGENIX INC.
Query Match 12.9%; Score 58; DB 5; Length 236;
Best Local Similarity 28.4%; Pred. No. 4e+02;
RESULT 1269
ID ADR28586 standard; protein; 236 AA.
DE Human anti-IGF-1R antibody heavy chain A30/Jk1 protein SEQ ID NO:52.
PN WO2004071529-A2.
PD 26-AUG-2004.
PA (PFIZ) PFIZER PROD INC.
Query Match 12.9%; Score 58; DB 8; Length 236;
Best Local Similarity 28.4%; Pred. No. 4e+02;
RESULT 1270
ID ADX57906 standard; protein; 236 AA.
DE Human germline A30/Jk1 protein sequence SeqID6.
PN WO2005016967-A2.
PD 24-FEB-2005.
PA (PFIZ) PFIZER PROD INC.
Query Match 12.9%; Score 58; DB 9; Length 236;

Best Local Similarity 28.4%; Pred. No. 4e+02;
RESULT 1271
ID ADS43001 standard; protein; 375 AA.
DE Bacterial polypeptide #21431.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.9%; Score 58; DB 8; Length 375;
Best Local Similarity 24.2%; Pred. No. 7.1e+02;
RESULT 1272
ID ADS15092 standard; protein; 405 AA.
DE Pseudomonas aeruginosa quorum sensing controlled protein, SEQ ID 647.
PN WO2004083385-A2.
PD 30-SEP-2004.
PA (IOWA) UNIV IOWA RES FOUND.
Query Match 12.9%; Score 58; DB 8; Length 405;
Best Local Similarity 38.6%; Pred. No. 7.8e+02;
RESULT 1273
ID ADX90494 standard; protein; 418 AA.
DE Plant full length insert polypeptide seqid 53158.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABAR/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 12.9%; Score 58; DB 8; Length 418;
Best Local Similarity 31.7%; Pred. No. 8.1e+02;
RESULT 1274
ID AAU31533 standard; protein; 450 AA.
DE Novel human secreted protein #2024.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.9%; Score 58; DB 4; Length 450;
Best Local Similarity 29.5%; Pred. No. 8.9e+02;
RESULT 1275
ID ABO78245 standard; protein; 469 AA.
DE Pseudomonas aeruginosa polypeptide #10420.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.9%; Score 58; DB 7; Length 469;
Best Local Similarity 38.6%; Pred. No. 9.4e+02;
RESULT 1276
ID AAW05408 standard; protein; 486 AA.
DE Mouse Hsi protein.
PN WO9631625-A1.
PD 10-OCT-1996.
PA (CYTO-) CYTOGEN CORP.
PA (UYNC-) UNIV NORTH CAROLINA.
Query Match 12.9%; Score 58; DB 2; Length 486;
Best Local Similarity 36.6%; Pred. No. 9.8e+02;
RESULT 1277
ID AA03795 standard; protein; 486 AA.
DE Murine Lck binding protein, LckBP1.
PN US5891673-A.
PD 06-APR-1999.
PA (SVNT) SYNTEX USA INC.
Query Match 12.9%; Score 58; DB 2; Length 486;
Best Local Similarity 36.6%; Pred. No. 9.8e+02;
RESULT 1278
ID ABR44110 standard; protein; 486 AA.
DE Human protein expressed in haematopoietic cells.
PN EP1295895-A1.
PD 26-MAR-2003.
PA (INSR) INST ROUSSY GUSTAVE.
PA (UYPA-) UNIV PARIS SUD.
Query Match 12.9%; Score 58; DB 6; Length 486;
Best Local Similarity 36.8%; Pred. No. 9.8e+02;
RESULT 1279
ID ABO7214 standard; protein; 486 AA.
DE Human p53 modifying protein, SEQ ID 174.
PN WO200299122-A1.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 12.9%; Score 58; DB 6; Length 486;
Best Local Similarity 36.6%; Pred. No. 9.8e+02;
RESULT 1280
ID ADD67624 standard; protein; 486 AA.
DE Human Lyl729P protein SEQ ID NO:101.
PN WO2003062401-A2.
PD 31-JUL-2003.
PA (CORI-) CORIXA CORP.
Query Match 12.9%; Score 58; DB 7; Length 486;
Best Local Similarity 36.6%; Pred. No. 9.8e+02;
RESULT 1281
ID ADM67192 standard; protein; 486 AA.
DE Human haematopoietic cell specific Lyn substrate 1 protein SeqID 546.
PN WO2004011618-A2.
PD 05-FEB-2004.
PA (HMGB-) HMGB INC.
Query Match 12.9%; Score 58; DB 8; Length 486;
Best Local Similarity 36.8%; Pred. No. 9.8e+02;
RESULT 1282
ID ADM67191 standard; protein; 486 AA.
DE Murine haematopoietic cell specific Lyn substrate 1 protein SeqID 545.
PN WO2004011618-A2.
PD 05-FEB-2004.
PA (HMGB-) HMGB INC.
Query Match 12.9%; Score 58; DB 8; Length 486;
Best Local Similarity 36.6%; Pred. No. 9.8e+02;
RESULT 1283
ID ADN25984 standard; protein; 496 AA.
DE Bacterial polypeptide #8637.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.9%; Score 58; DB 8; Length 496;
Best Local Similarity 30.0%; Pred. No. 1e+03;
RESULT 1284
ID AEB41830 standard; protein; 499 AA.
DE L. pneumophila protein SEQ ID NO 6162.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 12.9%; Score 58; DB 9; Length 499;
Best Local Similarity 38.7%; Pred. No. 1e+03;
RESULT 1285
ID ABO58685 standard; protein; 501 AA.
DE Human genome derived single exon protein #4919.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 12.9%; Score 58; DB 8; Length 501;
Best Local Similarity 28.0%; Pred. No. 1e+03;
RESULT 1286
ID AEB38588 standard; protein; 507 AA.
DE L. pneumophila protein SEQ ID NO 2920.
PN WO2005049642-A2.
PD 02-JUN-2005.

PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UPLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 12.9%; Score 58; DB 9; Length 507;
Best Local Similarity 38.7%; Pred. No. 1e+03;
RESULT 1287
ID AAW90945 standard; protein; 540 AA.
DE Comenonas testosterone R5 phenol hydroxylase protein #4.
PN JP2000069968-A.
PD 07-MAR-2000.
PA (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.
Query Match 12.9%; Score 58; DB 3; Length 540;
Best Local Similarity 22.6%; Pred. No. 1.1e+03;
RESULT 1288
ID AJ49107 standard; protein; 528 AA.
DE Oll-associated gene related protein #607.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 12.9%; Score 58; DB 8; Length 628;
Best Local Similarity 26.9%; Pred. No. 1.4e+03;
RESULT 1289
ID AJ49064 standard; protein; 528 AA.
DE Oll-associated gene related protein #564.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 12.9%; Score 58; DB 8; Length 628;
Best Local Similarity 26.9%; Pred. No. 1.4e+03;
RESULT 1290
ID AM78503 standard; protein; 797 AA.
DE Human protein SEQ ID NO 1165.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.9%; Score 58; DB 4; Length 797;
Best Local Similarity 28.0%; Pred. No. 1.8e+03;
RESULT 1291
ID AAM40565 standard; protein; 801 AA.
DE Human polypeptide SEQ ID NO 5496.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.9%; Score 58; DB 4; Length 801;
Best Local Similarity 28.0%; Pred. No. 1.8e+03;
RESULT 1292
ID ABB11940 standard; peptide; 973 AA.
DE Human secreted protein homologue, SEQ ID NO:2310.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.9%; Score 58; DB 4; Length 973;
Best Local Similarity 28.0%; Pred. No. 2.4e+03;
RESULT 1293
ID AAM79487 standard; protein; 973 AA.
DE Human protein SEQ ID NO 3133.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.9%; Score 58; DB 4; Length 973;
Best Local Similarity 28.0%; Pred. No. 2.4e+03;
RESULT 1294
ID ADC31585 standard; protein; 1094 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1667.
PN WO2003048323-A2.

PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 12.9%; Score 58; DB 7; Length 1094;
Best Local Similarity 28.0%; Pred. No. 2.7e+03;
RESULT 1295
ID ADC31584 standard; protein; 1114 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1666.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 12.9%; Score 58; DB 7; Length 1114;
Best Local Similarity 28.0%; Pred. No. 2.8e+03;
RESULT 1296
ID ADQ66563 standard; protein; 1139 AA.
DE Novel human protein sequence #1536.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 12.9%; Score 58; DB 8; Length 1139;
Best Local Similarity 28.0%; Pred. No. 2.9e+03;
RESULT 1297
ID ABP74029 standard; protein; 1177 AA.
DE Candida albicans essential protein SEQ ID NO 7866.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 12.9%; Score 58; DB 5; Length 1177;
Best Local Similarity 23.3%; Pred. No. 3e+03;
RESULT 1298
ID AAE29358 standard; protein; 1331 AA.
DE Plasmodium falciparum BBP-5 protein.
PN WO200270542-A2.
PD 12-SEP-2002.
PA (SELI-) ST ELIZABETH'S MEDICAL CENT INC.
Query Match 12.9%; Score 58; DB 5; Length 1331;
Best Local Similarity 23.8%; Pred. No. 3.5e+03;
RESULT 1299
ID AAM84121 standard; protein; 95 AA.
DE Human immune/haematopoietic antigen SEQ ID NO:11714.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.8%; Score 57.5; DB 4; Length 95;
Best Local Similarity 28.0%; Pred. No. 1.4e+02;
RESULT 1300
ID AAU31789 standard; protein; 213 AA.
DE Novel human secreted protein #2280.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.8%; Score 57.5; DB 4; Length 213;
Best Local Similarity 26.3%; Pred. No. 4e+02;
RESULT 1301
ID ADL70801 standard; protein; 213 AA.
DE Anti-TNFalpha antibody VL region, SEQ ID 74.
PN WO2004020588-A2.
PD 11-MAR-2004.
PA (BIOR-) BIOREXIS PHARM CORP.
Query Match 12.8%; Score 57.5; DB 8; Length 213;
Best Local Similarity 28.8%; Pred. No. 4e+02;
RESULT 1302
ID ABM83745 standard; protein; 221 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3994.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 12.8%; Score 57.5; DB 8; Length 221;
Best Local Similarity 30.8%; Pred. No. 4.2e+02;
RESULT 1303
ID ADE34554 standard; protein; 269 AA.
DE Human MHC class II HLA-DR2/Dw12 #SEQ ID 38.
PN WO2003048323-A2.

PD 12-JUN-2003.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (CARM) CARMAN J.
PA (NADL) NADLER S G.
PA (BOWE) BOWEN M.
PA (NEUB) NEUBAUER M.
PA (LUPP) LU P.
Query Match 12.8%; Score 57.5; DB 7; Length 269;
Best Local Similarity 21.0%; Pred. No. 5.3e+02;
RESULT 1304
ID ADX91260 standard; protein; 273 AA.
DE Plant full length insert polypeptide seqid 53924.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ) LIU J.
PA (ZHOU) ZHOU Y.
PA (KOVA) KOVALIC D K.
PA (SCRE) SCREEN S E.
PA (TABA) TABASKA J E.
PA (CAOY) CAO Y.
Query Match 12.8%; Score 57.5; DB 8; Length 273;
Best Local Similarity 26.6%; Pred. No. 5.4e+02;
RESULT 1305
ID ABU15131 standard; protein; 275 AA.
DE Protein encoded by Prokaryotic essential gene #658.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT) ELITRA PHARM INC.
Query Match 12.8%; Score 57.5; DB 6; Length 275;
Best Local Similarity 35.6%; Pred. No. 5.5e+02;
RESULT 1306
ID ABO62158 standard; protein; 281 AA.
DE Klebsiella pneumoniae polypeptide seqid 8675.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO) GENOME THERAPEUTICS CORP.
Query Match 12.8%; Score 57.5; DB 7; Length 281;
Best Local Similarity 22.2%; Pred. No. 5.6e+02;
RESULT 1307
ID ARA26355 standard; protein; 286 AA.
DE Stress tolerant plant-related transcription factor protein SeqID196.
PN WO2005047516-A2.
PD 26-MAY-2005.
PA (MEND) MENDEL BIOTECHNOLOGY INC.
Query Match 12.8%; Score 57.5; DB 9; Length 286;
Best Local Similarity 32.3%; Pred. No. 5.8e+02;
RESULT 1308
ID ABU31908 standard; protein; 308 AA.
DE Protein encoded by Prokaryotic essential gene #17435.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT) ELITRA PHARM INC.
Query Match 12.8%; Score 57.5; DB 6; Length 308;
Best Local Similarity 28.6%; Pred. No. 6.3e+02;
RESULT 1309
ID ADN22689 standard; protein; 546 AA.
DE Bacterial polypeptide #5342.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK) HINKLE G J.
PA (SLAT) SLATER S C.
PA (CHEN) CHEN X.
PA (GOLD) GOLDMAN B S.
Query Match 12.8%; Score 57.5; DB 8; Length 546;
Best Local Similarity 33.8%; Pred. No. 1.3e+03;
RESULT 1310
ID ABB48487 standard; protein; 574 AA.
DE Listeria monocytogenes protein #1191.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 12.8%; Score 57.5; DB 5; Length 574;
Best Local Similarity 26.9%; Pred. No. 2.4e+03;

Best Local Similarity 27.9%; Pred. No. 1.4e+03;
RESULT 1311
ID ADY09430 standard; protein; 715 AA.
DE Plant full length insert polypeptide seqid 65245.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ) LIU J.
PA (ZHOU) ZHOU Y.
PA (KOVA) KOVALIC D K.
PA (SCRE) SCREEN S E.
PA (TABA) TABASKA J E.
PA (CAOY) CAO Y.
Query Match 12.8%; Score 57.5; DB 8; Length 715;
Best Local Similarity 25.3%; Pred. No. 1.8e+03;
RESULT 1312
ID ABB60747 standard; protein; 722 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 9033.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.8%; Score 57.5; DB 4; Length 722;
Best Local Similarity 21.0%; Pred. No. 1.8e+03;
RESULT 1313
ID AAW34501 standard; protein; 804 AA.
DE Obesity receptor protein splice variant.
PN WO9725424-A1.
PD 17-JUL-1997.
PA (AMGE) AMGEN INC.
Query Match 12.8%; Score 57.5; DB 2; Length 804;
Best Local Similarity 26.9%; Pred. No. 2.1e+03;
RESULT 1314
ID ADB12853 standard; protein; 804 AA.
DE Human leptin receptor, OB-RE , splice variant protein.
PN US2003073829-A1.
PD 17-APR-2003.
PA (ADHA) ADHAM N.
PA (BORO) BOROWSKY B.
PA (LEVE) LEVENS N.
PA (SKOD) SKODA R C.
Query Match 12.8%; Score 57.5; DB 7; Length 804;
Best Local Similarity 26.9%; Pred. No. 2.1e+03;
RESULT 1315
ID AAW34502 standard; protein; 839 AA.
DE Obesity receptor protein.
PN WO9725424-A1.
PD 17-JUL-1997.
PA (AMGE) AMGEN INC.
Query Match 12.8%; Score 57.5; DB 2; Length 839;
Best Local Similarity 26.9%; Pred. No. 2.2e+03;
RESULT 1316
ID ADG63038 standard; protein; 867 AA.
DE Human OBR truncated protein.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 8; Length 867;
Best Local Similarity 26.9%; Pred. No. 2.3e+03;
RESULT 1317
ID ADG63030 standard; protein; 868 AA.
DE Human OBR truncated protein, delta 868.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 8; Length 868;
Best Local Similarity 26.9%; Pred. No. 2.3e+03;
RESULT 1318
ID AAW50003 standard; protein; 896 AA.
DE Human OB-R variant Form 3.
PN WO9741263-A1.
PD 06-NOV-1997.
PA (PROG) PROGENITOR INC.
Query Match 12.8%; Score 57.5; DB 2; Length 896;
Best Local Similarity 26.9%; Pred. No. 2.4e+03;

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RESULT 1319
ID AAW24052 standard; protein; 896 AA.
DE Human WSX receptor variant 6.4.
PN WO9725425-A1.
PD 17-JUL-1997.
PA (GETH ) GENENTECH INC.
Query Match 12.8%; Score 57.5; DB 2; Length 896;
Best Local Similarity 26.9%; Pred. No. 2.4e+03;
RESULT 1320
ID AAW14841 standard; protein; 896 AA.
DE Human haemopoietin receptor NR2.
PN WO9712037-A1.
PD 03-APR-1997.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
Query Match 12.8%; Score 57.5; DB 2; Length 896;
Best Local Similarity 26.9%; Pred. No. 2.4e+03;
RESULT 1321
ID ABUS7939 standard; protein; 896 AA.
DE Human WSX receptor splice variant 6.4.
PN US2003004109-A1.
PD 02-JAN-2003.
PA (BENN/) BENNETT B.
PA (MATT/) MATTHEWS W.
Query Match 12.8%; Score 57.5; DB 6; Length 896;
Best Local Similarity 26.9%; Pred. No. 2.4e+03;
RESULT 1322
ID ABO53758 standard; protein; 896 AA.
DE Human WSX receptor variant 6.4.
PN US6541604-B1.
PD 01-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.8%; Score 57.5; DB 6; Length 896;
Best Local Similarity 26.9%; Pred. No. 2.4e+03;
RESULT 1323
ID ADC08904 standard; protein; 896 AA.
DE Human WSX receptor variant 6.4.
PN US2002193571-A1.
PD 19-DEC-2002.
PA (CART/) CARTER P J.
PA (CHIA/) CHIANG N Y.
PA (KIMK/) KIM K J.
PA (MATT/) MATTHEWS W.
PA (RODR/) RODRIGUES M L.
Query Match 12.8%; Score 57.5; DB 7; Length 896;
Best Local Similarity 26.9%; Pred. No. 2.4e+03;
RESULT 1324
ID ADD95274 standard; protein; 896 AA.
DE Human leptin receptor OBRI.
PN WO2003072787-A2.
PD 04-SEP-2003.
PA (AVET ) AVENTIS PHARMA SA.
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA (CNRS ) CENT NAT RECH SCI.
Query Match 12.8%; Score 57.5; DB 7; Length 896;
Best Local Similarity 26.9%; Pred. No. 2.4e+03;
RESULT 1325
ID ADN04458 standard; protein; 896 AA.
DE Antipsoriatic protein sequence #422.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 12.8%; Score 57.5; DB 8; Length 896;
Best Local Similarity 26.9%; Pred. No. 2.4e+03;
RESULT 1326
ID ADR27661 standard; protein; 896 AA.
DE Human leptin receptor related protein OB-RGRP related sequence SEQ ID 10.
PN FR2850971-A1.
PD 13-AUG-2004.
PA (AVET ) AVENTIS PHARMA SA.
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 12.8%; Score 57.5; DB 8; Length 896;
Best Local Similarity 26.9%; Pred. No. 2.4e+03;
RESULT 1327
ID ADW88112 standard; protein; 896 AA.
DE Human WSX receptor variant 6.4 protein.
PN US2005019325-A1.
PD 27-JAN-2005.
PA (CART/) CARTER P J.
PA (CHIA/) CHIANG N Y.
PA (KIMK/) KIM K J.
PA (MATT/) MATTHEWS W.
PA (RODR/) RODRIGUES M L.
Query Match 12.8%; Score 57.5; DB 9; Length 896;
Best Local Similarity 26.9%; Pred. No. 2.4e+03;
RESULT 1328
ID AAR88912 standard; protein; 898 AA.
DE Haematopoietin receptor Hu-B1.219 Form 3 protein.
PN WO9608510-A1.
PD 21-MAR-1996.
PA (PROG-) PROGENITOR INC.
Query Match 12.8%; Score 57.5; DB 2; Length 898;
Best Local Similarity 26.9%; Pred. No. 2.4e+03;
RESULT 1329
ID AAW50002 standard; protein; 904 AA.
DE Human OB-R variant Form 2.
PN WO9741263-A1.
PD 06-NOV-1997.
PA (PROG-) PROGENITOR INC.
Query Match 12.8%; Score 57.5; DB 2; Length 904;
Best Local Similarity 26.9%; Pred. No. 2.5e+03;
RESULT 1330
ID AAR88911 standard; protein; 908 AA.
DE Haematopoietin receptor Hu-B1.219 Form 2 protein.
PN WO9608510-A1.
PD 21-MAR-1996.
PA (PROG-) PROGENITOR INC.
Query Match 12.8%; Score 57.5; DB 2; Length 908;
Best Local Similarity 26.9%; Pred. No. 2.5e+03;
RESULT 1331
ID AAW19536 standard; protein; 908 AA.
DE Variant form of human leptin receptor OB-R.
PN WO9726523-A2.
PD 24-JUL-1997.
PA (PROG-) PROGENITOR INC.
Query Match 12.8%; Score 57.5; DB 2; Length 908;
Best Local Similarity 26.9%; Pred. No. 2.5e+03;
RESULT 1332
ID AAW24053 standard; protein; 923 AA.
DE Human WSX receptor variant 12.1.
PN WO9725425-A1.
PD 17-JUL-1997.
PA (GETH ) GENENTECH INC.
Query Match 12.8%; Score 57.5; DB 2; Length 923;
Best Local Similarity 26.9%; Pred. No. 2.5e+03;
RESULT 1333
ID ABUS7940 standard; protein; 923 AA.
DE Human WSX receptor splice variant 12.1.
PN US2003004109-A1.
PD 02-JAN-2003.
PA (BENN/) BENNETT B.
PA (MATT/) MATTHEWS W.
Query Match 12.8%; Score 57.5; DB 6; Length 923;
Best Local Similarity 26.9%; Pred. No. 2.5e+03;
RESULT 1334
ID ABO53759 standard; protein; 923 AA.
DE Human WSX receptor variant 12.1.
PN US6541604-B1.
PD 01-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.8%; Score 57.5; DB 6; Length 923;
Best Local Similarity 26.9%; Pred. No. 2.5e+03;
RESULT 1335
ID ADC08905 standard; protein; 923 AA.
DE Human WSX receptor variant 12.1.
PN US2002193571-A1.
PD 19-DEC-2002.

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PA (CART/) CARTER P J. 12.8%; Score 57.5; DB 7; Length 923;
PA (CHIA/) CHIANG N Y. 26.9%; Pred. No. 2.5e+03;
PA (KIMK/) KIM K J.
PA (MATT/) MATTHEWS W. L.
PA (RODR/) RODRIGUES M L.
Query Match 12.8%; Score 57.5; DB 7; Length 923;
Best Local Similarity 26.9%; Pred. No. 2.5e+03;
RESULT 1336
ID ADW8813 standard; protein; 923 AA.
DE Human WSX receptor variant 12.1 protein.
PN US2005019325-A1.
PD 27-JAN-2005.
PA (CART/) CARTER P J.
PA (CHIA/) CHIANG N Y.
PA (KIMK/) KIM K J.
PA (MATT/) MATTHEWS W. L.
PA (RODR/) RODRIGUES M L.
Query Match 12.8%; Score 57.5; DB 9; Length 923;
Best Local Similarity 26.9%; Pred. No. 2.5e+03;
RESULT 1337
ID ADO23831 standard; protein; 925 AA.
DE Leptin receptor extracellular domain-GPI fusion protein.
PN WO2003034275-A2.
PD 24-APR-2003.
PA (ASTE-) ASTERION LTD.
Query Match 12.8%; Score 57.5; DB 7; Length 925;
Best Local Similarity 26.9%; Pred. No. 2.5e+03;
RESULT 1338
ID AAW38214 standard; protein; 958 AA.
DE Human OB-R variant Form 1.
PN WO9741263-A1.
PD 06-NOV-1997.
PA (PROG-) PROGENITOR INC.
Query Match 12.8%; Score 57.5; DB 2; Length 958;
Best Local Similarity 26.9%; Pred. No. 2.6e+03;
RESULT 1339
ID AAW31911 standard; protein; 958 AA.
DE Human OB-R leptin receptor variant.
PN WO9726370-A1.
PD 24-JUL-1997.
PA (PROG-) PROGENITOR INC.
Query Match 12.8%; Score 57.5; DB 2; Length 958;
Best Local Similarity 26.9%; Pred. No. 2.6e+03;
RESULT 1340
ID AAW19535 standard; protein; 958 AA.
DE Human OB-R leptin receptor variant.
PN WO9726272-A1.
PD 24-JUL-1997.
PA (PROG-) PROGENITOR INC.
Query Match 12.8%; Score 57.5; DB 2; Length 958;
Best Local Similarity 26.9%; Pred. No. 2.6e+03;
RESULT 1341
ID AAW22773 standard; protein; 958 AA.
DE Human haematopoietin receptor variant Hu-B1.219 form 1.
PN WO9727286-A1.
PD 31-JUL-1997.
PA (PROG-) PROGENITOR INC.
Query Match 12.8%; Score 57.5; DB 2; Length 958;
Best Local Similarity 26.9%; Pred. No. 2.6e+03;
RESULT 1342
ID AAR88910 standard; protein; 960 AA.
DE Haematopoietin receptor Hu-B1.219 Form 1 protein.
PN WO9608510-A1.
PD 21-MAR-1996.
PA (PROG-) PROGENITOR INC.
Query Match 12.8%; Score 57.5; DB 2; Length 960;
Best Local Similarity 26.9%; Pred. No. 2.6e+03;
RESULT 1343
ID ADG63037 standard; protein; 964 AA.
DE Human OB-R truncated protein.
PN US2002182676-A1.
PD 03-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 8; Length 1155;
Best Local Similarity 26.9%; Pred. No. 3.3e+03;
RESULT 1344
ID ADG63031 standard; protein; 965 AA.
DE Human OB-R truncated protein, delta 965.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 8; Length 964;
Best Local Similarity 26.9%; Pred. No. 2.7e+03;
RESULT 1345
ID AAW34499 standard; protein; 970 AA.
DE Obesity receptor C protein.
PN WO9725424-A1.
PD 17-JUL-1997.
PA (AMGB-) AMGEN INC.
Query Match 12.8%; Score 57.5; DB 2; Length 970;
Best Local Similarity 26.9%; Pred. No. 2.7e+03;
RESULT 1346
ID AAW34497 standard; protein; 972 AA.
DE Obesity receptor A protein.
PN WO9725424-A1.
PD 17-JUL-1997.
PA (AMGB-) AMGEN INC.
Query Match 12.8%; Score 57.5; DB 2; Length 972;
Best Local Similarity 26.9%; Pred. No. 2.7e+03;
RESULT 1347
ID AAW34498 standard; protein; 999 AA.
DE Obesity receptor B protein.
PN WO9725424-A1.
PD 17-JUL-1997.
PA (AMGB-) AMGEN INC.
Query Match 12.8%; Score 57.5; DB 2; Length 999;
Best Local Similarity 26.9%; Pred. No. 2.8e+03;
RESULT 1348
ID ADG63032 standard; protein; 1065 AA.
DE Human OB-R truncated protein, delta 1065.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 8; Length 1065;
Best Local Similarity 26.9%; Pred. No. 3e+03;
RESULT 1349
ID ADG63039 standard; protein; 1067 AA.
DE Human OB-R truncated protein.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 8; Length 1067;
Best Local Similarity 26.9%; Pred. No. 3e+03;
RESULT 1350
ID ADG63033 standard; protein; 1115 AA.
DE Human OB-R truncated protein, delta 1115.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 8; Length 1115;
Best Local Similarity 26.9%; Pred. No. 3.2e+03;
RESULT 1351
ID AEA19287 standard; protein; 1152 AA.
DE Mouse B220.
PN WO2005049865-A2.
PD 02-JUN-2005.
PA (REPR-) REPROCELL INC.
Query Match 12.8%; Score 57.5; DB 9; Length 1152;
Best Local Similarity 21.7%; Pred. No. 3.3e+03;
RESULT 1352
ID ADG63040 standard; protein; 1155 AA.
DE Human OB-R truncated protein.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 8; Length 1155;

Best Local Similarity 26.9%; Pred. No. 3.3e+03;
RESULT 1353
ID ABO84453 standard; protein; 1157 AA.
DE Mouse cancer-associated protein MPI3-011.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 12.8%; Score 57.5; DB 8; Length 1157;
Best Local Similarity 21.7%; Pred. No. 3.3e+03;
RESULT 1354
ID ADG63041 standard; protein; 1161 AA.
DE Human OBR truncated protein.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 8; Length 1161;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1355
ID AAW24051 standard; protein; 1165 AA.
DE Human WSX receptor variant 13.2.
PN WO9725425-A1.
PD 17-JUL-1997.
PA (GETH) GENENTECH INC.
Query Match 12.8%; Score 57.5; DB 2; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1356
ID AAW19116 standard; protein; 1165 AA.
DE Human Ob receptor.
PN WO9719952-A1.
PD 05-JUN-1997.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 2; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1357
ID AAY13474 standard; protein; 1165 AA.
DE Peptide Seq ID No: 4 of WO9923493.
PN WO9923493-A1.
PD 14-MAY-1999.
PA (YTRQ) UNIV ROCKEFELLER.
Query Match 12.8%; Score 57.5; DB 2; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1358
ID AAE12551 standard; protein; 1165 AA.
DE Human Ob receptor (OBR) protein mutant (Y1141F).
PN US6287782-B1.
PD 11-SEP-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 4; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1359
ID AAE12609 standard; protein; 1165 AA.
DE Human Ob receptor (OBR) protein.
PN US6287782-B1.
PD 11-SEP-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 4; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1360
ID AAE25455 standard; protein; 1165 AA.
DE Human Ob receptor (OBR) protein.
PN US6395498-B1.
PD 28-MAY-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 5; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1361
ID AAE25774 standard; protein; 1165 AA.
DE Human obesity receptor (OBR) mutant protein, Y1079F.
PN US6403552-B1.
PD 11-JUN-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 5; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1362
ID AAE25765 standard; protein; 1165 AA.
DE Human obesity receptor (OBR) protein.
PN US6403552-B1.
PD 11-JUN-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 5; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1363
ID AAE25772 standard; protein; 1165 AA.
DE Human obesity receptor (OBR) mutant protein, Y1141F.
PN US6403552-B1.
PD 11-JUN-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 5; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1364
ID AAE25773 standard; protein; 1165 AA.
DE Human obesity receptor (OBR) mutant protein, Y986F.
PN US6403552-B1.
PD 11-JUN-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 5; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1365
ID AAE23859 standard; protein; 1165 AA.
DE Human Ob receptor (OBR) protein.
PN US6380363-B1.
PD 30-APR-2002.
PA (TART) TARTAGLIA L A.
PA (TEPP) TEPPER R I.
PA (CULP) CULPEPPER J A.
PA (WHIT) WHITE D W.
Query Match 12.8%; Score 57.5; DB 5; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1366
ID ABU87938 standard; protein; 1165 AA.
DE Human DNA full length WSX receptor.
PN US2003004109-A1.
PD 02-JAN-2003.
PA (BENN) BENNETT B.
PA (MATT) MATTHEWS W.
Query Match 12.8%; Score 57.5; DB 6; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1367
ID ABP72720 standard; protein; 1165 AA.
DE Human leptin receptor long form.
PN WO2003017825-A2.
PD 06-MAR-2003.
PA (JOSL-) JOSLIN DIABETES CENT INC.
Query Match 12.8%; Score 57.5; DB 6; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1368
ID ABO53757 standard; protein; 1165 AA.
DE Human full length WSX receptor variant 13.2.
PN US6541604-B1.
PD 01-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 12.8%; Score 57.5; DB 6; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1369
ID ADC08903 standard; protein; 1165 AA.
DE Human WSX receptor variant 13.2.
PN US2002193571-A1.
PD 19-DEC-2002.
PA (CART) CARTER P J.
PA (CHIA) CHIANG N Y.
PA (KIMK) KIM K J.
PA (MATT) MATTHEWS W.
PA (RODR) RODRIGUES M L.
Query Match 12.8%; Score 57.5; DB 7; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1370

ID ADE62888 standard; protein; 1165 AA.
DE Human Protein P48357, SEQ ID NO 8822.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 12.8%; Score 57.5; DB 7; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1371
ID ADD46275 standard; protein; 1165 AA.
DE Human Protein P48357, SEQ ID NO 11950.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 12.8%; Score 57.5; DB 7; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1372
ID ADG63035 standard; protein; 1165 AA.
DE Human OBR mutant protein, Y986F.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 8; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1373
ID ADG62979 standard; protein; 1165 AA.
DE Human OBR protein from clone famj5312.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 8; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1374
ID ADG63036 standard; protein; 1165 AA.
DE Human OBR mutant protein, Y1141F.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 8; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1375
ID ADG63034 standard; protein; 1165 AA.
DE Human OBR mutant protein, Y1079F.
PN US2002182676-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 57.5; DB 8; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1376
ID ADW88111 standard; protein; 1165 AA.
DE Human WSX receptor variant 13.2 protein.
PN US2005019325-A1.
PD 27-JAN-2005.
PA (CART/) CARTER P J.
PA (CHIA/) CHIANG N Y.
PA (KIMK/) KIM K J.
PA (MATT/) MATTHEWS W.
PA (RODR/) RODRIGUES M L.
Query Match 12.8%; Score 57.5; DB 9; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1377
ID AEB32310 standard; protein; 1165 AA.
DE Human protein #12.
PN US2005147987-A1.
PD 07-JUL-2005.
PA (APPL-) APPLERA CORP NY.
Query Match 12.8%; Score 57.5; DB 9; Length 1165;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1378
ID AEB32324 standard; protein; 1167 AA.
DE Human protein #26.
PN US2005147987-A1.

PD 07-JUL-2005.
PA (APPL-) APPLERA CORP NY.
Query Match 12.8%; Score 57.5; DB 9; Length 1167;
Best Local Similarity 26.9%; Pred. No. 3.4e+03;
RESULT 1379
ID AAW34500 standard; protein; 1220 AA.
DE Obesity receptor D protein.
PN W09725424-A1.
PD 17-JUL-1997.
PA (AMGE-) AMGEN INC.
Query Match 12.8%; Score 57.5; DB 2; Length 1220;
Best Local Similarity 26.9%; Pred. No. 3.6e+03;
RESULT 1380
ID AAW62544 standard; protein; 1221 AA.
DE Human ob-receptor replacement mutant.
PN W09824881-A1.
PD 11-JUN-1998.
PA (MERI) MERCK & CO INC.
Query Match 12.8%; Score 57.5; DB 2; Length 1221;
Best Local Similarity 26.9%; Pred. No. 3.6e+03;
RESULT 1381
ID ADL16234 standard; protein; 1291 AA.
DE Mouse protein tyrosine phosphatase #7.
PN W02003068984-A2.
PD 21-AUG-2003.
PA (COLD-) COLD SPRING HARBOR LAB.
PA (CEPT-) CEPTUR INC.
Query Match 12.8%; Score 57.5; DB 7; Length 1291;
Best Local Similarity 21.7%; Pred. No. 3.8e+03;
RESULT 1382
ID ADM67208 standard; protein; 1343 AA.
DE Murine adipocyte specific leukocyte common antigen protein SeqID 562.
PN W02004011618-A2.
PD 05-FEB-2004.
PA (HMGE-) HMGNE INC.
Query Match 12.8%; Score 57.5; DB 8; Length 1343;
Best Local Similarity 21.7%; Pred. No. 4e+03;
RESULT 1383
ID AAW52217 standard; protein; 105 AA.
DE Antibody LDI-84-VL chain sequence.
PN W09749809-A1.
PD 31-DEC-1997.
PA (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
Query Match 12.7%; Score 57; DB 2; Length 105;
Best Local Similarity 35.6%; Pred. No. 1.9e+02;
RESULT 1384
ID ADY66220 standard; protein; 135 AA.
DE S. mansoni protein SEQ ID 1638.
PN W02005023979-A2.
PD 17-MAR-2005.
PA (AMPA-) FUNDACAO AMPARO A PESQUISA DO ESTADO.
Query Match 12.7%; Score 57; DB 9; Length 135;
Best Local Similarity 33.3%; Pred. No. 2.6e+02;
RESULT 1385
ID AAB13367 standard; protein; 136 AA.
DE Eucalyptus grandis diphenol oxidase protein sequence SEQ ID NO:293.
PN W0200022099-A1.
PD 20-APR-2000.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 12.7%; Score 57; DB 3; Length 136;
Best Local Similarity 31.7%; Pred. No. 2.6e+02;
RESULT 1386
ID ADD41543 standard; protein; 136 AA.
DE Diphenol oxidase #4.
PN US200311373-A1.
PD 10-JUL-2003.
PA (BLOK/) BLOKSBERG L N.
PA (HAVU/) HAVUKKALA I.
Query Match 12.7%; Score 57; DB 7; Length 136;
Best Local Similarity 31.7%; Pred. No. 2.6e+02;
RESULT 1387
ID AAY34312 standard; protein; 147 AA.

DE Igm antibody CEM 10.12 G5 kappa chain sequence.
PN W09945031-A2.
PD 10-SEP-1999.
PA (ABGE-) ABGENIX INC. 12.7%; Score 57; DB 2; Length 147;
Query Match 28.4%; Pred. No. 2.9e+02;
Best Local Similarity 28.4%; Pred. No. 2.9e+02;
RESULT 1388
ID ADP44641 standard; protein; 213 AA.
DE Human anti-CD20 light chain protein.
PN W02004050041-A2.
PD 17-JUN-2004.
PA (MOLB-) APPLIED MOLECULAR EVOLUTION INC.
Query Match 12.7%; Score 57; DB 8; Length 213;
Best Local Similarity 28.4%; Pred. No. 4.5e+02;
RESULT 1389
ID ADU80277 standard; protein; 213 AA.
DE CD20 binding AME 33 complete light chain variable protein.
PN W02004103404-A1.
PD 02-DEC-2004.
PA (MOLB-) APPLIED MOLECULAR EVOLUTION.
Query Match 12.7%; Score 57; DB 8; Length 213;
Best Local Similarity 28.4%; Pred. No. 4.5e+02;
RESULT 1390
ID AEA60641 standard; protein; 213 AA.
DE Human butyrylcholinesterase variant protein SEQ ID NO:198.
PN US22005136044-A1.
PD 23-JUN-2005.
PA (WATK/) WATKINS J D.
PA (PANC/) PANCOOK J D.
Query Match 12.7%; Score 57; DB 9; Length 213;
Best Local Similarity 28.4%; Pred. No. 4.5e+02;
RESULT 1391
ID ABO73390 standard; protein; 218 AA.
DE Pseudomonas aeruginosa polypeptide #5565.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.7%; Score 57; DB 7; Length 218;
Best Local Similarity 24.5%; Pred. No. 4.7e+02;
RESULT 1392
ID AAR59416 standard; protein; 219 AA.
DE 6D9 antibody light chain.
PN JP06220072-A.
PD 09-AUG-1994.
PA (TANP-) TANPAKU KOGAKU KENKYUSHO KK.
Query Match 12.7%; Score 57; DB 2; Length 219;
Best Local Similarity 28.4%; Pred. No. 4.7e+02;
RESULT 1393
ID AEB08093 standard; protein; 220 AA.
DE Murine Ig kappa light chain constant domain, SEQ ID NO: 55.
PN W02005058251-A2.
PD 30-JUN-2005.
PA (DEND-) DENDREON CORP.
Query Match 12.7%; Score 57; DB 9; Length 220;
Best Local Similarity 28.4%; Pred. No. 4.7e+02;
RESULT 1394
ID ADZ57707 standard; protein; 236 AA.
DE Anti-cMet antibody 8.90.3 light chain protein.
PN GE2404660-A.
PD 09-FEB-2005.
PA (PFIZ) PFIZER PROD INC.
PA (ABGE-) ABGENIX INC.
Query Match 12.7%; Score 57; DB 9; Length 236;
Best Local Similarity 26.9%; Pred. No. 5.2e+02;
RESULT 1395
ID ADX95267 standard; protein; 321 AA.
DE Plant full length insert polypeptide seqid 57931.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.

PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 12.7%; Score 57; DB 8; Length 321;
Best Local Similarity 29.7%; Pred. No. 7.6e+02;
RESULT 1396
ID ADT57341 standard; protein; 370 AA.
DE Plant polypeptide, SEQ ID 7418.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 12.7%; Score 57; DB 8; Length 370;
Best Local Similarity 29.7%; Pred. No. 9.1e+02;
RESULT 1397
ID ADG83832 standard; protein; 454 AA.
DE Red belly black snake venom protease.
PN W02003082914-A1.
PD 09-OCT-2003.
PA (UYQU) UNIV QUEENSLAND.
Query Match 12.7%; Score 57; DB 8; Length 454;
Best Local Similarity 32.8%; Pred. No. 1.2e+03;
RESULT 1398
ID AAG64459 standard; protein; 573 AA.
DE Mouse 6D9 catalytic antibody.
PN JP2001128681-A.
PD 15-MAY-2001.
PA (NISB) JAPAN TOBACCO INC.
PA (SEIB-) SEIBUTSU BUNSHI KOGAKU KENKYUSHO KK.
PA (TANP-) TANPAKU KOGAKU KENKYUSHO KK.
Query Match 12.7%; Score 57; DB 4; Length 573;
Best Local Similarity 28.4%; Pred. No. 1.6e+03;
RESULT 1399
ID ABO77277 standard; protein; 576 AA.
DE Pseudomonas aeruginosa polypeptide #9452.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.7%; Score 57; DB 7; Length 576;
Best Local Similarity 38.2%; Pred. No. 1.6e+03;
RESULT 1400
ID ADC08221 standard; protein; 676 AA.
DE Rice protein sequence Seq ID526 related to grain filling.
PN W02003000905-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 12.7%; Score 57; DB 7; Length 676;
Best Local Similarity 45.5%; Pred. No. 1.9e+03;
RESULT 1401
ID ADC07938 standard; protein; 729 AA.
DE Rice protein sequence Seq ID204 related to grain filling.
PN W02003000905-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 12.7%; Score 57; DB 7; Length 729;
Best Local Similarity 45.5%; Pred. No. 2.1e+03;
RESULT 1402
ID AAO15273 standard; protein; 757 AA.
DE Human nervous serine protease inhibitor (PI12) 83-27.
PN CN1333249-A.
PD 30-JAN-2002.
PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
Query Match 12.7%; Score 57; DB 5; Length 757;
Best Local Similarity 28.0%; Pred. No. 2.2e+03;
RESULT 1403
ID ABB64716 standard; protein; 971 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 20940.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.7%; Score 57; DB 4; Length 971;
Best Local Similarity 35.2%; Pred. No. 3.1e+03;
RESULT 1404
ID ADR18920 standard; protein; 1225 AA.
DE Human tracheobronchial mucin protein, MUCSA.

PN WO2004069136-A2.
PD 19-AUG-2004.
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
Query Match 12.7%; Score 57; DB 8; Length 1225;
Best Local Similarity 27.7%; Pred. No. 4.1e+03;
RESULT 1405
ID AD93316 standard; protein; 1302 AA.
DE Zebrafish Flt1 protein required for angiogenesis.
PN WO2003079776-A2.
PD 02-OCT-2003.
PA (ARTE-) ARTEMIS PHARM GMBH.
Query Match 12.7%; Score 57; DB 7; Length 1302;
Best Local Similarity 30.0%; Pred. No. 4.4e+03;
RESULT 1406
ID ABR53378 standard; protein; 1411 AA.
DE Protein sequence #SEQ ID 1621.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 12.7%; Score 57; DB 6; Length 1411;
Best Local Similarity 36.4%; Pred. No. 4.9e+03;
RESULT 1407
ID ADK63342 standard; protein; 1411 AA.
DE Disease treating protein complex-derived protein #982.
PN EP138608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 12.7%; Score 57; DB 7; Length 1411;
Best Local Similarity 36.4%; Pred. No. 4.9e+03;
RESULT 1408
ID ADR18918 standard; protein; 2202 AA.
DE Mature Human mucin-like protein, SCS0005, SEQ ID 8.
PN WO2004069136-A2.
PD 19-AUG-2004.
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
Query Match 12.7%; Score 57; DB 8; Length 2202;
Best Local Similarity 27.7%; Pred. No. 8.6e+03;
RESULT 1409
ID ADR18917 standard; protein; 2227 AA.
DE Human mucin-like protein, SCS0005, SEQ ID 7.
PN WO2004069136-A2.
PD 19-AUG-2004.
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
Query Match 12.7%; Score 57; DB 8; Length 2227;
Best Local Similarity 27.7%; Pred. No. 8.7e+03;
RESULT 1410
ID ADR18919 standard; protein; 2233 AA.
DE H18-tagged Human mucin-like protein, SCS0005, SEQ ID 9.
PN WO2004069136-A2.
PD 19-AUG-2004.
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
Query Match 12.7%; Score 57; DB 8; Length 2233;
Best Local Similarity 27.7%; Pred. No. 8.7e+03;
RESULT 1411
ID ADV24899 standard; protein; 3869 AA.
DE Anabaena microcystin polyketide synthase mcyD protein.
PN WO2004104211-A2.
PD 02-DEC-2004.
PA (HEL-) HELSING YLIOPISTO.
PA (UYLI-) UNIV LIEGE.
Query Match 12.7%; Score 57; DB 9; Length 3869;
Best Local Similarity 35.4%; Pred. No. 1.7e+04;
RESULT 1412
ID ADP79571 standard; protein; 107 AA.
DE Humanised 2H7.v16 variant light chain variable domain SEQ ID NO:2.
PN WO2004056312-A2.
PD 08-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 8; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
RESULT 1413
ID ADS33301 standard; protein; 107 AA.

DE Anti-CD20 humanised antibody hu2H7.v16, light chain variable domain.
PN US2004202658-A1.
PD 14-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 8; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
RESULT 1414
ID ADW03407 standard; protein; 107 AA.
DE Humanized anti-CD20 antibody light chain variable region - SEQ ID 13.
PN WO2005000351-A2.
PD 06-JAN-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 9; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
RESULT 1415
ID ADW21304 standard; protein; 107 AA.
DE Mouse anti-CD20 antibody 2H7 VL, humanized clone v16.
PN WO2005005462-A2.
PD 20-JAN-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 9; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
RESULT 1416
ID ADX00802 standard; protein; 107 AA.
DE Humanized 2H7 v16 antibody light chain variable region, SEQ ID 1.
PN US2005032130-A1.
PD 10-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 9; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
RESULT 1417
ID ADY62622 standard; protein; 107 AA.
DE Humanized 2H7 antibody variable light chain.
PN US2005053602-A1.
PD 10-MAR-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 9; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
RESULT 1418
ID AEB27725 standard; protein; 107 AA.
DE Humanized 2H7 antibody light chain variable region sequence.
PN WO2005060999-A2.
PD 07-JUL-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 9; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
RESULT 1419
ID AEB17635 standard; peptide; 107 AA.
DE Variable light peptide sequence of humanized 2H7 antibody.
PN WO2005061542-A2.
PD 07-JUL-2005.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 9; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
RESULT 1420
ID ADA89110 standard; protein; 109 AA.
DE MS-Pro-28-VL amino acid sequence SEQ ID NO:98.
PN WO2002102973-A2.
PD 27-DEC-2002.
PA (PROC-) PROCHON BIOTECH LTD.
Query Match 12.8%; Score 56.5; DB 6; Length 109;
Best Local Similarity 36.1%; Pred. No. 2.2e+02;
RESULT 1421
ID ADG74361 standard; protein; 109 AA.
DE MSPRO light chain variable region protein, SEQ ID No 98.
PN WO2002102972-A2.
PD 27-DEC-2002.
PA (PROC-) PROCHON BIOTECH LTD.
PA (MORP-) MORPHOSYS AG.
Query Match 12.6%; Score 56.5; DB 7; Length 109;
Best Local Similarity 36.1%; Pred. No. 2.2e+02;
RESULT 1422
ID ADI26478 standard; protein; 114 AA.

DE H. pylori HPu-18-L SEQ ID NO:14.
PN W02004009805-A1.
PD 29-JAN-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 12.6%; Score 56.5; DB 8; Length 114;
Best Local Similarity 38.9%; Pred. No. 2.4e+02;
RESULT 1423
ID ABO59078 standard; protein; 169 AA.
DE Human genome derived single exon protein #4312.
PN U2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 12.6%; Score 56.5; DB 8; Length 169;
Best Local Similarity 24.2%; Pred. No. 3.9e+02;
RESULT 1424
ID ADP55680 standard; protein; 175 AA.
DE Human PRO protein sequence SEQ ID NO:1656.
PN W02004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 12.6%; Score 56.5; DB 8; Length 175;
Best Local Similarity 29.3%; Pred. No. 4.1e+02;
RESULT 1425
ID ADY22634 standard; protein; 186 AA.
DE Plant full length insert polypeptide seqid 70418.
PN U2004034888-A1.
PD 19-FEB-2004.
PA (LIU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 12.6%; Score 56.5; DB 8; Length 186;
Best Local Similarity 29.1%; Pred. No. 4.4e+02;
RESULT 1426
ID ARM84939 standard; protein; 221 AA.
DE Human diagnostic and therapeutic Pprotein SEQ ID NO:5188.
PN W02004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 12.6%; Score 56.5; DB 8; Length 221;
Best Local Similarity 32.7%; Pred. No. 5.4e+02;
RESULT 1427
ID ABO69554 standard; protein; 235 AA.
DE Pseudomonas aeruginosa polypeptide #1729.
PN U86551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.6%; Score 56.5; DB 7; Length 235;
Best Local Similarity 28.2%; Pred. No. 5.9e+02;
RESULT 1428
ID ADN25938 standard; protein; 273 AA.
DE Bacterial polypeptide #8591.
PN U2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 12.6%; Score 56.5; DB 8; Length 273;
Best Local Similarity 27.7%; Pred. No. 7.1e+02;
RESULT 1429
ID ADC19732 standard; protein; 324 AA.
DE H. influenzae Orf15 polypeptide SEQ ID NO:29.
PN W02003055905-A2.
PD 10-JUL-2003.
PA (GLAX) GLAXOSMITHKLINE BIOLOGICALS SA.
Query Match 12.6%; Score 56.5; DB 7; Length 324;
Best Local Similarity 34.3%; Pred. No. 8.8e+02;
RESULT 1430
ID ADT55522 standard; protein; 335 AA.
DE Plant polypeptide, SEQ ID 5599.
PN U2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 12.6%; Score 56.5; DB 8; Length 335;
Best Local Similarity 36.0%; Pred. No. 9.2e+02;
RESULT 1431
ID ABB58822 standard; protein; 351 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 3258.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.6%; Score 56.5; DB 4; Length 351;
Best Local Similarity 25.3%; Pred. No. 9.7e+02;
RESULT 1432
ID ADA55440 standard; protein; 412 AA.
DE Human protein, SEQ ID 3008.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 12.6%; Score 56.5; DB 6; Length 412;
Best Local Similarity 22.0%; Pred. No. 1.2e+03;
RESULT 1433
ID ABB11538 standard; peptide; 416 AA.
DE Human TRAP150 homologue, SEQ ID NO:1908.
PN W0200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.6%; Score 56.5; DB 4; Length 416;
Best Local Similarity 23.3%; Pred. No. 1.2e+03;
RESULT 1434
ID AAW59836 standard; protein; 438 AA.
DE Maize Id protein.
PN W09837201-A1.
PD 27-AUG-1998.
PA (COLD-) COLD SPRING HARBOR LAB.
Query Match 12.6%; Score 56.5; DB 2; Length 438;
Best Local Similarity 39.6%; Pred. No. 1.3e+03;
RESULT 1435
ID ADY72479 standard; protein; 475 AA.
DE HIV-2/VCP clone 8c.3 gp120 protein SEQ ID NO:29.
PN U2005064392-A1.
PD 24-MAR-2005.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 12.6%; Score 56.5; DB 9; Length 475;
Best Local Similarity 30.6%; Pred. No. 1.4e+03;
RESULT 1436
ID ADY72487 standard; protein; 482 AA.
DE HIV-2/VCP gp120 protein with a V3(6,6) deletion.
PN U2005064392-A1.
PD 24-MAR-2005.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 12.6%; Score 56.5; DB 9; Length 482;
Best Local Similarity 30.6%; Pred. No. 1.5e+03;
RESULT 1437
ID ADY72491 standard; protein; 484 AA.
DE HIV-2/VCP gp120 protein p16.9 clone.
PN U2005064392-A1.
PD 24-MAR-2005.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 12.6%; Score 56.5; DB 9; Length 484;
Best Local Similarity 30.6%; Pred. No. 1.5e+03;
RESULT 1438
ID ADY72473 standard; protein; 485 AA.
DE HIV-2/VCP clone p16.9 gp120 protein SEQ ID NO:23.
PN U2005064392-A1.
PD 24-MAR-2005.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 12.6%; Score 56.5; DB 9; Length 485;
Best Local Similarity 30.6%; Pred. No. 1.5e+03;

RESULT 1439
ID ADW69549 standard; protein; 500 AA.
DE HIV-1 gp120 protein, U-228cl.
PN WO2004110384-A2.
PD 23-DEC-2004.
PA (VAXG-) VAXGEN INC. 12.6%; Score 56.5; DB 9; Length 500;
Query Match Best Local Similarity 23.2%; Pred. No. 1.5e+03;
RESULT 1440
ID ADY72455 standard; protein; 501 AA.
DE HIV-2/VCP gp120 protein SEQ ID NO:5.
PN US2005064392-A1.
PD 24-MAR-2005.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match Best Local Similarity 30.6%; Score 56.5; DB 9; Length 501;
RESULT 1441
ID ADY72481 standard; protein; 503 AA.
DE HIV-2/VCP gp120 protein.
PN US2005064392-A1.
PD 24-MAR-2005.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match Best Local Similarity 30.6%; Score 56.5; DB 9; Length 503;
RESULT 1442
ID ADX94611 standard; protein; 553 AA.
DE Plant full length insert polypeptide seqid 57275.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABR/) TABASKA J B.
PA (CAOV/) CAO Y.
Query Match Best Local Similarity 28.6%; Score 56.5; DB 8; Length 553;
RESULT 1443
ID AAB31664 standard; protein; 610 AA.
DE Amino acid sequence of a codon optimised TGEV S-gene.
PN CA2272793-A1.
PD 11-DEC-2000.
PA (YUGU-) UNIV GUELPH.
Query Match Best Local Similarity 29.0%; Score 56.5; DB 4; Length 610;
RESULT 1444
ID ADB65251 standard; protein; 629 AA.
DE Human protein encoded by clone TESTI20049410.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match Best Local Similarity 22.0%; Score 56.5; DB 7; Length 629;
RESULT 1445
ID ADS21458 standard; protein; 708 AA.
DE Bacterial polypeptide #10491.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOV/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match Best Local Similarity 22.7%; Score 56.5; DB 8; Length 708;
RESULT 1446
ID ADY72478 standard; protein; 713 AA.
DE HIV-2/VCP clone 8c.3 env protein SEQ ID NO:28.
PN US2005064392-A1.
PD 24-MAR-2005.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match Best Local Similarity 12.6%; Score 56.5; DB 9; Length 713;
Best Local Similarity 30.6%; Pred. No. 2.4e+03;
RESULT 1447
ID ADY72472 standard; protein; 723 AA.
DE HIV-2/VCP clone p16.9 env protein SEQ ID NO:22.
PN US2005064392-A1.
PD 24-MAR-2005.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match Best Local Similarity 30.6%; Score 56.5; DB 9; Length 723;
RESULT 1448
ID ADY72454 standard; protein; 739 AA.
DE HIV-2/VCP env protein SEQ ID NO:4.
PN US2005064392-A1.
PD 24-MAR-2005.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match Best Local Similarity 30.6%; Score 56.5; DB 9; Length 739;
RESULT 1449
ID ASG15572 standard; protein; 804 AA.
DE Novel human diagnostic protein #15563.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match Best Local Similarity 31.6%; Score 56.5; DB 4; Length 804;
RESULT 1450
ID AAG90560 standard; protein; 811 AA.
DE C glutamicum protein fragment SEQ ID NO: 4314.
PN EPI108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match Best Local Similarity 24.7%; Score 56.5; DB 4; Length 811;
RESULT 1451
ID ADL65931 standard; protein; 811 AA.
DE C. glutamicum RXA-associated protein #144.
PN DE10154177-A1.
PD 08-MAY-2003.
PA (BADI) BASF AG.
Query Match Best Local Similarity 24.7%; Score 56.5; DB 7; Length 811;
RESULT 1452
ID ASY00038 standard; protein; 1447 AA.
DE Transmissible gastroenteritis virus spike (S) protein, SEQ:6057.
PN WO2004092360-A2.
PD 28-OCT-2004.
PA (CHIR) CHIRON CORP.
Query Match Best Local Similarity 29.0%; Score 56.5; DB 8; Length 1447;
RESULT 1453
ID ASG12703 standard; protein; 1468 AA.
DE Novel human diagnostic protein #12694.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match Best Local Similarity 31.1%; Score 56.5; DB 4; Length 1468;
RESULT 1454
ID AAP80474 standard; protein; 1483 AA.
DE Sequence of protein of transmissible gastroenteritis virus (TGEV) encoded on peplomer gene.
PN EP278541-A.
PD 17-AUG-1988.
PA (DUIN) DUPHAR INT RES BV.
Query Match Best Local Similarity 29.0%; Score 56.5; DB 1; Length 1483;
RESULT 1455
ID ASG23183 standard; protein; 1513 AA.
DE Novel human diagnostic protein #23174.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match Best Local Similarity 12.6%; Score 56.5; DB 4; Length 1513;

Best Local Similarity 31.1%; Pred. No. 6.1e+03;
RESULT 1456
ID ABG17328 standard; protein; 1513 AA.
DE Novel human diagnostic protein #17319.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.6%; Score 56.5; DB 4; Length 1513;
Best Local Similarity 31.1%; Pred. No. 6.1e+03;
RESULT 1457
ID ABG08688 standard; protein; 1516 AA.
DE Novel human diagnostic protein #8679.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.6%; Score 56.5; DB 4; Length 1516;
Best Local Similarity 31.1%; Pred. No. 6.1e+03;
RESULT 1458
ID AAR93933 standard; protein; 2353 AA.
DE Haemophilus adhesion protein HA2.
PN WO9630519-A1.
PD 03-OCT-1996.
PA (UNIW) UNIV WASHINGTON.
PA (UYSL-) UNIV ST LOUIS.
Query Match 12.6%; Score 56.5; DB 2; Length 2353;
Best Local Similarity 25.8%; Pred. No. 1.1e+04;
RESULT 1459
ID AAB23860 standard; protein; 2411 AA.
DE Haemophilus influenzae adhesin (Hia) protein from type c strain API.
PN WO200055191-A2.
PD 21-SEP-2000.
PA (CONN-) CONNAUGHT LAB LTD.
Query Match 12.6%; Score 56.5; DB 3; Length 2411;
Best Local Similarity 25.8%; Pred. No. 1.1e+04;
RESULT 1460
ID ABB58102 standard; protein; 3005 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 1098.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.6%; Score 56.5; DB 4; Length 3005;
Best Local Similarity 27.3%; Pred. No. 1.5e+04;
RESULT 1461
ID ADG42622 standard; protein; 4351 AA.
DE RAT MEGFI.
PN US2003204052-A1.
PD 30-OCT-2003.
PA (HERR) HERRMANN J L.
PA (RAST) RASTELLI L.
PA (SHIM) SHINKETS R A.
Query Match 12.6%; Score 56.5; DB 7; Length 4351;
Best Local Similarity 26.0%; Pred. No. 2.3e+04;
RESULT 1462
ID ADN73145 standard; protein; 5155 AA.
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 1040.
PN WO2004035798-A2.
PD 28-APR-2004.
PA (CROP-) CROFDISIGN NV.
Query Match 12.6%; Score 56.5; DB 8; Length 5155;
Best Local Similarity 33.8%; Pred. No. 2.8e+04;
RESULT 1463
ID ABB66811 standard; protein; 6815 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 27225.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 12.6%; Score 56.5; DB 4; Length 6815;
Best Local Similarity 25.8%; Pred. No. 4e+04;
RESULT 1464
ID AAO10725 standard; protein; 91 AA.
DE Human polypeptide SEQ ID NO 24617.
PN WO200164835-A2.
PD 07-SEP-2001.

PA (HYSE-) HYSEQ INC.
Query Match 12.5%; Score 56; DB 4; Length 91;
Best Local Similarity 27.1%; Pred. No. 2e+02;
RESULT 1465
ID ABO76764 standard; protein; 137 AA.
DE Pseudomonas aeruginosa polypeptide #8939.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 12.5%; Score 56; DB 7; Length 137;
Best Local Similarity 25.8%; Pred. No. 3.4e+02;
RESULT 1466
ID AAE12999 standard; protein; 145 AA.
DE Arabidopsis thaliana SDS protein cyclin box.
PN WO200174144-A1.
PD 11-OCT-2001.
PA (UYPE-) UNIV PENNSYLVANIA STATE.
Query Match 12.5%; Score 56; DB 4; Length 145;
Best Local Similarity 30.4%; Pred. No. 3.7e+02;
RESULT 1467
ID ABP66595 standard; protein; 213 AA.
DE Human RSV antibody variable light chain.
PN WO200243660-A2.
PD 06-JUN-2002.
PA (MEDI-) MEDIMMUNE INC.
Query Match 12.5%; Score 56; DB 5; Length 213;
Best Local Similarity 26.9%; Pred. No. 5.9e+02;
RESULT 1468
ID ABU69458 standard; protein; 213 AA.
DE Respiratory syncytial virus (RSV) antibody #72.
PN US2002177126-A1.
PD 28-NOV-2002.
PA (MEDI-) MEDIMMUNE INC.
Query Match 12.5%; Score 56; DB 6; Length 213;
Best Local Similarity 26.9%; Pred. No. 5.9e+02;
RESULT 1469
ID ADE35953 standard; protein; 213 AA.
DE SYNAGIS antibody based light chain #17.
PN US2003091584-A1.
PD 15-MAY-2003.
PA (YOUN) YOUNG J F.
PA (KOEN) KOENIG S.
PA (JOHN) JOHNSON L S.
Query Match 12.5%; Score 56; DB 7; Length 213;
Best Local Similarity 26.9%; Pred. No. 5.9e+02;
RESULT 1470
ID ADW20095 standard; protein; 213 AA.
DE RSV antigen binding antibody variable light chain, SEQ ID 241.
PN US2005002926-A1.
PD 06-JAN-2005.
PA (MEDI-) MEDIMMUNE INC.
Query Match 12.5%; Score 56; DB 9; Length 213;
Best Local Similarity 26.9%; Pred. No. 5.9e+02;
RESULT 1471
ID AEB07077 standard; protein; 213 AA.
DE RSV-specific antibody-related protein - SEQ ID 241.
PN US2005147616-A1.
PD 07-JUL-2005.
PA (YOUN) YOUNG J F.
PA (KOEN) KOENIG S.
PA (JOHN) JOHNSON L S.
PA (HUSE) HUSE W D.
PA (WATK) WATKINS J D.
PA (WUHH) WU H.
Query Match 12.5%; Score 56; DB 9; Length 213;
Best Local Similarity 26.9%; Pred. No. 5.9e+02;
RESULT 1472
ID ADC26157 standard; protein; 214 AA.
DE Anti-VEGF Y0101 antibody mutant light chain protein 2.
PN WO2003068801-A2.
PD 21-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 12.5%; Score 56; DB 7; Length 214;

Best Local Similarity 26.9%; Pred. No. 6e+02;
RESULT 1473
ID ADC26154 standard; protein; 214 AA.
DE Parent anti-VEGF Y0101 antibody wild-type light chain protein.
PN WO2003068801-A2.
PD 21-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 12.5%; Score 56; DB 7; Length 214;
Best Local Similarity 26.9%; Pred. No. 6e+02;
RESULT 1474
ID ADC26156 standard; protein; 214 AA.
DE Anti-VEGF Y0101 antibody mutant light chain protein 1.
PN WO2003068801-A2.
PD 21-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 12.5%; Score 56; DB 7; Length 214;
Best Local Similarity 26.9%; Pred. No. 6e+02;
RESULT 1475
ID ADL93656 standard; protein; 233 AA.
DE Human CD44-binding antibody light chain HAE-F1-kappa-light SEQ ID NO:151.
PN WO2004024750-A2.
PD 25-MAR-2004.
PA (DYAX-) DYAX CORP.
Query Match 12.5%; Score 56; DB 8; Length 233;
Best Local Similarity 28.1%; Pred. No. 6.6e+02;
RESULT 1476
ID ADS84458 standard; protein; 234 AA.
DE Human anti-EPO-R antibody Ab412 light chain SEQ ID NO:97.
PN WO2004035603-A2.
PD 29-APR-2004.
PA (ABBO) ABBOTT LAB.
Query Match 12.5%; Score 56; DB 8; Length 234;
Best Local Similarity 28.4%; Pred. No. 6.7e+02;
RESULT 1477
ID ADS84476 standard; protein; 234 AA.
DE Human anti-EPO-R antibody Ab484 light chain SEQ ID NO:115.
PN WO2004035603-A2.
PD 29-APR-2004.
PA (ABBO) ABBOTT LAB.
Query Match 12.5%; Score 56; DB 8; Length 234;
Best Local Similarity 28.4%; Pred. No. 6.7e+02;
RESULT 1478
ID ADS84464 standard; protein; 234 AA.
DE Human anti-EPO-R antibody Ab430 light chain SEQ ID NO:103.
PN WO2004035603-A2.
PD 29-APR-2004.
PA (ABBO) ABBOTT LAB.
Query Match 12.5%; Score 56; DB 8; Length 234;
Best Local Similarity 29.7%; Pred. No. 6.7e+02;
RESULT 1479
ID ADR68618 standard; protein; 234 AA.
DE Human antibody Ab484 light chain polypeptide seqid 115.
PN US2004175379-A1.
PD 09-SEP-2004.
PA (DEVIR/) DEVRIES P J.
PA (OSTR/) OSTROW D H.
PA (REIL/) REILLY E B.
PA (GREE/) GREEN L L.
PA (WIEL/) WIELER J.
Query Match 12.5%; Score 56; DB 8; Length 234;
Best Local Similarity 28.4%; Pred. No. 6.7e+02;
RESULT 1480
ID ADR68600 standard; protein; 234 AA.
DE Human antibody Ab412 light chain polypeptide seqid 97.
PN US2004175379-A1.
PD 09-SEP-2004.
PA (DEVIR/) DEVRIES P J.
PA (OSTR/) OSTROW D H.
PA (REIL/) REILLY E B.
PA (GREE/) GREEN L L.
PA (WIEL/) WIELER J.
Query Match 12.5%; Score 56; DB 8; Length 234;
Best Local Similarity 28.4%; Pred. No. 6.7e+02;

RESULT 1481
ID ADR68606 standard; protein; 234 AA.
DE Human antibody Ab430 light chain polypeptide seqid 103.
PN US2004175379-A1.
PD 09-SEP-2004.
PA (DEVIR/) DEVRIES P J.
PA (OSTR/) OSTROW D H.
PA (REIL/) REILLY E B.
PA (GREE/) GREEN L L.
PA (WIEL/) WIELER J.
Query Match 12.5%; Score 56; DB 8; Length 234;
Best Local Similarity 29.7%; Pred. No. 6.7e+02;
RESULT 1482
ID AAU74297 standard; protein; 236 AA.
DE Anti-human AILIM monoclonal antibody clone Jmab-136, light chain.
PN WO200187981-A2.
PD 22-NOV-2001.
PA (NISB) JAPAN TOBACCO INC.
Query Match 12.5%; Score 56; DB 5; Length 236;
Best Local Similarity 26.9%; Pred. No. 6.7e+02;
RESULT 1483
ID ABB81107 standard; protein; 237 AA.
DE Anti-VEGF light chain fragment.
PN WO200261090-A2.
PD 08-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 12.5%; Score 56; DB 5; Length 237;
Best Local Similarity 26.9%; Pred. No. 6.8e+02;
RESULT 1484
ID ABP51952 standard; protein; 237 AA.
DE Plasmid pY0317 anti-VEGF Fab amino acid sequence SEQ ID NO:2 #1.
PN WO200248376-A2.
PD 20-JUN-2002.
PA (GETH) GENENTECH INC.
Query Match 12.5%; Score 56; DB 5; Length 237;
Best Local Similarity 26.9%; Pred. No. 6.8e+02;
RESULT 1485
ID ADO14128 standard; protein; 237 AA.
DE Plasmid pXVG2AP11 expression cassette light chain protein SEQ ID NO:8.
PN WO2004042017-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 12.5%; Score 56; DB 8; Length 237;
Best Local Similarity 26.9%; Pred. No. 6.8e+02;
RESULT 1486
ID ADO14131 standard; protein; 237 AA.
DE Plasmid pXVG11VNERK expression cassette light chain protein SEQ ID NO:11.
PN WO2004042017-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 12.5%; Score 56; DB 8; Length 237;
Best Local Similarity 26.9%; Pred. No. 6.8e+02;
RESULT 1487
ID ADQ90703 standard; protein; 237 AA.
DE Anti-VEGF antibody Y0317 light chain protein SEQ ID NO:7.
PN WO2004065417-A2.
PD 05-AUG-2004.
PA (GETH) GENENTECH INC.
Query Match 12.5%; Score 56; DB 8; Length 237;
Best Local Similarity 26.9%; Pred. No. 6.8e+02;
RESULT 1488
ID ADQ90701 standard; protein; 237 AA.
DE Anti-VEGF antibody VNERK light chain protein SEQ ID NO:5.
PN WO2004065417-A2.
PD 05-AUG-2004.
PA (GETH) GENENTECH INC.
Query Match 12.5%; Score 56; DB 8; Length 237;
Best Local Similarity 26.9%; Pred. No. 6.8e+02;
RESULT 1489
ID ADQ90705 standard; protein; 237 AA.
DE Anti-VEGF antibody VNERK light chain protein SEQ ID NO:9.
PN WO2004065417-A2.
PD 05-AUG-2004.

PA (GETH) GENENTECH INC.
Query Match 12.5%; Score 56; DB 8; Length 237;
Best Local Similarity 26.9%; Pred. No. 6.8e+02;
RESULT 1490
ID ADQ90709 standard; protein; 237 AA.
DE Anti-VEGF antibody VNERK light chain protein SEQ ID NO:13.
PN WO2004065417-A2.
PD 05-AUG-2004.
PA (GETH) GENENTECH INC.
Query Match 12.5%; Score 56; DB 8; Length 237;
Best Local Similarity 26.9%; Pred. No. 6.8e+02;
RESULT 1491
ID ADQ90723 standard; protein; 237 AA.
DE Anti-VEGF antibody VNERK light chain protein SEQ ID NO:27.
PN WO2004065417-A2.
PD 05-AUG-2004.
PA (GETH) GENENTECH INC.
Query Match 12.5%; Score 56; DB 8; Length 237;
Best Local Similarity 26.9%; Pred. No. 6.8e+02;
RESULT 1492
ID ADQ90721 standard; protein; 237 AA.
DE Anti-VEGF antibody light chain protein SEQ ID NO:25.
PN WO2004065417-A2.
PD 05-AUG-2004.
PA (GETH) GENENTECH INC.
Query Match 12.5%; Score 56; DB 8; Length 237;
Best Local Similarity 26.9%; Pred. No. 6.8e+02;
RESULT 1493
ID ADQ90707 standard; protein; 237 AA.
DE Anti-VEGF antibody VNERK light chain protein SEQ ID NO:11.
PN WO2004065417-A2.
PD 05-AUG-2004.
PA (GETH) GENENTECH INC.
Query Match 12.5%; Score 56; DB 8; Length 237;
Best Local Similarity 26.9%; Pred. No. 6.8e+02;
RESULT 1494
ID ADY06952 standard; protein; 237 AA.
DE Plant full length insert polypeptide seqid 62767.
PN US2004034888-A1.
PD 13-FEB-2004.
PA (LIUJ) LIU J.
PA (ZHOU) ZHOU Y.
PA (KOVA) KOVALIC D K.
PA (SCRE) SCREEN S E.
PA (TABA) TABASKA J B.
PA (CAOY) CAO Y.
Query Match 12.5%; Score 56; DB 8; Length 237;
Best Local Similarity 31.0%; Pred. No. 6.8e+02;
RESULT 1495
ID ABU97115 standard; protein; 250 AA.
DE Recombinant anti-infective bursal disease virus-antibody fragment #1.
PN WO200298921-A1.
PD 12-DEC-2002.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
Query Match 12.5%; Score 56; DB 6; Length 250;
Best Local Similarity 26.8%; Pred. No. 7.3e+02;
RESULT 1496
ID AEM69176 standard; protein; 258 AA.
DE Photorhabdus luminescens protein sequence #2273.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 12.5%; Score 56; DB 6; Length 258;
Best Local Similarity 25.5%; Pred. No. 7.5e+02;
RESULT 1497
ID ADE57818 standard; protein; 261 AA.
DE Human Protein P01919, SEQ ID NO 3683.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 12.5%; Score 56; DB 7; Length 261;
Best Local Similarity 30.8%; Pred. No. 8e+02;
RESULT 1498
ID ADE62851 standard; protein; 261 AA.
DE Human Protein P01919, SEQ ID NO 8785.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 12.5%; Score 56; DB 7; Length 261;
Best Local Similarity 30.8%; Pred. No. 7.7e+02;
RESULT 1499
ID ADQ17236 standard; protein; 261 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 52.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 12.5%; Score 56; DB 8; Length 261;
Best Local Similarity 30.8%; Pred. No. 7.7e+02;
RESULT 1500
ID AAY68284 standard; peptide; 269 AA.
DE Class II beta chain protein DQ-beta SEQ ID NO:116.
PN US6011146-A.
PD 04-JAN-2000.
PA (INSP) INST NAT SANTE & RECH MEDICALE.
Query Match 12.5%; Score 56; DB 3; Length 269;
Best Local Similarity 30.8%; Pred. No. 8e+02;

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OM protein - protein search, using sw model

Run on: December 22, 2005, 02:54:14 ; Search time 39.1837 Seconds
(without alignments)
196.443 Million cell updates/sec

Title: US-10-063-553-48_COPY_111_190
Perfect score: 449
Sequence: 1 KQPLMCNPSNANCFSL.....RASSFHFDSEKNKRLIHFS 80

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78.5	17.5	281	2 T51961	ATRAFI-like protein
2	73	16.3	413	2 S01076	aspartate transami
3	70	15.6	490	2 S52830	RMS1 protein - yea
4	70	15.6	1011	2 T13669	neuromusculin - fr
5	68	15.1	2201	2 A32160	tenascin-C - human
6	67	14.9	296	2 AH1173	conserved hypothet
7	66	14.7	575	2 A54861	tenascin - rat (fr
8	66	14.7	1217	2 T00270	hypothetical prote
9	65.5	14.6	620	2 T49067	transcription fact
10	65.5	14.6	656	2 B49423	semaphorin I - fru
11	65	14.5	652	2 H96524	probable phospho
12	64.5	14.4	330	2 T43061	hypothetical prote
13	64.5	14.4	461	2 T25671	hypothetical prote
14	64.5	14.4	475	2 T39486	hypothetical prote
15	64.5	14.4	503	2 T38303	SWI/SNF complex tr
16	64	14.3	228	2 T16578	hypothetical prote
17	64	14.3	992	2 A42318	glycogen phosphory
18	64	14.3	1500	2 T03824	probable immediate
19	63	14.0	418	2 R86395	hypothetical prote
20	63	14.0	1165	1 S45879	chitin synthase (E
21	63	14.0	2051	2 T13164	plexin B - fruit f
22	62.5	13.9	296	2 A11530	conserved hypothet
23	62.5	13.9	413	2 S29027	aspartate transami
24	62.5	13.9	646	2 JQ2150	B west mating prot
25	62.5	13.9	1748	1 JN0786	integrin beta-4 ch
26	62.5	13.9	1811	2 T00035	nonstructural poly
27	62	13.8	971	2 S50912	probable membrane
28	61.5	13.7	417	2 AG1934	folylpolyglutamate
29	61.5	13.7	487	2 T49424	hypothetical prote

30	61.5	13.7	647	2 JQ2149	B west mating prot
31	61.5	13.7	1034	2 S49947	SMT4 protein - yea
32	61	13.6	326	2 G84748	hypothetical prote
33	61	13.6	412	2 S13035	aspartate transami
34	61	13.6	413	2 S29028	aspartate transami
35	61	13.6	413	2 JTO439	tenascin precursor
36	61	13.6	1810	1 A32230	tenascin precursor
37	61	13.6	2019	1 JQ1322	surface-layer rela
38	60.5	13.5	444	2 D97142	beta-fructofuranos
39	60.5	13.5	661	2 S37592	beta-fructofuranos
40	60.5	13.5	661	2 S37591	beta-fructofuranos
41	60.5	13.5	661	2 S37590	beta-fructofuranos
42	60.5	13.5	937	2 A56517	nucleoporin Nup98
43	60.5	13.5	992	2 S49835	hypothetical prote
44	60	13.4	292	2 T19669	hypothetical prote
45	60	13.4	292	2 G88783	protein C33A12.16
46	60	13.4	292	2 T32336	hypothetical prote
47	59.5	13.3	557	2 JCS487	cellulase (EC 3.2.
48	59.5	13.3	821	2 T41364	hypothetical prote
49	59	13.1	284	2 T06129	zinc finger protei
50	59	13.1	412	2 A26341	aspartate transami
51	59	13.1	433	2 S31436	ig upsilon chain -
52	59	13.1	493	2 I39541	cytolytic enteroto
53	59	13.1	554	2 G96598	protein F20N2.6 [i
54	59	13.1	677	1 A45264	system b(0,+) amin
55	59	13.1	741	2 JG0606	homeobox protein A
56	59	13.1	763	2 S17998	gene COX1 intron 4
57	59	13.1	838	2 B89473	protein F52D2.6 [i
58	59	13.1	1006	2 T41104	probable transcrip
59	59	13.1	2352	2 T43431	alpha-glucan synth
60	58.5	13.0	508	2 T19350	hypothetical prote
61	58.5	13.0	640	2 S23008	insulin-like growt
62	58.5	13.0	1615	2 JG0372	low density lipopre
63	58.5	13.0	1748	1 JQ1555	genome polyprotein
64	58	12.9	261	2 I68718	MHC class II histo
65	58	12.9	375	2 A64300	aspartate transami
66	58	12.9	405	2 A83038	hypothetical prote
67	58	12.9	465	2 S03325	transforming prote
68	58	12.9	486	2 S07633	hematopoietic line
69	58	12.9	486	2 I49760	lckBp1 protein - m
70	58	12.9	528	2 S63009	hypothetical prote
71	58	12.9	795	2 T31180	hypothetical prote
72	58	12.9	1666	2 T43169	hypothetical prote
73	57.5	12.8	176	2 I53630	cell surface glyco
74	57.5	12.8	269	2 I54432	MHC class II histo
75	57.5	12.8	275	1 F65090	3',5'-cyclic-nucle
76	57.5	12.8	275	1 G85963	3',5'-cyclic-nucle
77	57.5	12.8	275	1 H91118	3',5'-cyclic-nucle
78	57.5	12.8	413	2 S51567	serine/threonine k
79	57.5	12.8	546	2 T32382	hypothetical prote
80	57.5	12.8	574	2 AC1414	ABC transporter re
81	57.5	12.8	640	2 B84887	probable SCARECROW
82	57.5	12.8	959	2 T25704	hypothetical prote
83	57.5	12.8	1291	1 A28334	protein-tyrosine-p
84	57.5	12.8	1807	2 JG6319	integrin beta-4 ch
85	57.5	12.8	3005	2 S33642	homeotic protein z
86	57	12.7	219	2 S52028	ig kappa chain - m
87	57	12.7	307	2 A45600	asparagine-rich bl
88	57	12.7	446	2 F84506	En/Spm-like transp
89	57	12.7	471	2 AH1810	isochoiamate synt
90	57	12.7	619	1 KSNCL0	laccase (EC 1.10.3
91	57	12.7	619	1 T04220	laccase (EC 1.10.3
92	57	12.7	813	2 KSNCLT	H+-transporting AT
93	57	12.7	1042	2 T29307	hypothetical prote
94	57	12.7	1411	2 S55123	hypothetical prote
95	57	12.7	2761	2 T21064	hypothetical prote
96	56.5	12.6	169	2 T31484	hypothetical prote
97	56.5	12.6	180	1 HLHUC3	MHC class II histo
98	56.5	12.6	251	2 S40995	hypothetical prote
99	56.5	12.6	263	2 T46093	hypothetical prote
100	56.5	12.6	457	2 S18239	glycerol-3-phospha
101	56.5	12.6	569	2 B84904	probable laccase (
102	56.5	12.6	740	2 H82807	beta-glucosidase X

103	56.5	12.6	768	2	JC6564	cellobiose oxidase	176	55	12.2	601	2	T00119	probable transcrip
104	56.5	12.6	874	1	AC2287	hypothetical prote	177	55	12.2	650	2	S23217	beta-fructofuranos
105	56.5	12.6	891	1	RDBNH7	nitrate reductase	178	55	12.2	708	2	S52317	quinohemoprotein e
106	56.5	12.6	1018	2	T30986	period protein - C	179	55	12.2	956	1	QOBBK2	Uti105 protein - hu
107	56.5	12.6	1125	2	T39052	hypothetical serin	180	55	12.2	1052	1	A44937	kinetoplast-associ
108	56.5	12.6	1447	1	VGIH83	E2 glycoprotein pr	181	55	12.2	1191	2	T13850	gene u-shaped prot
109	56.5	12.6	1447	1	VGIH82	E2 glycoprotein pr	182	55	12.2	1194	2	E96624	hypothetical prote
110	56.5	12.6	4351	2	T00252	MEGF1 protein - ra	183	55	12.2	1245	2	G86404	probable P-glycopr
111	56.5	12.6	5138	2	B96695	hypothetical prote	184	55	12.2	1280	2	A39117	170K lectin precur
112	56	12.5	238	2	A45544	BoIA-DQ beta-1 - b	185	55	12.2	1450	2	C86880	hypothetical prote
113	56	12.5	247	2	I45942	MHC class II - bov	186	55	12.2	2843	1	RBHUAP	adenomatous polyo
114	56	12.5	259	2	S64423	probable membrane	187	54.5	12.1	155	2	T49557	hypothetical prote
115	56	12.5	261	1	HLHU2C	MHC class II histo	188	54.5	12.1	219	2	I45937	MHC cell surface g
116	56	12.5	261	1	I45928	MHC class II - bov	189	54.5	12.1	232	2	I47094	MHC class II OLA-D
117	56	12.5	447	2	A84718	hypothetical prote	190	54.5	12.1	237	2	S68702	tryptase (EC 3.4.2
118	56	12.5	468	2	T22397	hypothetical prote	191	54.5	12.1	261	2	I45943	MHC class II - bov
119	56	12.5	492	2	I39591	hemolysin - Aeromo	192	54.5	12.1	323	2	T06506	glutenin low molec
120	56	12.5	518	2	T23745	hypothetical prote	193	54.5	12.1	348	2	S57601	ribonuclease H (EC
121	56	12.5	555	2	C83444	probable AMP-bindi	194	54.5	12.1	361	2	A91037	probable peptidase
122	56	12.5	703	2	A97312	membrane associat	195	54.5	12.1	361	2	C85881	probable peptidase
123	56	12.5	711	2	D83897	catalase katB (imp	196	54.5	12.1	373	2	D71636	hypothetical prote
124	56	12.5	714	2	S56208	hypothetical prote	197	54.5	12.1	396	2	S01660	glycerol-3-phospha
125	56	12.5	729	2	T46328	probable adenosine	198	54.5	12.1	448	2	S40439	tubulin alpha-2 ch
126	56	12.5	731	2	S56028	protein YKR018c ho	199	54.5	12.1	449	2	S55911	tubulin alpha-1 ch
127	56	12.5	953	2	T01093	luminidependens pr	200	54.5	12.1	449	2	T21415	hypothetical prote
128	56	12.5	1161	2	B70172	DNA polymerase III	201	54.5	12.1	477	2	S53362	mucin 5AC (clone J
129	56	12.5	1308	2	B32494	transposable eleme	202	54.5	12.1	482	2	T02538	hypothetical prote
130	55.5	12.4	218	2	B49346	butyrate-acetoacet	203	54.5	12.1	506	2	D84609	hypothetical prote
131	55.5	12.4	276	2	A69437	dehydrase homolog	204	54.5	12.1	528	1	A31854	lanosterol 14alpha
132	55.5	12.4	288	2	A90135	SAM-dependent meth	205	54.5	12.1	681	1	A36500	transferrin precur
133	55.5	12.4	417	2	B97249	fusion HD-GYP doma	206	54.5	12.1	760	2	S70294	FUN21 protein - ye
134	55.5	12.4	441	2	S29921	hypothetical prote	207	54.5	12.1	774	2	A86454	hypothetical prote
135	55.5	12.4	501	2	S51160	nitrate reductase	208	54.5	12.1	811	1	VCJLJSP	gag polyprotein -
136	55.5	12.4	544	2	C96943	uncharacterized me	209	54.5	12.1	859	1	FOLJCT	env polyprotein pr
137	55.5	12.4	646	2	JN0473	P-selectin precurs	210	54.5	12.1	859	2	S24571	env protein - huma
138	55.5	12.4	683	2	T03146	probable glycoprot	211	54.5	12.1	916	2	S07554	nitrate reductase
139	55.5	12.4	699	2	I37369	epican - human	212	54.5	12.1	1034	2	AB2013	hypothetical prote
140	55.5	12.4	704	1	S39004	finger protein MSN	213	54.5	12.1	1036	2	A29832	HPI layer surface
141	55.5	12.4	858	1	A42239	adenylate cyclase	214	54.5	12.1	1106	2	T25065	hypothetical prote
142	55.5	12.4	884	2	S66308	nitrate reductase	215	54.5	12.1	1133	2	T01757	hypothetical prote
143	55.5	12.4	886	2	A59223	nitrate reductase	216	54.5	12.1	1241	2	JU0466	potassium transpor
144	55.5	12.4	912	1	RDBHNS	nitrate reductase	217	54.5	12.1	1599	2	T16210	hypothetical prote
145	55.5	12.4	915	1	RDBHNS	nitrate reductase	218	54.5	12.1	1776	1	RRWPMY	genome polyprotein
146	55.5	12.4	1016	2	T30990	period protein - C	219	54.5	12.1	2524	2	A35844	Xotch protein - Af
147	55.5	12.4	1056	2	A53767	mucin MUC5B, trach	220	54.5	12.1	6658	2	T13931	projectin - fruit
148	55.5	12.4	1874	1	JQ0533	genome polyprotein	221	54	12.0	115	2	AB2223	hypothetical prote
149	55	12.2	183	2	A32339	MHC class II histo	222	54	12.0	140	2	S20914	lysosyme (EC 3.2.1
150	55	12.2	183	2	I54288	MHC class II DQ3.1	223	54	12.0	140	2	S41577	lysosyme (EC 3.2.1
151	55	12.2	183	2	I79496	MHC HLA-DQ-beta ch	224	54	12.0	140	2	S41574	lysosyme (EC 3.2.1
152	55	12.2	218	2	G71260	probable ribulose-	225	54	12.0	140	2	S41573	lysosyme (EC 3.2.1
153	55	12.2	224	2	A31459	MHC class II histo	226	54	12.0	214	2	S45465	heat shock protein
154	55	12.2	233	2	B83580	conserved hypotet	227	54	12.0	221	2	S25168	CHT28 protein - ch
155	55	12.2	261	1	HLHU1C	MHC class II histo	228	54	12.0	223	1	CSNCM	peptidylprolyl iso
156	55	12.2	261	1	HLHU1B	MHC class II histo	229	54	12.0	237	2	C86309	Similar to Ubiquit
157	55	12.2	261	2	I55996	MHC class II histo	230	54	12.0	260	2	I45938	MHC cell surface g
158	55	12.2	261	2	B37044	MHC class II histo	231	54	12.0	261	2	I68732	MHC class II histo
159	55	12.2	261	2	I54480	HLA DQ-beta - huma	232	54	12.0	276	2	H96985	probable hydrolase
160	55	12.2	261	2	B32527	class II histocomp	233	54	12.0	360	2	S48365	hypothetical prote
161	55	12.2	268	2	D29312	MHC class II histo	234	54	12.0	422	2	I50516	retinoid X recepto
162	55	12.2	287	2	T26411	hypothetical prote	235	54	12.0	425	2	T50484	mammalian swi/snf
163	55	12.2	358	2	I38429	connexin40 - human	236	54	12.0	447	2	T13204	hypothetical prote
164	55	12.2	359	2	E86706	hypothetical prote	237	54	12.0	485	2	S26575	hemolysin - Aeromo
165	55	12.2	363	2	JC7570	CVC domain-contain	238	54	12.0	504	2	S54744	cellulase (EC 3.2.
166	55	12.2	406	2	S60982	hypothetical prote	239	54	12.0	513	2	T41011	hypothetical prote
167	55	12.2	413	2	S21560	aspartate transami	240	54	12.0	614	2	A32608	thyroid hormone re
168	55	12.2	443	2	F87488	prolyl-tRNA synth	241	54	12.0	636	2	T41673	hypothetical zinc
169	55	12.2	458	2	S50919	hypothetical prote	242	54	12.0	713	2	B75489	hypothetical prote
170	55	12.2	486	2	A25976	aerolysin precurs	243	54	12.0	771	2	T38616	hypothetical prote
171	55	12.2	571	1	HNNZP2	hemagglutinin-neur	244	54	12.0	802	2	T21315	probable RNA-bind
172	55	12.2	571	1	HNNZP2	hemagglutinin-neur	245	54	12.0	849	2	T01286	hypothetical prote
173	55	12.2	582	2	T38743	hypothetical zinc	246	54	12.0	851	2	S12159	env protein - huma
174	55	12.2	586	2	JC7277	Sarcophaga-derived	247	54	12.0	890	2	T11805	nitrate reductase
175	55	12.2	593	2	T38547	probable cell divi	248	54	12.0	920	2	S52301	nitrate reductase

249	54	12.0	938	2	T39006	related to yeast z	322	53	11.8	504	2	S00390	Ig gamma chain (cl
250	54	12.0	964	2	T41547	hypothetical prote	323	53	11.8	530	2	F89581	protein xol-1 (imp
251	54	12.0	978	2	T16948	hypothetical prote	324	53	11.8	533	1	TVFVFP	protein tyrosine k
252	54	12.0	989	2	A54505	serine-repeat anti	325	53	11.8	536	2	S66716	glutamate-tRNA lig
253	54	12.0	997	2	B71617	SBRA antigen/papai	326	53	11.8	634	2	S31925	beta-fructofuranos
254	54	12.0	1224	2	T07446	DNA-directed RNA p	327	53	11.8	642	1	S34416	transcription fact
255	54	12.0	1446	2	T30916	carboxypeptidase D	328	53	11.8	649	2	AH3546	outer membrane pro
256	54	12.0	1742	2	S24600	projectin - fruit	329	53	11.8	660	2	T00902	hypothetical prote
257	54	12.0	1746	1	S19694	tenascin precursor	330	53	11.8	666	2	I52648	class A helix-loop
258	54	12.0	1945	2	T13937	plexin A - fruit f	331	53	11.8	667	2	A41311	transcription fact
259	54	12.0	2718	2	A23475	G surface protein	332	53	11.8	687	2	S69723	hypothetical prote
260	53.5	11.9	114	2	A34353	anti-peptide Fab'	333	53	11.8	744	2	S68115	catalase (EC 1.11.
261	53.5	11.9	122	2	A11116	hypothetical prote	334	53	11.8	782	1	G64157	probable organic s
262	53.5	11.9	125	2	S40315	Ig kappa chain - h	335	53	11.8	838	2	T04449	hypothetical prote
263	53.5	11.9	175	2	T23437	hypothetical prote	336	53	11.8	852	2	S41886	DNA repair protein
264	53.5	11.9	261	2	F96722	hypothetical prote	337	53	11.8	858	1	VCLJG2	env polyprotein pr
265	53.5	11.9	264	2	S65070	hypothetical prote	338	53	11.8	911	2	T08108	nitrate reductase
266	53.5	11.9	289	2	A48913	KRAB zinc finger p	339	53	11.8	917	2	E96807	nitrate reductase
267	53.5	11.9	308	2	B71697	probable proteinas	340	53	11.8	917	2	S35228	nitrate reductase
268	53.5	11.9	357	2	S09269	Ig alpha chain C r	341	53	11.8	969	2	T23256	hypothetical prote
269	53.5	11.9	403	2	S42521	A39R protein - vac	342	53	11.8	1121	2	T52631	1-phosphatidylinos
270	53.5	11.9	427	2	G82827	6-phosphofructokin	343	53	11.8	1159	2	S62562	probable nuclear p
271	53.5	11.9	448	2	T22194	hypothetical prote	344	53	11.8	1337	1	I38670	protein-tyrosine-p
272	53.5	11.9	451	2	S13337	tubulin alpha-2 ch	345	53	11.8	1344	2	H84557	hypothetical prote
273	53.5	11.9	455	2	T32189	zinc finger protei	346	53	11.8	1365	2	T00833	RNA-directed DNA p
274	53.5	11.9	474	2	A90520	ABC transporter pe	347	53	11.8	1806	2	T23298	hypothetical prote
275	53.5	11.9	482	2	B83113	catalase PA4236 [i	348	53	11.8	4688	2	F82885	hypothetical prote
276	53.5	11.9	517	2	S77255	hypothetical prote	349	52.5	11.7	99	2	D70582	probable PE protei
277	53.5	11.9	617	2	S19254	nitrate reductase	350	52.5	11.7	210	2	T49785	hypothetical prote
278	53.5	11.9	642	2	S55521	beta-fructofuranos	351	52.5	11.7	222	2	S22517	s-allele-associate
279	53.5	11.9	661	2	T16597	hypothetical prote	352	52.5	11.7	257	1	S50294	hypothetical prote
280	53.5	11.9	678	2	H88187	protein C18H9.8 [i	353	52.5	11.7	261	2	G90612	cytochrome c oxida
281	53.5	11.9	751	2	T15230	hypothetical prote	354	52.5	11.7	272	2	T09132	26S proteasome bet
282	53.5	11.9	823	2	H83724	hypothetical prote	355	52.5	11.7	304	2	A97768	probable proteasee
283	53.5	11.9	835	2	T47164	hypothetical prote	356	52.5	11.7	337	1	JQ0965	chitinase [EC 3.2.
284	53.5	11.9	900	2	S47029	nitrate reductase	357	52.5	11.7	357	2	C69223	anion permease - M
285	53.5	11.9	909	2	JN0665	nitrate reductase	358	52.5	11.7	361	2	A41535	glutamyl-peptide
286	53.5	11.9	936	2	T26521	hypothetical prote	359	52.5	11.7	414	2	A70214	hypothetical prote
287	53.5	11.9	1131	2	T38744	hypothetical prote	360	52.5	11.7	419	2	T18420	hypothetical prote
288	53.5	11.9	1239	1	A32579	neuroglian - fruit	361	52.5	11.7	449	2	A48466	tubulin alpha chai
289	53.5	11.9	1513	2	T44045	hypothetical prote	362	52.5	11.7	457	2	T15271	hypothetical prote
290	53.5	11.9	1520	2	C42311	hypothetical prote	363	52.5	11.7	462	2	S44490	RXR type hormone r
291	53.5	11.9	1712	2	T76181	hypothetical prote	364	52.5	11.7	470	2	T10193	glycerol-3-phospha
292	53.5	11.9	2399	2	H71879	toxin-like outer m	365	52.5	11.7	472	2	S51768	glycerol-3-phospha
293	53	11.8	140	2	A83285	hypothetical prote	366	52.5	11.7	491	1	CSRZ	catalase (EC 1.11.
294	53	11.8	142	2	A83285	hypothetical prote	367	52.5	11.7	499	1	S30007	probable UTP-gluco
295	53	11.8	203	2	T23943	hypothetical prote	368	52.5	11.7	536	2	T04222	hypothetical prote
296	53	11.8	207	2	T34054	hypothetical prote	369	52.5	11.7	556	2	S51858	probable membrane
297	53	11.8	232	2	B90129	26S proteasome SU	370	52.5	11.7	795	2	T21487	hypothetical prote
298	53	11.8	263	2	D83085	conserved hypothet	371	52.5	11.7	798	2	B27079	fibronectin recept
299	53	11.8	302	2	E64800	probable glutamate	372	52.5	11.7	803	2	S45916	hypothetical prote
300	53	11.8	302	2	A85566	probable periplasm	373	52.5	11.7	837	2	S54624	ROD1 protein - yea
301	53	11.8	302	2	F90715	probable periplasm	374	52.5	11.7	844	2	T00529	hypothetical prote
302	53	11.8	310	2	JL0119	Fc gamma (IgG) rec	375	52.5	11.7	852	1	VCLJGG	env polyprotein pr
303	53	11.8	317	2	JL0118	Fc gamma (IgG) rec	376	52.5	11.7	891	2	G89957	hypothetical prote
304	53	11.8	323	2	S06946	Fc gamma (IgG) rec	377	52.5	11.7	985	2	I51549	receptor tyrosine
305	53	11.8	339	2	A42259	endo-beta-N-acetyl	378	52.5	11.7	1015	2	A42915	type II cAMP-depen
306	53	11.8	341	2	S31236	hypothetical prote	379	52.5	11.7	1017	2	T42384	inositol-1,4,5-tri
307	53	11.8	350	2	B82281	ferric vibriobacti	380	52.5	11.7	1036	1	A34755	nitrogen regulator
308	53	11.8	352	2	T23464	hypothetical prote	381	52.5	11.7	1106	2	T19948	hypothetical prote
309	53	11.8	355	1	A55473	early switch prote	382	52.5	11.7	1146	2	S64402	probable transcrip
310	53	11.8	355	2	T07160	glutamate-ammonia	383	52.5	11.7	1211	2	S45500	alpha,alpha-trehal
311	53	11.8	360	2	T06786	6a-hydroxymaackiai	384	52.5	11.7	1367	1	IGHUR1	insulin-like growt
312	53	11.8	367	2	T00815	probable Tail-like	385	52.5	11.7	1445	2	A59437	KIAA1204 protein (
313	53	11.8	413	1	XNPGDC	aspartate transami	386	52.5	11.7	1449	1	A43573	E2 glycoprotein pr
314	53	11.8	417	2	B55473	early switch prote	387	52.5	11.7	1449	1	VGIHFS	E2 glycoprotein pr
315	53	11.8	426	2	C55473	early switch prote	388	52.5	11.7	1449	2	S47423	E2 glycoprotein pr
316	53	11.8	428	2	A53689	transcription fact	389	52.5	11.7	1806	2	AF1717	probable peptidogl
317	53	11.8	436	2	B86469	protein F12K21.16	390	52.5	11.7	3014	1	JC5620	genome polyprotein
318	53	11.8	443	2	T14916	mitosis-specific c	391	52	11.6	133	2	S57885	T-cell receptor al
319	53	11.8	445	2	D84385	oligopeptide ABC t	392	52	11.6	167	2	I58352	p16INK4a - mouse
320	53	11.8	461	2	T11819	glycerol-3-phospha	393	52	11.6	174	1	YQEC7P	fimbrial protein 9
321	53	11.8	484	2	T16695	hypothetical prote	394	52	11.6	215	2	JE0243	Ig kappa chain NIG

395	52	11.6	239	2	T34305	hypothetical prote	468	51.5	11.5	551	2	S05667	glucan 1,4-alpha-m
396	52	11.6	287	2	A45854	leucocyte common a	469	51.5	11.5	570	2	S56132	cellulase (EC 3.2.
397	52	11.6	289	2	T25277	hypothetical prote	470	51.5	11.5	576	2	S75958	hypothetical prote
398	52	11.6	291	2	T01241	probable MBP famil	471	51.5	11.5	576	2	T38293	hypothetical serin
399	52	11.6	301	2	C69143	hypothetical prote	472	51.5	11.5	578	1	BVBD1	GCD1 protein - yea
400	52	11.6	305	2	AD3378	hypothetical prote	473	51.5	11.5	578	2	S66353	hypothetical prote
401	52	11.6	373	2	T10341	late expression fa	474	51.5	11.5	610	2	S50539	l-ascorbate oxidas
402	52	11.6	426	2	T20253	hypothetical prote	475	51.5	11.5	618	2	T49177	hypothetical prote
403	52	11.6	437	2	S55392	meh ptein - fruit	476	51.5	11.5	620	2	JC4925	Xm1 methyltransfe
404	52	11.6	471	2	D90094	hypothetical prote	477	51.5	11.5	648	2	B81686	conserved hypochet
405	52	11.6	505	2	P71218	hypothetical prote	478	51.5	11.5	717	1	S29923	transforming prote
406	52	11.6	514	2	T11249	cytochrome-c oxida	479	51.5	11.5	766	2	B85440	receptor kinase-11
407	52	11.6	516	2	F82070	2-isopropylmalate	480	51.5	11.5	792	2	T26050	hypothetical prote
408	52	11.6	533	2	H86282	protein F10B6.34 [481	51.5	11.5	854	2	AC2309	hypothetical prote
409	52	11.6	572	2	S77249	hypothetical prote	482	51.5	11.5	862	2	I49583	hypothetical prote
410	52	11.6	597	2	T23561	hypothetical prote	483	51.5	11.5	888	2	A46512	differentiation an
411	52	11.6	611	2	T21747	hypothetical prote	484	51.5	11.5	911	2	T08105	CD22 homolog/B lym
412	52	11.6	638	2	B83890	hypothetical prote	485	51.5	11.5	959	2	B44402	nitrate reductase
413	52	11.6	681	2	S33316	structural protein	486	51.5	11.5	965	2	T12545	nuclear pore compl
414	52	11.6	681	2	A45705	type I transembra	487	51.5	11.5	1007	2	G96606	hypothetical prote
415	52	11.6	729	2	T52187	probable transposa	488	51.5	11.5	1107	2	S61667	disease resistance
416	52	11.6	799	1	TVRTTB	nerve growth facto	489	51.5	11.5	1142	2	S59359	probable membrane
417	52	11.6	855	2	A45713	Env transmembrane	490	51.5	11.5	1335	2	H86489	GIN4 protein - Yea
418	52	11.6	865	2	E84718	hypothetical prote	491	51.5	11.5	1338	2	T18416	protein T3E20.13
419	52	11.6	903	2	E88221	protein T0IH3.2 [i	492	51.5	11.5	1518	2	A44811	hypothetical prote
420	52	11.6	926	2	T48391	protein kinase-lik	493	51.5	11.5	1528	2	S13743	glucosyltransferas
421	52	11.6	1273	1	TDRPLT	leukocyte common a	494	51.5	11.5	1635	2	T10053	DNA strand transfe
422	52	11.6	1398	2	S56814	microtubule-intera	495	51.5	11.5	1753	1	A47437	laminin alpha 5 ch
423	52	11.6	1444	1	A30588	140K adhesin precu	496	51.5	11.5	5005	2	F82884	LDL-receptor-relat
424	52	11.6	2958	2	S64921	probable membrane	497	51.5	11.5	26926	1	I38344	hypothetical prote
425	52	11.6	491	2	T18489	hypothetical prote	498	51	11.4	160	2	C64171	hypothetical prote
426	51.5	11.5	98	2	PH1069	Ig light chain V r	499	51	11.4	174	2	T48419	hypothetical prote
427	51.5	11.5	102	2	S35882	AL0 protein - Indi	500	51	11.4	191	2	E75132	molhydropterin-guan
428	51.5	11.5	113	2	G71071	hypothetical prote	501	51	11.4	205	2	B31906	hypothetical prote
429	51.5	11.5	124	2	A40336	Ig kappa chain V-J	502	51	11.4	221	2	T03954	hypothetical prote
430	51.5	11.5	143	2	A95253	PTS system, IIA co	503	51	11.4	253	2	T40687	hypothetical prote
431	51.5	11.5	145	2	T16598	hypothetical prote	504	51	11.4	287	2	C82158	hypothetical prote
432	51.5	11.5	146	2	D42402	cell surface glyco	505	51	11.4	290	2	G72858	ROK family protein
433	51.5	11.5	148	2	G98117	hypothetical prote	506	51	11.4	319	2	AD1108	AcOrf-70 protein -
434	51.5	11.5	194	2	H22845	hypothetical prote	507	51	11.4	322	2	T25416	other proteins hom
435	51.5	11.5	207	2	G69381	hypothetical prote	508	51	11.4	329	2	H83907	hypothetical prote
436	51.5	11.5	210	2	A85018	probable copper-co	509	51	11.4	331	2	F86142	cytochrome aa3 qul
437	51.5	11.5	211	2	E71334	flagellin (flaB1-2	510	51	11.4	333	2	AF0407	F633.5 protein - A
438	51.5	11.5	257	2	I54285	hypothetical prote	511	51	11.4	352	2	G85606	lipoprotein [impor
439	51.5	11.5	261	2	A26344	MHC class II histo	512	51	11.4	352	2	F90797	hypothetical prote
440	51.5	11.5	262	2	G81954	carbonate dehydrat	513	51	11.4	388	2	S59860	hypothetical prote
441	51.5	11.5	262	2	T34547	cytochrome C1 prec	514	51	11.4	397	2	I39184	hypothetical prote
442	51.5	11.5	266	2	D81011	hypothetical prote	515	51	11.4	402	2	A84581	bomapiin - human
443	51.5	11.5	278	2	D36791	ubiquinol-cytochro	516	51	11.4	407	2	C45600	probable disease r
444	51.5	11.5	280	2	AF3144	hypothetical prote	517	51	11.4	417	2	A45794	asparagine-rich bl
445	51.5	11.5	312	2	C84511	non-heme chloroper	518	51	11.4	430	2	T23899	tubulin alpha chai
446	51.5	11.5	312	2	C75124	hypothetical prote	519	51	11.4	430	2	I39727	hypothetical prote
447	51.5	11.5	313	2	T49129	hypothetical prote	520	51	11.4	470	2	T25578	mannopine biosynth
448	51.5	11.5	320	2	A40216	flavonol 4'-sulfol	521	51	11.4	481	2	F97472	hypothetical prote
449	51.5	11.5	334	2	E85513	probable integrase	522	51	11.4	488	2	E70234	conserved hypochet
450	51.5	11.5	342	2	G90652	probable integrase	523	51	11.4	512	2	H86216	protein T23G18.16
451	51.5	11.5	346	2	F98143	non-heme chloroper	524	51	11.4	555	2	H96762	hypothetical prote
452	51.5	11.5	332	2	AH2533	hypothetical prote	525	51	11.4	578	2	S55102	HP2 protein - yea
453	51.5	11.5	344	2	T29264	hypothetical prote	526	51	11.4	580	2	T46024	hypothetical prote
454	51.5	11.5	376	2	T05420	cyclin delta-3 - A	527	51	11.4	642	2	S53434	plasma protein S p
455	51.5	11.5	454	2	T31604	hypothetical prote	528	51	11.4	684	2	S45758	proliferating-cell
456	51.5	11.5	387	2	D88968	protein T27B7.3 [i	529	51	11.4	710	2	T41352	probable transcrip
457	51.5	11.5	395	2	S51449	probable membrane	530	51	11.4	714	2	C90100	hypothetical prote
458	51.5	11.5	446	2	S46786	serine-tRNA ligase	531	51	11.4	722	2	F84394	integrin beta-1 ch
459	51.5	11.5	447	2	T06004	1-aminocyclopropan	532	51	11.4	753	2	A27041	fibronectin recept
460	51.5	11.5	465	2	B71716	transhydrogenase c	533	51	11.4	758	2	S47866	integrin beta olig
461	51.5	11.5	484	2	D64214	hypothetical prote	534	51	11.4	773	2	D89010	hypothetical prote
462	51.5	11.5	492	2	T09756	catalase (EC 1.11	535	51	11.4	795	2	T20939	hypothetical prote
463	51.5	11.5	511	1	VGVN	spike glycoprotein	536	51	11.4	798	2	S01659	integrin beta-1 ch
464	51.5	11.5	513	2	S58200	probable membrane	537	51	11.4	799	1	UCM5FB	fibronectin recept
465	51.5	11.5	527	2	JE0373	low density lipopr	538	51	11.4	799	2	JC4126	integrin beta olig
466	51.5	11.5	537	2	S26857	isocitrate lyase (539	51	11.4	805	2	T21957	hypothetical prote
467	51.5	11.5	538	2	S62566	PHD finger protein	540	51	11.4	807	2	T02916	hypothetical prote

541	51	11.4	839	1	TQZMCA	probable transposase	614	50.5	11.2	827	2	T04789	hypothetical prote
542	51	11.4	874	2	S62486	probable leucyl tr	615	50.5	11.2	869	2	S53098	envelope polyprote
543	51	11.4	879	2	S64755	hypothetical prote	616	50.5	11.2	904	1	RDNTNS	nitrate reductase
544	51	11.4	882	2	C83234	hypothetical prote	617	50.5	11.2	904	1	RDNTNT	nitrate reductase
545	51	11.4	890	2	A98017	probable 2-compone	618	50.5	11.2	911	1	RDTONH	nitrate reductase
546	51	11.4	890	2	C85861	probable 2-compone	619	50.5	11.2	926	1	RDSPNH	nitrate reductase
547	51	11.4	890	2	P64991	yojN protein - Esc	620	50.5	11.2	960	2	T50383	homolog to yeast c
548	51	11.4	900	2	T19689	hypothetical prote	621	50.5	11.2	964	2	JC5545	integrin beta-4 pr
549	51	11.4	995	2	S67564	hypothetical prote	622	50.5	11.2	974	1	A40213	optic lobe develop
550	51	11.4	1021	2	S64506	hypothetical prote	623	50.5	11.2	1050	2	T27753	hypothetical prote
551	51	11.4	1034	2	A36108	protein kinase BUB	624	50.5	11.2	1070	2	T34385	hypothetical prote
552	51	11.4	1041	2	D82792	conserved hypotet	625	50.5	11.2	1087	2	S58147	protein kinase - f
553	51	11.4	1079	2	PC7034	Na+ bicarbonate co	626	50.5	11.2	1148	2	T09073	splicing factor Si
554	51	11.4	1092	2	JK0312	differentiation-st	627	50.5	11.2	1185	2	S61886	chitin synthase (E
555	51	11.4	1097	2	S17308	leukemia inhibitor	628	50.5	11.2	1228	2	G90581	hypothetical prote
556	51	11.4	1112	2	S28289	hypothetical prote	629	50.5	11.2	1292	2	T09229	galactose binding
557	51	11.4	1187	1	TVHVY2	protein-tyrosine k	630	50.5	11.2	1325	2	S62497	probable nucleopor
558	51	11.4	1205	2	T41987	hypothetical prote	631	50.5	11.2	1466	2	A36426	SP2 protein - yea
559	51	11.4	1209	2	T46027	hypothetical prote	632	50.5	11.2	1607	2	T04583	TMV resistance pro
560	51	11.4	1247	2	F86405	probable P-glycopr	633	50.5	11.2	1692	2	A33988	adenylate cyclase
561	51	11.4	1265	2	T51498	hypothetical prote	634	50.5	11.2	1708	2	F69189	protoporphyrin IX
562	51	11.4	1379	1	S01254	hepatocyte growth	635	50.5	11.2	1875	2	A36429	integrin beta-4 ch
563	51	11.4	1385	2	A88554	protein C38C10.5a	636	50.5	11.2	2167	2	S50658	intrinsic factor-B
564	51	11.4	1391	2	B88554	protein C38C10.5b	637	50.5	11.2	3623	2	T08618	hypothetical prote
565	51	11.4	1424	2	T03851	thyroid hormone re	638	50	11.1	115	2	T51208	hypothetical prote
566	51	11.4	1604	2	B86287	F9L1.23 protein -	639	50	11.1	118	2	F58932	ribosomal protein
567	51	11.4	1839	2	S77626	mannuronan C-5-epi	640	50	11.1	165	2	A82246	probable phosphata
568	51	11.4	2197	2	B71600	variant-specific s	641	50	11.1	175	1	CYBOAB	alpha-crystallin c
569	51	11.4	3124	2	A40020	collagen alpha 1(X	642	50	11.1	175	1	CYHUAB	alpha-crystallin c
570	50.5	11.2	125	2	A53627	fibroblast growth	643	50	11.1	175	2	A53871	alpha-crystallin c
571	50.5	11.2	233	2	T00202	occlusion-derived	644	50	11.1	191	2	T19668	hypothetical prote
572	50.5	11.2	254	2	S20741	chitinase (EC 3.2.	645	50	11.1	202	1	DHRT	lg delta chain C r
573	50.5	11.2	264	2	F90102	translational init	646	50	11.1	215	2	JB0242	lg kappa chain NIG
574	50.5	11.2	280	2	F81984	hypothetical prote	647	50	11.1	217	2	T50521	hypothetical prote
575	50.5	11.2	281	2	A97604	probable oxidoredu	648	50	11.1	243	2	T24981	hypothetical prote
576	50.5	11.2	281	2	AB2826	aldo/keto reducta	649	50	11.1	245	2	T41291	conserved hypotet
577	50.5	11.2	283	2	S73523	probable lipoprote	650	50	11.1	261	2	A60404	MHC class II histo
578	50.5	11.2	324	1	UBCH34	tubulin alpha-8 ch	651	50	11.1	261	2	B60404	MHC class II histo
579	50.5	11.2	325	2	G70334	hypothetical prote	652	50	11.1	270	2	T43491	hypothetical prote
580	50.5	11.2	332	2	S47358	probable membrane	653	50	11.1	271	2	C82841	cysteine proteinas
581	50.5	11.2	338	2	S73441	MG032 homolog B01	654	50	11.1	311	2	A69095	cobalt transport A
582	50.5	11.2	340	2	T48288	hypothetical prote	655	50	11.1	321	2	AG2936	transglycosylase A
583	50.5	11.2	342	2	S57814	oxidase like prote	656	50	11.1	321	2	H98345	hypothetical prote
584	50.5	11.2	361	1	F65014	hypothetical prote	657	50	11.1	327	1	HLHUCD	T-cell surface gly
585	50.5	11.2	361	2	S67590	mannose-1-phosphat	658	50	11.1	345	2	A12217	low specificity DNA-
586	50.5	11.2	361	2	AH1469	internalin protein	659	50	11.1	354	2	JT0594	site-specific DNA-
587	50.5	11.2	376	2	B96714	hypothetical prote	660	50	11.1	368	2	A46601	hypothetical prote
588	50.5	11.2	420	2	T47998	pectinacetylestera	661	50	11.1	370	2	A96547	hypothetical prote
589	50.5	11.2	427	2	AH2141	type I restriction	662	50	11.1	374	2	T24162	hypothetical prote
590	50.5	11.2	446	2	H90094	hypothetical prote	663	50	11.1	379	2	T04762	chitinase homolog
591	50.5	11.2	454	2	S65970	replicative DNA he	664	50	11.1	397	1	Z6BPT9	ribonucleoside-tri
592	50.5	11.2	455	2	T49176	hypothetical prote	665	50	11.1	410	2	G90362	hypothetical prote
593	50.5	11.2	459	2	T11489	NADH2 dehydrogenas	666	50	11.1	416	2	B86384	probable zinc fing
594	50.5	11.2	492	2	T09754	catalase (EC 1.11.	667	50	11.1	418	2	A37344	acrosin (EC 3.4.21
595	50.5	11.2	494	2	S62637	catalase (EC 1.11.	668	50	11.1	431	2	P90316	darP protein, prob
596	50.5	11.2	541	2	T33312	hypothetical prote	669	50	11.1	436	1	A70409	hypothetical prote
597	50.5	11.2	550	2	G86225	hypothetical prote	670	50	11.1	438	1	HVRKC2	lg mu chain C regi
598	50.5	11.2	561	2	T23564	hypothetical prote	671	50	11.1	456	2	T33822	hypothetical prote
599	50.5	11.2	567	2	B84650	probable selenium-	672	50	11.1	459	2	A25928	cellulase (EC 3.2.
600	50.5	11.2	568	2	T28041	hypothetical prote	673	50	11.1	473	2	B85187	glycoprotein homol
601	50.5	11.2	592	2	S25705	lg mu chain - shee	674	50	11.1	494	2	A48657	monophenol monooxy
602	50.5	11.2	620	2	S05807	SAN1 protein - yea	675	50	11.1	497	2	T15812	o-succinylbenzoate
603	50.5	11.2	624	2	A84150	hypothetical prote	676	50	11.1	497	2	T15812	hypothetical prote
604	50.5	11.2	660	2	S71276	beta-fructofuranos	677	50	11.1	505	2	S39962	endoglucanase - Er
605	50.5	11.2	664	2	B86257	beta-fructosidase	678	50	11.1	512	2	AF3628	nitrate reductase
606	50.5	11.2	683	1	A41785	system b(0,+).amin	679	50	11.1	513	2	T37806	probable flavoprot
607	50.5	11.2	687	2	S56939	probable membrane	680	50	11.1	520	2	C64213	ribose transport s
608	50.5	11.2	688	2	T32750	hypothetical prote	681	50	11.1	522	2	S77073	hypothetical prote
609	50.5	11.2	720	2	B72074	1,4-alpha-glucan b	682	50	11.1	524	2	G64243	hypothetical prote
610	50.5	11.2	720	2	G86549	glucan branching e	683	50	11.1	524	2	S46007	hypothetical prote
611	50.5	11.2	743	2	C56695	transducin-like en	684	50	11.1	568	2	B86400	T17H3.1 protein -
612	50.5	11.2	769	2	T08431	gene bobby sox pro	685	50	11.1	584	1	ALBY	alpha-glucosidase
613	50.5	11.2	795	2	B86247	receptor-like prot	686	50	11.1	584	2	S64627	alpha-glucosidase

687	50	11.1	584	2	S46183	alpha-glucosidase	760	49.5	11.0	264	2	S11650	class II histocomp
688	50	11.1	592	1	S13391	endo-1,4-beta-xyla	761	49.5	11.0	264	2	A30529	H-2 class II histo
689	50	11.1	603	2	S61504	glycogen(starch) s	762	49.5	11.0	264	2	I48422	MHC class II histo
690	50	11.1	605	2	T07123	nine-cis-epoxycaro	763	49.5	11.0	267	2	AC3232	conjugal transfer
691	50	11.1	621	2	T20307	hypothetical prote	764	49.5	11.0	269	2	S61633	YNT20 protein - ye
692	50	11.1	631	2	S67268	hypothetical prote	765	49.5	11.0	278	2	S65006	hypothetical prote
693	50	11.1	672	2	T20310	hypothetical prote	766	49.5	11.0	293	2	G86901	phosphomevalonate
694	50	11.1	676	1	KKHUS	plasma protein S p	767	49.5	11.0	317	2	F70185	hypothetical prote
695	50	11.1	682	2	T18847	hypothetical prote	768	49.5	11.0	319	2	F75420	hypothetical prote
696	50	11.1	710	2	S30154	low-temperature-in	769	49.5	11.0	324	2	S56694	chitinase (BC 3.2.
697	50	11.1	747	1	QRECFE	ferrichrome-iron r	770	49.5	11.0	325	2	A69930	conserved hypothet
698	50	11.1	747	2	B85499	outer membrane rec	771	49.5	11.0	326	2	A28129	sporulation-specif
699	50	11.1	747	2	B90648	outer membrane rec	772	49.5	11.0	328	2	E82324	immunogenic protei
700	50	11.1	750	2	S67100	protein-tyrosine-p	773	49.5	11.0	335	2	G82708	malate dehydrogena
701	50	11.1	758	1	S45477	SBC18 protein - ye	774	49.5	11.0	342	2	S63654	hypothetical COI i
702	50	11.1	758	2	S65169	hypothetical prote	775	49.5	11.0	361	2	T14800	hypothetical prote
703	50	11.1	771	1	WMV29J	ribonucleoside-dip	776	49.5	11.0	371	2	A61275	tubulin alpha-2 ch
704	50	11.1	771	1	WZV2H4	ribonucleoside-dip	777	49.5	11.0	376	2	S45763	hypothetical prote
705	50	11.1	771	2	T28496	ribonucleoside-dip	778	49.5	11.0	387	2	AG3218	acetylornithine de
706	50	11.1	771	2	B36843	ribonucleoside-dip	779	49.5	11.0	411	1	UBCHA	tubulin alpha chai
707	50	11.1	771	2	H72157	L4L protein - vari	780	49.5	11.0	418	2	JC7872	stearyl-CoA 9-des
708	50	11.1	788	2	F96714	probable protease	781	49.5	11.0	426	2	H97765	proline-tRNA ligas
709	50	11.1	813	2	A40601	ferripyoverdine re	782	49.5	11.0	432	2	G71695	conserved hypothet
710	50	11.1	815	2	H83345	ferripyoverdine re	783	49.5	11.0	434	2	AE0226	conserved hypothet
711	50	11.1	857	1	Q08B1L	glycoprotein B - h	784	49.5	11.0	444	2	A56635	tubulin alpha chai
712	50	11.1	879	2	B84765	hypothetical prote	785	49.5	11.0	444	2	S25004	tubulin alpha chai
713	50	11.1	961	2	A55380	faciogenital dyspl	786	49.5	11.0	448	1	UBCHA5	tubulin alpha-5 ch
714	50	11.1	974	2	S15038	cell division cont	787	49.5	11.0	448	2	A25873	tubulin alpha chai
715	50	11.1	1009	2	S61174	hypothetical prote	788	49.5	11.0	448	2	I77427	tubulin alpha chai
716	50	11.1	1046	2	T30199	chitinase (BC 3.2.	789	49.5	11.0	449	2	S00253	tubulin alpha chai
717	50	11.1	1048	2	S64758	SCD25 protein (ver	790	49.5	11.0	449	2	I77428	tubulin alpha chai
718	50	11.1	1139	1	B64234	cytadherence-acces	791	49.5	11.0	450	2	S43138	tubulin alpha chai
719	50	11.1	1145	2	T33606	hypothetical prote	792	49.5	11.0	451	1	UBPGA	tubulin alpha chai
720	50	11.1	1206	2	T30555	nitric-oxide synth	793	49.5	11.0	451	1	UBRTA	tubulin alpha chai
721	50	11.1	1323	2	S27224	N-methyl-D-asparta	794	49.5	11.0	451	2	A23035	tubulin alpha-3 ch
722	50	11.1	1323	2	I78557	N-methyl-D-asparta	795	49.5	11.0	451	2	C24903	tubulin alpha-1 ch
723	50	11.1	1356	1	C45219	N-methyl-D-asparta	796	49.5	11.0	451	2	JC4133	tubulin alpha-1 ch
724	50	11.1	1827	1	UUHU	sucrose alpha-gluc	797	49.5	11.0	451	2	I77403	tubulin alpha-1 ch
725	50	11.1	2279	2	T42531	acetyl-CoA carboxy	798	49.5	11.0	451	2	A24903	tubulin alpha-2 ch
726	50	11.1	2280	2	T38906	acetyl-CoA carboxy	799	49.5	11.0	451	2	B24903	tubulin alpha-2 ch
727	50	11.1	2327	2	T31733	hypothetical prote	800	49.5	11.0	451	2	I77424	tubulin alpha chai
728	50	11.1	2655	2	D96595	probable acetyl-Co	801	49.5	11.0	451	2	I77425	tubulin alpha chai
729	50	11.1	3328	2	T30835	breast cancer tumo	802	49.5	11.0	452	2	A60671	tubulin alpha chai
730	50	11.1	3329	2	T42005	breast cancer susc	803	49.5	11.0	452	2	S11207	tubulin alpha chai
731	50	11.1	3343	2	S44887	ZK112.7 protein -	804	49.5	11.0	477	2	J50597	t-plasminogen acti
732	50	11.1	4131	2	T21085	hypothetical prote	805	49.5	11.0	477	2	F64805	RhA protein (impo
733	50	11.1	4725	1	A44357	dynamin heavy chain	806	49.5	11.0	479	2	F82328	aspartokinase III,
734	49.5	11.0	92	2	S37512	Ig kappa chain V r	807	49.5	11.0	480	2	S38134	probable xanthine
735	49.5	11.0	102	2	B83934	hypothetical prote	808	49.5	11.0	493	2	F95940	hypothetical prote
736	49.5	11.0	119	2	D84845	hypothetical prote	809	49.5	11.0	495	2	T33065	hypothetical prote
737	49.5	11.0	165	2	S68776	myogenin - rainbow	810	49.5	11.0	522	2	T19762	hypothetical prote
738	49.5	11.0	187	2	I84461	MHC HLA-SB beta ch	811	49.5	11.0	529	2	T00677	hypothetical prote
739	49.5	11.0	187	2	T51876	hypothetical prote	812	49.5	11.0	542	2	AH2191	probable purine nu
740	49.5	11.0	207	2	AG2553	beta-phosphoglucom	813	49.5	11.0	543	2	S56830	beta-fructofuranos
741	49.5	11.0	222	2	F96918	MHC class II histo	814	49.5	11.0	562	2	S57951	hypothetical prote
742	49.5	11.0	224	1	HLHUS1	MHC class II lymph	815	49.5	11.0	608	2	T18437	noncaspase protein
743	49.5	11.0	224	2	I68751	MHC class II histo	816	49.5	11.0	620	1	UYVPAP	probable serine pr
744	49.5	11.0	229	2	A28909	MHC class II histo	817	49.5	11.0	632	2	D84921	similar to xli 1 p
745	49.5	11.0	232	1	HLMS92	H-2 class II histo	818	49.5	11.0	638	2	E84799	beta-fructofuranos
746	49.5	11.0	233	2	I55654	MHC class II prote	819	49.5	11.0	639	2	S71268	tumor cell suppres
747	49.5	11.0	237	2	A21200	H-2 class II histo	820	49.5	11.0	645	2	A49013	cysteine proteinas
748	49.5	11.0	241	2	I48657	I-E(b-beta) protei	821	49.5	11.0	658	2	T08153	envelope protein -
749	49.5	11.0	243	2	A53506	folate receptor ty	822	49.5	11.0	669	2	A46511	catalase (EC 1.11.
750	49.5	11.0	244	2	C90580	DNA processing pro	823	49.5	11.0	686	2	D96447	probable membrane
751	49.5	11.0	258	1	HLHDPB	MHC class II histo	824	49.5	11.0	728	2	A96652	amine oxidase (cop
752	49.5	11.0	258	1	HLHUS2	MHC class II histo	825	49.5	11.0	760	2	S19374	glucose-6-phosphat
753	49.5	11.0	258	2	I54458	MHC class II histo	826	49.5	11.0	762	2	A54411	cellobiose oxidase
754	49.5	11.0	258	2	I59621	HLA-DPB1 - human	827	49.5	11.0	763	2	A47563	beta-1 integrin su
755	49.5	11.0	261	2	AH2960	ABC transporter, m	828	49.5	11.0	770	2	S60676	nerve growth facto
756	49.5	11.0	261	2	F98322	nitrate transport	829	49.5	11.0	773	2	I46059	beta-1 integrin su
757	49.5	11.0	261	2	T11525	cytochrome-c oxida	830	49.5	11.0	790	1	TVHUTT	gastric mucin MUC5
758	49.5	11.0	264	1	HLMSB1	H-2 class II histo	831	49.5	11.0	850	2	S56015	nitrate reductase
759	49.5	11.0	264	1	HLMSB2	H-2 class II histo	832	49.5	11.0	859	2	S70584	

833	49.5	11.0	859	2	AE2217	hypotheical prote	906	49	10.9	362	2	TS2038	probable phytochel
834	49.5	11.0	868	1	JC4283	nitrate reductase	907	49	10.9	363	2	S56273	probable membrane
835	49.5	11.0	877	2	C46356	env polyprotein -	908	49	10.9	377	2	S67448	hypotheical prote
836	49.5	11.0	942	2	T37539	probable guanine n	909	49	10.9	385	2	A86165	protein F15K9.6 [i
837	49.5	11.0	985	2	B86084	hypotheical prote	910	49	10.9	389	2	S08031	nucleocapsid prote
838	49.5	11.0	997	2	S4457	period clock prote	911	49	10.9	393	1	HVRK1	Ig mu chain C regi
839	49.5	11.0	1028	2	G96769	unknown protein F9	912	49	10.9	410	2	I50494	serine proteinase
840	49.5	11.0	1030	2	T16114	hypotheical prote	913	49	10.9	426	2	I36948	Ig epsilon-chain -
841	49.5	11.0	1043	2	F97302	hypotheical prote	914	49	10.9	427	1	T49031	acid phosphatase (
842	49.5	11.0	1082	2	T31112	hypotheical prote	915	49	10.9	428	2	S22377	aspartate transami
843	49.5	11.0	1131	2	S22266	ATPase 2 (EC 3.6.1	916	49	10.9	438	1	HVRKCS	Ig mu chain C regi
844	49.5	11.0	1181	2	C86349	FUN30 protein - Ye	917	49	10.9	444	2	C84789	hypotheical prote
845	49.5	11.0	1237	2	A54080	protein-tyrosine-p	918	49	10.9	444	2	JC1141	metacyclic-form-sp
846	49.5	11.0	1377	2	E86034	rhsA protein in rh	919	49	10.9	461	1	HVRK1	Ig mu chain C regi
847	49.5	11.0	1377	2	C65159	rhsA protein precu	920	49	10.9	461	2	A31820	thyroid hormone re
848	49.5	11.0	1394	2	H91236	RhsC core protein	921	49	10.9	462	2	H64145	hypotheical prote
849	49.5	11.0	1397	2	A85570	RhsC protein in rh	922	49	10.9	472	2	E81784	glutamate-ammonia
850	49.5	11.0	1397	2	C64805	rhsC protein precu	923	49	10.9	472	2	F81208	neuroblast prolif
851	49.5	11.0	1399	2	A99720	RhsC core protein	924	49	10.9	474	2	A40721	testosterone 7alph
852	49.5	11.0	1402	2	F84480	probable retroelem	925	49	10.9	492	2	A34272	conserved hypotet
853	49.5	11.0	1409	2	F91187	rhsA core protein	926	49	10.9	510	2	T44810	conserved hypotet
854	49.5	11.0	1411	2	E65145	rhsB protein precu	927	49	10.9	510	2	H69893	nitrate reductase
855	49.5	11.0	1590	2	B86398	protein T7N9.24 [i	928	49	10.9	513	2	F83162	NADH2 dehydrogen
856	49.5	11.0	1661	2	T31330	head-activator bin	929	49	10.9	513	2	E71583	carboxypeptidase C
857	49.5	11.0	1677	2	T46095	hypotheical prote	930	49	10.9	523	1	S61713	cholesterol monoox
858	49.5	11.0	1677	2	T14267	Xin protein, stage	931	49	10.9	526	1	A34164	xylan 1,4-beta-xy
859	49.5	11.0	1711	2	T21432	hypotheical prote	932	49	10.9	536	2	G64752	receptor-like prot
860	49.5	11.0	1908	2	T42707	hypotheical prote	933	49	10.9	552	2	T04653	hypotheical prote
861	49.5	11.0	2123	2	F86348	hypotheical prote	934	49	10.9	558	2	T02704	regulatory protein
862	49.5	11.0	2330	1	PR1WV	genome polyprotein	935	49	10.9	562	2	S16594	hypotheical prote
863	49.5	11.0	2331	2	T09144	genome polyprotein	936	49	10.9	605	2	T27397	hypotheical prote
864	49.5	11.0	2559	2	S44054	probable guanine n	937	49	10.9	611	2	T03890	hypotheical prote
865	49.5	11.0	2957	2	T33152	hypotheical prote	938	49	10.9	613	2	T15489	probable exonuclea
866	49.5	11.0	4307	2	T20721	hypotheical prote	939	49	10.9	623	2	T39001	probable RNA-bind
867	49	10.9	55	2	AD1852	hypotheical prote	940	49	10.9	626	2	H96810	hypotheical prote
868	49	10.9	77	2	G28840	Ig kappa chain V r	941	49	10.9	649	2	S67787	beta-fructofuran
869	49	10.9	89	2	F69268	hypotheical prote	942	49	10.9	651	2	T12083	probable formyl tr
870	49	10.9	101	1	ARRA3	allergen Ra3 - com	943	49	10.9	667	2	AD0295	plasma protein S p
871	49	10.9	107	2	S57444	Ig kappa chain V-J	944	49	10.9	675	1	KXMS	meprin A (EC 3.4.2
872	49	10.9	111	1	CCTO	cytochrome c [vali	945	49	10.9	700	1	HYHMB	env polyprotein pr
873	49	10.9	128	2	T40464	probable RNA bind	946	49	10.9	712	1	VCLJSA	WD-40 repeat regul
874	49	10.9	130	2	A82853	hypotheical prote	947	49	10.9	713	2	JN0133	hypotheical prote
875	49	10.9	135	1	CBRTSM	cytochrome b5, out	948	49	10.9	779	2	C96805	hypotheical prote
876	49	10.9	157	2	S73704	hypotheical prote	949	49	10.9	802	2	T21464	hypotheical prote
877	49	10.9	158	2	B86169	hypotheical prote	950	49	10.9	843	2	S44868	kinesin heavy chai
878	49	10.9	175	2	JC5971	alpha-b crystallin	951	49	10.9	848	2	S48273	probable transcrip
879	49	10.9	213	2	G86195	hypotheical prote	952	49	10.9	849	2	I50617	protein-tyrosine k
880	49	10.9	226	2	AH1138	conserved hypotet	953	49	10.9	859	1	VCLJST	env polyprotein pr
881	49	10.9	228	2	B90369	hypotheical prote	954	49	10.9	860	1	C35905	endopeptidase Clp
882	49	10.9	234	2	D84768	hypotheical prote	955	49	10.9	874	2	JC4930	S-layer protein pr
883	49	10.9	239	2	S14470	asparagine-rich pr	956	49	10.9	876	2	G90592	hypotheical prote
884	49	10.9	247	1	QOBER1	B25R protein - vac	957	49	10.9	886	2	A57172	probable hormone r
885	49	10.9	259	2	F42528	probable rare lipo	958	49	10.9	887	2	T11566	envelope glycoprot
886	49	10.9	263	2	G82259	tenascin - chicken	959	49	10.9	905	2	G83314	NADH dehydrogenase
887	49	10.9	274	2	I50682	tenascin - chicken	960	49	10.9	927	2	F82818	conserved hypotet
888	49	10.9	285	1	YXERIC	isochorismatase (E	961	49	10.9	944	2	T41711	probable alpha-tre
889	49	10.9	285	2	F85558	isochorismatase (E	962	49	10.9	953	2	A86351	hypotheical prote
890	49	10.9	285	2	B90708	isochorismatase (E	963	49	10.9	1031	1	A38713	kinesin heavy chai
891	49	10.9	289	2	T12682	hypotheical prote	964	49	10.9	1089	2	T21582	hypotheical prote
892	49	10.9	294	2	S39606	class I histocompa	965	49	10.9	1143	2	T10636	hypotheical prote
893	49	10.9	294	2	G84504	probable VSR-1-lik	966	49	10.9	1191	1	A44051	DNA-binding protei
894	49	10.9	295	2	T22039	hypotheical prote	967	49	10.9	1193	2	G71605	hypotheical prote
895	49	10.9	301	2	S51439	hypotheical prote	968	49	10.9	1217	2	F97177	alpha-glucosidase
896	49	10.9	311	2	F83695	hypotheical prote	969	49	10.9	1250	2	S14177	SCD25 protein (ver
897	49	10.9	319	2	A72284	oligopeptide ABC t	970	49	10.9	1391	2	T20406	hypotheical prote
898	49	10.9	328	2	I51215	inhibin alpha-subu	971	49	10.9	1441	2	A86685	prophage p11 prote
899	49	10.9	328	2	T25231	hypotheical prote	972	49	10.9	1456	1	A36563	mannose receptor p
900	49	10.9	337	2	T15071	hypotheical prote	973	49	10.9	1463	2	C86482	protein F5J5.1 [im
901	49	10.9	343	2	S44834	F54H12.3 protein -	974	49	10.9	1524	2	S68553	surface layer prot
902	49	10.9	343	2	T27230	hypotheical prote	975	49	10.9	1844	2	D71612	hypotheical prote
903	49	10.9	354	1	S00574	alkanal monooxygen	976	49	10.9	2274	2	T30258	adenomatous polyo
904	49	10.9	356	2	B84495	En/Spm-like transp	977	49	10.9	2301	1	GNNYTN	genome polyprotein
905	49	10.9	358	2	F84053	transcription regu	978	49	10.9	2670	2	T37919	GCN1 homolog - fl

979	49	10.9	2704	2	S09118	G surface protein	1052	48.5	10.8	704	2	C81542	conserved hypothet
980	49	10.9	3848	2	T17414	TipC protein - sli	1053	48.5	10.8	704	2	B81051	hypothetical prote
981	49	10.9	4572	2	S57908	hypothetical 577K	1054	48.5	10.8	709	2	G83376	catalase HPII PA21
982	49	10.9	6642	2	T29757	protein UNC-89 - C	1055	48.5	10.8	726	2	A10147	probable ATP-depen
983	48.5	10.8	108	2	S30521	Ig kappa chain V r	1056	48.5	10.8	740	2	B81823	hypothetical prote
984	48.5	10.8	110	2	S22890	T-cell receptor al	1057	48.5	10.8	745	2	T12518	hypothetical prote
985	48.5	10.8	111	2	S57889	T cell receptor Er	1058	48.5	10.8	750	2	S55180	phospholipase D ho
986	48.5	10.8	114	2	S46375	Ig kappa chain V-J	1059	48.5	10.8	787	2	S54535	hypothetical prote
987	48.5	10.8	122	2	AE1477	hypothetical prote	1060	48.5	10.8	798	2	A28193	integrin beta-1 ch
988	48.5	10.8	128	2	S40345	Ig kappa chain V-J	1061	48.5	10.8	803	1	IJCH3	integrin band 3 p
989	48.5	10.8	132	2	S23374	T-cell receptor al	1062	48.5	10.8	807	2	B71605	hypothetical prote
990	48.5	10.8	153	2	JC5854	polyketide synthas	1063	48.5	10.8	811	2	T17863	valine-CRNA ligase
991	48.5	10.8	159	2	B84669	hypothetical prote	1064	48.5	10.8	814	2	B71675	vitellin-CRNA ligase
992	48.5	10.8	210	2	T27168	hypothetical prote	1065	48.5	10.8	823	2	B81282	probable integral
993	48.5	10.8	217	2	C86350	protein F8K7.12 [i	1066	48.5	10.8	830	2	A30359	P-selectin precurs
994	48.5	10.8	218	2	AB1764	late competence pr	1067	48.5	10.8	833	1	A31593	heat shock transcr
995	48.5	10.8	230	2	S09778	hypothetical prote	1068	48.5	10.8	835	2	T30030	hypothetical prote
996	48.5	10.8	236	2	B88923	protein W03F9.2 [i	1069	48.5	10.8	862	2	T49593	hypothetical prote
997	48.5	10.8	243	2	E37386	hypothetical prote	1070	48.5	10.8	863	2	F85343	hypothetical prote
998	48.5	10.8	243	2	S01923	hypothetical prote	1071	48.5	10.8	914	2	S46593	finger protein AZP
999	48.5	10.8	263	2	P84849	hypothetical prote	1072	48.5	10.8	949	2	T29334	hypothetical prote
1000	48.5	10.8	284	2	I56056	MHC E-beta-f - mou	1073	48.5	10.8	955	2	T21612	hypothetical prote
1001	48.5	10.8	274	2	T16003	hypothetical prote	1074	48.5	10.8	958	2	S64249	hypothetical prote
1002	48.5	10.8	276	2	JC4161	probable chloride	1075	48.5	10.8	989	2	C83035	hypothetical prote
1003	48.5	10.8	300	2	JC4367	NAD(P)-arginine AD	1076	48.5	10.8	1068	2	G86452	hypothetical prote
1004	48.5	10.8	302	1	ORB915	replication protei	1077	48.5	10.8	1121	2	S54504	hypothetical prote
1005	48.5	10.8	319	2	AH2062	aldo/keto reductas	1078	48.5	10.8	1167	2	T42704	hypothetical prote
1006	48.5	10.8	320	2	S59947	chitinase [EC 3.2.	1079	48.5	10.8	1199	2	A40670	nuclear envelope p
1007	48.5	10.8	320	2	T72421	oligopeptide ABC t	1080	48.5	10.8	1364	2	T00250	MEGF2 protein - hu
1008	48.5	10.8	331	2	G96785	protein F10A5.24 [1081	48.5	10.8	1400	2	T31555	hypothetical prote
1009	48.5	10.8	333	2	G95380	probable periplasm	1082	48.5	10.8	1403	2	T11583	probable translati
1010	48.5	10.8	337	2	S24222	CD44 protein - hum	1083	48.5	10.8	1487	1	CGH06C	collagen alpha 1(I
1011	48.5	10.8	341	2	S51766	dioxygenase - eggp	1084	48.5	10.8	1560	2	T00080	hypothetical prote
1012	48.5	10.8	343	2	T45987	hypothetical prote	1085	48.5	10.8	1589	2	T13826	translation initia
1013	48.5	10.8	358	2	AH1376	hypothetical prote	1086	48.5	10.8	1630	2	A53577	ascites siatoglyco
1014	48.5	10.8	360	2	T18529	protein phosphatas	1087	48.5	10.8	1770	2	S56221	hypothetical prote
1015	48.5	10.8	372	2	I52196	homeobox transcrip	1088	48.5	10.8	1804	2	H96597	hypothetical prote
1016	48.5	10.8	380	2	T09661	ascorbate oxidase	1089	48.5	10.8	2254	2	D86215	protein T6D22.14 [
1017	48.5	10.8	393	2	T23041	hypothetical prote	1090	48.5	10.8	2386	1	FNHU	fibronectin precur
1018	48.5	10.8	421	2	A56550	Krox-20 - African	1091	48.5	10.8	3511	2	A59295	unconventional myo
1019	48.5	10.8	428	2	S22379	aspartate transami	1092	48	10.7	99	2	B53116	Ig epsilon chain C
1020	48.5	10.8	433	2	S77340	hypothetical prote	1093	48	10.7	103	2	T50954	hypothetical prote
1021	48.5	10.8	446	2	T03021	mitosis-specific c	1094	48	10.7	108	1	K1HUHU	Ig kappa chain V-I
1022	48.5	10.8	446	2	A26724	tubulin alpha-2 ch	1095	48	10.7	111	1	CCMB	cytochrome c - mun
1023	48.5	10.8	433	2	T48240	hypothetical prote	1096	48	10.7	112	1	CCRZ	cytochrome c [vali
1024	48.5	10.8	458	2	AC1632	chromosome replica	1097	48	10.7	112	2	S22891	T-cell receptor al
1025	48.5	10.8	459	2	B86446	glycerol-3-phospha	1098	48	10.7	112	2	S64448	hypothetical prote
1026	48.5	10.8	462	2	B86262	F13K23.11 protein	1099	48	10.7	115	2	E53116	Ig epsilon chain C
1027	48.5	10.8	473	2	A10587	deoxyribodipyrimid	1100	48	10.7	118	2	S61051	hypothetical prote
1028	48.5	10.8	473	2	S22321	deoxyribodipyrimid	1101	48	10.7	136	2	C53116	Ig epsilon chain C
1029	48.5	10.8	482	2	S60757	catalase (EC 1.11.	1102	48	10.7	134	2	S53074	hypothetical prote
1030	48.5	10.8	487	2	S42442	nuclear protein EB	1103	48	10.7	138	2	T34049	hypothetical prote
1031	48.5	10.8	499	2	A49388	catalase (EC 1.11.	1104	48	10.7	145	2	T48552	glutaredoxin-like
1032	48.5	10.8	502	2	A48678	differentiated ker	1105	48	10.7	151	2	S21987	probable heme-bind
1033	48.5	10.8	514	2	T11859	cytochrome-c oxida	1106	48	10.7	151	2	S17326	probable heme-bind
1034	48.5	10.8	518	2	T05196	hypothetical prote	1107	48	10.7	151	2	S17322	probable heme-bind
1035	48.5	10.8	524	2	T27177	catalase (EC 1.11.	1108	48	10.7	160	2	T29392	hypothetical prote
1036	48.5	10.8	535	2	D96586	hypothetical prote	1109	48	10.7	185	2	H90355	hypothetical prote
1037	48.5	10.8	547	2	T39250	hypothetical prote	1110	48	10.7	189	2	A12534	transposase all756
1038	48.5	10.8	586	2	T20816	hypothetical prote	1111	48	10.7	198	1	A06620	prolactin - green
1039	48.5	10.8	590	2	I39685	polyhydroxyalkanoi	1112	48	10.7	213	1	JX0295	ribonuclease (EC 3
1040	48.5	10.8	596	2	T26950	hypothetical prote	1113	48	10.7	217	2	F82612	hypothetical prote
1041	48.5	10.8	601	2	T47249	nuclear envelope p	1114	48	10.7	219	2	PC4203	Ig kappa chain (mo
1042	48.5	10.8	608	2	T14731	glycogen(starch) s	1115	48	10.7	226	2	AG1496	conserved hypothet
1043	48.5	10.8	624	2	T48587	peptide transporte	1116	48	10.7	227	2	PH1215	Ig epsilon chain C
1044	48.5	10.8	641	2	S41439	gene NS-1 protein	1117	48	10.7	228	2	S03050	Ig gamma chain (cl
1045	48.5	10.8	650	2	S75072	probable phytoene	1118	48	10.7	236	2	T45067	hypothetical prote
1046	48.5	10.8	653	2	B82872	transketolase I UU	1119	48	10.7	242	2	S60143	cellulase (EC 3.2.
1047	48.5	10.8	665	2	T46570	dosage-dependent c	1120	48	10.7	243	2	PH1216	Ig epsilon chain C
1048	48.5	10.8	679	2	S90560	hypothetical prote	1121	48	10.7	246	2	T32510	hypothetical prote
1049	48.5	10.8	690	2	F97164	flagellar biosynth	1122	48	10.7	258	1	DHMS	Ig delta chain C r
1050	48.5	10.8	695	2	B72129	probable outer mem	1123	48	10.7	262	1	JQ1738	coat protein - sha
1051	48.5	10.8	695	2	F86493	probable outer mem	1124	48	10.7	263	2	T43629	hypothetical prote

1125	48	10.7	278	2	S29615	whiG protein - Str	1198	48	10.7	534	2	T23305	hypothetical prote
1126	48	10.7	280	2	E96589	hypothetical prote	1199	48	10.7	543	2	T48239	hypothetical prote
1127	48	10.7	285	2	I51412	hypothetical trans	1200	48	10.7	546	2	AF2268	type II site-speci
1128	48	10.7	289	2	S48664	distal-less 3 prot	1201	48	10.7	553	2	A47504	epoxide hydrolase
1129	48	10.7	289	2	I53082	homeoprotein - rat	1202	48	10.7	554	2	A47503	epoxide hydrolase
1130	48	10.7	291	1	DHMSM	Ig delta chain C r	1203	48	10.7	566	2	S50979	RHC21 protein - ye
1131	48	10.7	294	2	G85474	homeodomain-like P	1204	48	10.7	573	2	B86247	hypothetical prote
1132	48	10.7	301	2	T06112	homeotic protein T	1205	48	10.7	578	2	T41715	hypothetical prote
1133	48	10.7	307	2	AF3239	conserved hypotet	1206	48	10.7	582	2	S37047	beta-fructofuranos
1134	48	10.7	309	2	B84550	hypothetical prote	1207	48	10.7	587	2	D84426	hypothetical prote
1135	48	10.7	316	2	T74129	hypothetical prote	1208	48	10.7	591	2	T48395	GR2-like protein -
1136	48	10.7	317	2	T24468	hypothetical prote	1209	48	10.7	595	2	B86798	prophage p13 prote
1137	48	10.7	318	1	S75765	stearyl-CoA 9-des	1210	48	10.7	601	2	S27777	80K protein (allel
1138	48	10.7	319	2	AE1469	other protein homo	1211	48	10.7	604	2	T08302	hypothetical prote
1139	48	10.7	321	2	S75026	hypothetical prote	1212	48	10.7	605	2	H86640	protein F52C12.2 [
1140	48	10.7	334	2	T47693	hypothetical prote	1213	48	10.7	607	2	T24172	hypothetical prote
1141	48	10.7	342	2	T29557	hypothetical prote	1214	48	10.7	614	2	T29937	hypothetical prote
1142	48	10.7	348	2	B83920	hypothetical prote	1215	48	10.7	621	2	S35092	plakoglobin - mous
1143	48	10.7	351	2	T32093	hypothetical prote	1216	48	10.7	625	2	T06184	sucrose-fructan 6-
1144	48	10.7	355	2	C39725	hypothetical prote	1217	48	10.7	642	2	T15708	hypothetical prote
1145	48	10.7	363	2	A56940	integral membrane	1218	48	10.7	644	2	JQ0160	3-isopropylmalate
1146	48	10.7	367	2	AF1188	hypothetical prote	1219	48	10.7	656	2	T38741	major facilitator
1147	48	10.7	369	1	S57525	alcohol dehydrogen	1220	48	10.7	670	2	T28391	ORF MSV230 hypot
1148	48	10.7	369	2	B71624	hypothetical prote	1221	48	10.7	703	2	T12696	NADH2 dehydrogenas
1149	48	10.7	375	2	T39329	hypothetical prote	1222	48	10.7	717	2	T06041	hypothetical prote
1150	48	10.7	377	2	F72165	Al17L protein - var	1223	48	10.7	717	2	E86812	sugar hydrolase [i
1151	48	10.7	377	2	T28558	hypothetical prote	1224	48	10.7	719	2	T00266	hypothetical prote
1152	48	10.7	379	2	H36849	Al6L protein - var	1225	48	10.7	724	2	D96949	secreted protein c
1153	48	10.7	379	2	H82284	queuine tRNA-ribos	1226	48	10.7	731	2	B86132	hypothetical prote
1154	48	10.7	380	1	S73751	high affinity tran	1227	48	10.7	732	1	EKHUX	protein-glutamine
1155	48	10.7	382	2	T19869	hypothetical prote	1228	48	10.7	735	2	G91290	hypothetical prote
1156	48	10.7	394	2	AH1858	3-dehydroquinat s	1229	48	10.7	745	2	D84661	F14M2.9 protein -
1157	48	10.7	408	2	T38386	hypothetical wd-40	1230	48	10.7	758	2	S54522	hypothetical prote
1158	48	10.7	408	2	T34467	hypothetical prote	1231	48	10.7	792	1	A39914	dipeptidyl-peptida
1159	48	10.7	409	2	S40740	cyclin A homolog -	1232	48	10.7	872	2	S73785	DNA polymerase III
1160	48	10.7	412	2	G82406	long-chain fatty a	1233	48	10.7	914	1	S07047	iodide peroxidase
1161	48	10.7	417	2	S44062	phosphoglycerate k	1234	48	10.7	915	2	T03589	probable aspartate
1162	48	10.7	417	2	H96733	hypothetical prote	1235	48	10.7	919	2	T16459	hypothetical prote
1163	48	10.7	417	2	T33376	hypothetical prote	1236	48	10.7	940	2	D89723	protein F3908.1b [
1164	48	10.7	418	2	T25092	hypothetical prote	1237	48	10.7	945	2	T21998	hypothetical prote
1165	48	10.7	420	2	C86197	hypothetical prote	1238	48	10.7	961	2	S67568	probable membrane
1166	48	10.7	421	2	T33523	hypothetical prote	1239	48	10.7	962	2	JC5808	G protein-coupled
1167	48	10.7	426	2	H71636	3-oxoacyl-facyl-ca	1240	48	10.7	992	2	T38817	hypothetical prote
1168	48	10.7	428	1	EHHU	Ig epsilon chain C	1241	48	10.7	1035	2	T13962	sodium bicarbonate
1169	48	10.7	430	2	JC5125	aspartate transami	1242	48	10.7	1062	2	G86325	hypothetical prote
1170	48	10.7	430	2	D70193	hypothetical prote	1243	48	10.7	1070	2	F90106	IAP100 protein [im
1171	48	10.7	430	2	A65215	hypothetical 49.4	1244	48	10.7	1079	2	T14031	sodium bicarbonate
1172	48	10.7	435	2	E86266	protein F3F19.23 [1245	48	10.7	1093	1	S50614	regulatory protein
1173	48	10.7	435	2	S52203	vaf-1 protein - to	1246	48	10.7	1096	2	A96607	protein disease re
1174	48	10.7	436	2	T07816	S-locus-specific g	1247	48	10.7	1172	2	AD3110	hypothetical prote
1175	48	10.7	437	2	S11925	S-locus-specific g	1248	48	10.7	1215	2	C84848	hypothetical prote
1176	48	10.7	438	1	S11325	transcription fact	1249	48	10.7	1261	2	E59430	PTP41-associated R
1177	48	10.7	440	2	C71863	probable aminotran	1250	48	10.7	1341	2	S66835	probable membrane
1178	48	10.7	440	2	E64570	nifs-like protein	1251	48	10.7	1480	2	T05566	hypothetical prote
1179	48	10.7	440	2	T26471	CAP59 protein - Cr	1252	48	10.7	1583	2	F86366	protein F2F24.8 [
1180	48	10.7	458	2	A56055	glycerol-3-phospho	1253	48	10.7	1606	2	T34073	paranemin - chicke
1181	48	10.7	459	1	S31083	endo-xylanase homo	1254	48	10.7	1635	2	A10452	hemolysin [impor
1182	48	10.7	462	2	T17480	paired box transcr	1255	48	10.7	1795	2	T30332	avirulence protein
1183	48	10.7	479	1	S15031	hypothetical prote	1256	48	10.7	1840	2	T29091	transit-in - chicke
1184	48	10.7	482	2	S55950	hypothetical prote	1257	48	10.7	2004	2	T30185	hypothetical prote
1185	48	10.7	484	2	G82825	leucine aminopepti	1258	48	10.7	2109	1	ZLVNJJ	genome polypotein
1186	48	10.7	501	2	D88548	protein ZK507.6 [i	1259	48	10.7	2303	1	GNNYTM	genome polypotein
1187	48	10.7	501	2	T39801	hypothetical sh3-c	1260	48	10.7	2485	1	H71621	serine/threonine-s
1188	48	10.7	503	2	A84434	Mutator-like trans	1261	48	10.7	2630	2	T08868	polypotein P1 - A
1189	48	10.7	505	2	T15159	hypothetical prote	1262	48	10.7	2902	2	C71953	toxin-like outer m
1190	48	10.7	506	2	A99252	hypothetical prote	1263	48	10.7	4563	1	LPHUB	apolipoprotein B-1
1191	48	10.7	506	2	AC3034	hypothetical prote	1264	48	10.7	4639	1	A54794	dynamin heavy chain
1192	48	10.7	515	2	AF2321	hypothetical prote	1265	48	10.7	6831	2	A88852	protein unc-22 [im
1193	48	10.7	517	2	I40798	cellulase [EC 3.2.	1266	48	10.7	6839	2	S57242	twitchin [similar
1194	48	10.7	525	2	T47409	hypothetical prote	1267	48	10.7	7160	2	T27935	hypothetical prote
1195	48	10.7	525	2	T23304	hypothetical prote	1268	47.5	10.6	76	2	B88318	protein age-1 [imp
1196	48	10.7	532	2	C97228	probable peptide A	1269	47.5	10.6	85	2	A42056	ribosomal protein
1197	48	10.7	532	2	T49467	related to CopI-in	1270	47.5	10.6	92	2	S37516	Ig kappa chain V r

1271	10.6	47.5	10.6	108	2	S34007	Ig kappa chain V r	1344	47.5	10.6	450	2	A56622	tubulin alpha chai
1272	10.6	47.5	10.6	114	2	S54905	Ig kappa chain V r	1345	47.5	10.6	450	2	I77426	tubulin alpha chai
1273	10.6	47.5	10.6	118	2	S21918	T-cell receptor al	1346	47.5	10.6	450	2	S52152	tubulin alpha chai
1274	10.6	47.5	10.6	129	2	JC2144	lysozyme (EC 3.2.1	1347	47.5	10.6	451	2	A48433	tubulin alpha chai
1275	10.6	47.5	10.6	156	1	WZB525	gene 25 protein -	1348	47.5	10.6	451	2	S43425	tubulin alpha chai
1276	10.6	47.5	10.6	161	1	UBURAL	tubulin alpha chai	1349	47.5	10.6	451	2	F97337	uncharacterized se
1277	10.6	47.5	10.6	172	2	AG3532	D-lactate dehydrog	1350	47.5	10.6	452	2	S42033	tubulin alpha chai
1278	10.6	47.5	10.6	177	2	C42463	hypothetical prote	1351	47.5	10.6	473	1	RGBYM3	regulatory protein
1279	10.6	47.5	10.6	197	2	T19892	hypothetical prote	1352	47.5	10.6	488	1	WMBE42	RNA-binding protei
1280	10.6	47.5	10.6	222	2	F64757	membrane protein y	1353	47.5	10.6	489	2	S23410	FUN19 protein - ye
1281	10.6	47.5	10.6	227	2	B37206	class II histocomp	1354	47.5	10.6	493	2	H69634	glutamate synthase
1282	10.6	47.5	10.6	231	2	S62530	hypothetical prote	1355	47.5	10.6	500	2	JC7668	dipeptidyl-peptida
1283	10.6	47.5	10.6	239	2	H81674	ubiquinone/menaqui	1356	47.5	10.6	513	2	T20068	hypothetical prote
1284	10.6	47.5	10.6	240	2	A61544	tubulin alpha chai	1357	47.5	10.6	513	2	A41504	structural protein
1285	10.6	47.5	10.6	244	2	B64220	tRNA-pseudouridine	1358	47.5	10.6	514	2	T10974	cytochrome-c oxida
1286	10.6	47.5	10.6	252	2	A86449	hypothetical prote	1359	47.5	10.6	518	2	S50465	PAC2 protein - yea
1287	10.6	47.5	10.6	256	2	S02855	class II histocomp	1360	47.5	10.6	527	2	S64060	probable membrane
1288	10.6	47.5	10.6	267	2	B64644	hypothetical prote	1361	47.5	10.6	534	2	T41081	hypothetical prote
1289	10.6	47.5	10.6	274	1	B64065	3',5'-cyclic-nucle	1362	47.5	10.6	537	2	A23770	asparagine-rich pr
1290	10.6	47.5	10.6	275	1	AG0889	3',5'-cyclic-nucle	1363	47.5	10.6	550	2	B84900	hypothetical prote
1291	10.6	47.5	10.6	278	2	H71119	hypothetical prote	1364	47.5	10.6	551	2	T02752	probable lactase (
1292	10.6	47.5	10.6	280	2	H81038	conserved hypotet	1365	47.5	10.6	562	2	H82077	type IV pilus asse
1293	10.6	47.5	10.6	291	2	A81696	stationary-phase s	1366	47.5	10.6	568	2	S70873	tapB protein - Aer
1294	10.6	47.5	10.6	291	2	B70562	hypothetical prote	1367	47.5	10.6	571	2	S24789	orphan nuclear hor
1295	10.6	47.5	10.6	294	2	S68784	cathepsin L - Para	1368	47.5	10.6	579	2	A57057	Jararagin C precu
1296	10.6	47.5	10.6	294	2	S36932	chitinase (EC 3.2.	1369	47.5	10.6	582	1	BNRT3S	myelin-associated
1297	10.6	47.5	10.6	309	2	T52453	ATP-dependent Clp	1370	47.5	10.6	591	2	T30895	sugar transport pr
1298	10.6	47.5	10.6	310	2	T52041	probable ATP-depen	1371	47.5	10.6	605	1	S07314	glycogen(starch) s
1299	10.6	47.5	10.6	312	2	AG1789	secreted protein w	1372	47.5	10.6	614	1	S36173	fragile X mental r
1300	10.6	47.5	10.6	314	2	E70116	hypothetical prote	1373	47.5	10.6	618	2	T20450	hypothetical prote
1301	10.6	47.5	10.6	318	2	S23155	envelope glycoprot	1374	47.5	10.6	626	1	BNRT3	myelin-associated
1302	10.6	47.5	10.6	319	1	S61150	thioredoxin-disulf	1375	47.5	10.6	629	2	T48940	hypothetical prote
1303	10.6	47.5	10.6	321	2	S57482	chitinase class 1	1376	47.5	10.6	632	1	A40724	beta-fructofuranos
1304	10.6	47.5	10.6	321	2	A85829	chitinase	1377	47.5	10.6	636	1	S31157	beta-fructofuranos
1305	10.6	47.5	10.6	321	2	F90983	glucose synthetase	1378	47.5	10.6	636	1	S31155	myelin-associated
1306	10.6	47.5	10.6	322	2	T28190	hypothetical prote	1379	47.5	10.6	637	2	S33785	gene NS-1 protein
1307	10.6	47.5	10.6	325	2	AC1047	lysine-tRNA ligase	1380	47.5	10.6	641	2	S41434	protein T0881.1 [i
1308	10.6	47.5	10.6	326	2	A45452	transcription fact	1381	47.5	10.6	644	2	T15652	hypothetical prote
1309	10.6	47.5	10.6	326	2	T33343	hypothetical prote	1382	47.5	10.6	648	2	E88960	probable homeodoma
1310	10.6	47.5	10.6	330	2	G91204	hypothetical prote	1383	47.5	10.6	680	2	H84774	hypothetical prote
1311	10.6	47.5	10.6	330	2	H95166	transcription regu	1384	47.5	10.6	680	2	T25832	env polypeptide -
1312	10.6	47.5	10.6	334	2	T03157	probable capsid as	1385	47.5	10.6	688	2	A43491	hypothetical prote
1313	10.6	47.5	10.6	334	2	S25785	hypothetical prote	1386	47.5	10.6	688	2	A12516	tran protein homol
1314	10.6	47.5	10.6	334	2	T17213	hypothetical prote	1387	47.5	10.6	704	2	T31227	enhancer-of-zeste
1315	10.6	47.5	10.6	339	2	S39979	chitinase (EC 3.2.	1388	47.5	10.6	746	2	G02838	hypothetical prote
1316	10.6	47.5	10.6	340	2	S40414	chitinase (EC 3.2.	1389	47.5	10.6	752	2	S23818	hypothetical prote
1317	10.6	47.5	10.6	342	1	S48948	thioredoxin-disulf	1390	47.5	10.6	758	2	D71072	transcription regu
1318	10.6	47.5	10.6	346	2	T27812	hypothetical prote	1391	47.5	10.6	769	2	C83710	endopeptidase Ia (
1319	10.6	47.5	10.6	355	2	D71429	hypothetical prote	1392	47.5	10.6	795	1	A70322	conserved domain p
1320	10.6	47.5	10.6	367	2	A86051	hypothetical prote	1393	47.5	10.6	802	2	C95136	sucrose synthase (
1321	10.6	47.5	10.6	371	2	B83900	gentisate 1,2-diox	1394	47.5	10.6	804	1	YUMU	microbial serine p
1322	10.6	47.5	10.6	379	2	T51784	AcPP-like protein	1395	47.5	10.6	806	2	A41341	scarce-like pro
1323	10.6	47.5	10.6	387	2	S46123	hypothetical prote	1396	47.5	10.6	808	2	T51232	membrane carboxype
1324	10.6	47.5	10.6	390	2	H86388	probable bHLH tran	1397	47.5	10.6	809	2	F97183	valine-tRNA ligase
1325	10.6	47.5	10.6	396	2	T51387	UVB-resistance pro	1398	47.5	10.6	812	2	E97831	hypothetical prote
1326	10.6	47.5	10.6	396	2	A57090	CSA protein - huma	1399	47.5	10.6	817	2	S53919	hypothetical prote
1327	10.6	47.5	10.6	398	2	B30565	phospholipase C (E	1400	47.5	10.6	828	2	E98004	hypothetical prote
1328	10.6	47.5	10.6	400	1	JQ1575	major surface anti	1401	47.5	10.6	841	1	S39365	outer membrane ush
1329	10.6	47.5	10.6	409	2	T11743	pP47 protein - pig	1402	47.5	10.6	861	2	A48825	Notch homolog Notc
1330	10.6	47.5	10.6	413	1	S03631	homeotic protein S	1403	47.5	10.6	869	2	A47665	env protein gp120 (
1331	10.6	47.5	10.6	415	2	PC4407	envelope protein -	1404	47.5	10.6	872	1	S53319	acetaldehyde dehyd
1332	10.6	47.5	10.6	417	2	B59392	Wnt10a protein pro	1405	47.5	10.6	873	2	T50171	hypothetical prote
1333	10.6	47.5	10.6	418	1	A53888	thermolabile hemol	1406	47.5	10.6	881	2	S25445	nitrate reductase
1334	10.6	47.5	10.6	419	2	A90888	hypothetical prote	1407	47.5	10.6	906	2	E84948	NADH2 dehydrogenas
1335	10.6	47.5	10.6	419	2	H85729	hypothetical prote	1408	47.5	10.6	911	1	B3HU	band 3 anion trans
1336	10.6	47.5	10.6	421	2	F83316	aspartate transami	1409	47.5	10.6	917	1	RDMUNH	nitrate reductase
1337	10.6	47.5	10.6	430	2	T48142	B-lymphocyte anti	1410	47.5	10.6	918	2	A41667	protein R0807.6 [i
1338	10.6	47.5	10.6	435	2	E96784	hypothetical prote	1411	47.5	10.6	918	2	D88544	protein F5982.12 [
1339	10.6	47.5	10.6	439	2	S58327	cobalt accumulatio	1412	47.5	10.6	943	2	G88545	hypothetical prote
1340	10.6	47.5	10.6	446	1	D69340	cobalam biosynth	1413	47.5	10.6	948	2	T31132	conserved hypotet
1341	10.6	47.5	10.6	448	2	F71862	glutamate dehydrog	1414	47.5	10.6	948	2	T41496	hypothetical prote
1342	10.6	47.5	10.6	449	2	B26488	tubulin alpha-2 ch	1415	47.5	10.6	974	2	T04910	regulatory protein
1343	10.6	47.5	10.6	450	2	A26488	tubulin alpha-1 ch	1416	47.5	10.6	980	2	S54986	regulatory protein

Best Local Similarity 28.3%; Pred. NO. 17;
Matches 28; Conservative 12; Mismatches 19; Indels 40; Gaps 7;

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Db 494 LFCNVLDANPSVLTKVRMYANSTLLKELPDCEETEDLCHIDPDKLLLSIGRGFFNY 553

Qy 41 CAPPTGKNKTSNDTMASGWPRASSPHFDSEENKHRLIHF 79
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Db 554 C---EGFN-----AAGWGPRS-----EDKELLVHY 575

RESULT 5
tenascin-C - human
N:Alternate names: hexabrachion
C:Species: Homo sapiens (man)
C>Date: 31-Jul-1989 #sequence revision 12-Apr-1996 #text change 09-Jul-2004
C:Accession: I38337; A32160; S14015; S16166; S50208; S49354
R:Gherzi, R.; Carnemolla, B.; Siri, A.; Ponassi, M.; Balza, E.; Zardi, L.
J. Biol. Chem. 270, 3429-3434, 1995
A:Title: Human tenascin gene. Structure of the 5'-region, identification, and character:
A:Reference number: A55974; MUID:95155442; PMID:7531707
A:Accession: I38337
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2201 <RES>
A:Cross-references: UNIPROT:P24821; UNIPARC:UPI0000034A0B; EMBL:X78565; NID:G556844; PID:
R:Gulcher, J.R.; Nies, D.E.; Marton, L.S.; Stefansson, K.
Proc. Natl. Acad. Sci. U.S.A. 86, 1588-1592, 1989
A:Title: An alternatively spliced region of the human hexabrachion contains a repeat of 1
A:Reference number: A32160; MUID:89160821; PMID:2466295
A:Accession: A32160
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 431-538, 'H', 540-1065, 'H', 1067-1599, 'LWLHPRASN', 1609-2054, 'L' <GUL>
A:Cross-references: UNIPARC:UPI000016AAC6; GB:IM24630; NID:G514363; PIDN:AA52703.1; PID:
R:Siri, A.; Carnemolla, B.; Saginati, M.; Lepri, A.; Casari, G.; Baralle, F.; Zardi, L.
Nucleic Acids Res. 19, 525-531, 1991
A:Title: Human tenascin: primary structure, pre-mRNA splicing patterns and localization (
A:Reference number: S14015; MUID:91187670; PMID:1707164
A:Accession: S14015
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-243, 245-369, 'V', 371-679, 'R', 681-1676, 'I', 1678-2139, 'TR', 2142, 2144-2201 <SI
A:Cross-references: UNIPARC:UPI0000155D15; EMBL:X56160; NID:G37226; PIDN:CAA39628.1; PID
R:Nies, D.E.; Hemesath, T.J.; Kim, J.H.; Gulcher, J.R.; Stefansson, K.
J. Biol. Chem. 266, 2818-2823, 1991
A:Title: The complete cDNA sequence of human hexabrachion (tenascin). A multidomain prot
A:Reference number: S16166; MUID:91131572; PMID:1704365
A:Accession: S16166
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-538, 'R', 540-1065, 'H', 1067-1599, 'LWLHPRASN', 1609-2054, 'LH', 2055-2201 <NIE>
A:Cross-references: UNIPARC:UPI000016AAC5; EMBL:M55618; NID:G184483; PIDN:AAA80803.1; PI
R:Glumoff, V.; Savontaus, M.; Vehanen, J.; Vuorio, E.
Biochim. Biophys. Acta 1219, 613-622, 1994
A:Title: Analysis of aggrecan and tenascin gene expression in mouse skeletal tissues by 1
A:Reference number: S50206; MUID:95035091; PMID:7524681
A:Accession: S50208
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 46-125 <GUU>
A:Cross-references: UNIPARC:UPI0000177AF4; EMBL:X80280
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
C:Genetics:
A:Gene: GDB:HXB
A:Cross-references: GDB:120073; OMIM:187380
A:Map position: 9q33-q33
C:Superfamily: tenascin; EGF homology; fibrinogen beta/gamma homology; fibronectin type
C:Keywords: alternative splicing; extracellular matrix
F:408-434/Domain: EGF homology <EGF>
F:622-703/Domain: fibronectin type III repeat homology <FN3>

P:171-794/Domain: fibronectin type III repeat homology <FN3>
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P:1437-1519/Domain: fibronectin type III repeat homology <FN3>
P:1619-1701/Domain: fibronectin type III repeat homology <FN3>
P:1709-1770/Domain: fibronectin type III repeat homology <FN3>
P:1798-1879/Domain: fibronectin type III repeat homology <FN3>
P:1886-1966/Domain: fibronectin type III repeat homology <FN3>
P:1981-2189/Domain: fibronectin beta/gamma homology <FG>

A;Reference number: Z21858
A;Accession: T39486
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-475 <LYN>
A;Cross-references: UNIPROT:O74315; UNIPARC:UPI000006A222; EMBL:AL031349; PIDN:CAA20485
A;Experimental source: strain 972h-; cosmid c15D4
C;Genetics:
A;Gene: SPDB:SPBC15D4.10c
A;Map position: 2
A;Introns: 419/1

Query Match 14.4%; Score 64.5; DB 2; Length 475;
Best Local Similarity 30.3%; Pred. No. 30;
Matches 27; Conservative 7; Mismatches 32; Indels 23; Gaps 5;

Qy 7 NSPSNS---NANCFPSLKNISD-----THPSFNLQ---WPFNDS---CAPPT 45
Db 318 NQOQSFAQNLTQFSLPNNSQPVGHTSLTQPVNPNNGFTVQPPATFMQOQPGFPVPNT 377

Qy 46 GFNKPTSNDTWSGWRASSPHFDSEENKH 74
Db 378 TFSPPFANVT--SKISASGFSNDNPANKN 404

RESULT 15
T38303
SWI/SNF complex transcription regulator - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T38303
R;Skellton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.; Wood, V.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z21785
A;Accession: T38303
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-503 <SKE>
A;Cross-references: UNIPROT:O14470; UNIPARC:UPI000006C8C4; EMBL:Z99163; PIDN:CAB16236.1;
A;Experimental source: strain 972h-; cosmid c23H3
C;Genetics:
A;Gene: SPDB:SPAC23H3.10
A;Map position: 1

Query Match 14.4%; Score 64.5; DB 2; Length 503;
Best Local Similarity 30.0%; Pred. No. 32;
Matches 27; Conservative 5; Mismatches 33; Indels 25; Gaps 6;

Qy 15 NCE-----FSLKNIS-DIHPSFNLQWP---FNDS---CAPPTGFN---KFTSN----- 53
Db 199 NCSQTWYHNLKKNKKYDPCNCKQGRFSSFSNDSDFLCMDAIDFNHDBEKPWSNQETILL 258

Qy 54 ----DTWASGWRASSPHFDSEENKRLIHF 79
Db 259 LEAITYGDDWNQIALHVGSRTEQCLIH 288

Search completed: December 22, 2005, 03:06:18
Job time : 59.1837 secs

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